

GenCore version 5.1.6
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OM protein - nucleic search, using frame_plus_p2n model

Run on: November 15, 2004, 21:05:47 ; Search time 727 Seconds

(without alignments)
3704.199 Million cell updates/sec

Title: US-10-729-807-10

Perfect score: 2763

Sequence: 1 MKRLLLCLEFFITFSAPPL.....SLSLFIHGIVHLKNTSIYQ 513

Scoring table:

BLOSUM62
Xgapop 10.0 , Xgapext 0.5
Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 4134886 seqs, 2624710521 residues

Total number of hits satisfying chosen parameters: 8269772

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Command line parameters:

-MODEL=frame_p2n.model -DEV=xlh
-Q=/cgn2_1/USPro.spool/US10729807/runat_15112004_131726_16835/app_query.fasta_1.711
-DB=N Geneseq 23Sep04 -QFMT=fastap -SUFFIX=ring -MINMATCH=0.1 -LOOPCL=0
-LOOPEXT=0 -UNITS=bits -START=1 -END=1 -MATRIX=blosum62 -TRANS=human40.cdi
-LIST=45 -DOCALIGN=200 -THR SCORE=pct -THR MAX=100 -THR MIN=0 -ALIGN=15
-MODE=LOCAL -OUTFMT=ptc -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=2000000000
-USER=US10729807@cgn_1_1_470 @runat_15112004_131726_16835 -NCPU=6 -ICPU=3
-NO_MMAP -LARGEQUERY -NEG_SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG
-DEV TIMEOUT=120 -WARN TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database :

N Geneseq 23Sep04:*
1: Geneseqn1980s:*
2: Geneseqn1990s:*
3: Geneseqn2000s:*
4: Geneseqn2001as:*
5: Geneseqn2001bs:*
6: Geneseqn2002as:*
7: Geneseqn2002bs:*
8: Geneseqn2003as:*
9: Geneseqn2003bs:*
10: Geneseqn2003cs:*
11: Geneseqn2003ds:*
12: Geneseqn2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	2763	100.0	1627	3	Aa337666 Human pep
2	2763	100.0	1845	6	Aad23963 Human mac
3	2752	99.6	1542	8	Acdb6740 Secreted
4	2752	99.6	1542	12	Adq10208 Human pol
5	2752	99.6	1647	4	Aas21339 Human cdn
6	2752	99.6	1647	8	Aca03698 CDNA enco

RESULT 1
AAA37666
ID AAA37666 standard; DNA; 1627 BP.
XX
AC AAA37666;
XX
DT 24-OCT-2000 (first entry)
XX
DE Human peptidase, HPEP-10 coding sequence.

XX Human; peptidase; cell proliferative disorder; arteriosclerosis;
KW psoriasis; myelofibrosis; cancer; autoimmune disorder; Crohn's disease;
KW inflammatory disorder; AIDS; anaemia; allergy; asthma; arteriosclerosis;
KW Grave's disease; multiple sclerosis; scleroderma; infection; diabetes;
KW metabolic disorder; Addison's disease; cystic fibrosis; diagnosis;
KW glycogen storage disease; obesity; therapy; HPEP-10; ds.
XX Homo sapiens.
XX Key Location/Qualifiers
XX CDS 24..1565
XX FT /*tag= a
XX FT /product= "HPEP-10"

ALIGNMENTS

7 2752 99.6 1647 8 ABX89236
8 2752 99.6 1647 8 ACD41890
9 2752 99.6 1647 8 ACA04119
10 2752 99.6 1647 9 ADA45710
11 2752 99.6 1647 9 ADA76141
12 2752 99.6 1647 9 ADA18791
13 2752 99.6 1647 9 ADA61414
14 2752 99.6 1647 9 ADA19199
15 2752 99.6 1647 9 AD227740
16 2752 99.6 1647 9 ADA86219
17 2752 99.6 1647 9 ADB15783
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44 2752 99.6 1647 9 ADA93286
45 2752 99.6 1647 9 ADB26636

ABX89236 DNA enco
ACD41890 Human sec
ACA04119 Human cdn
ADA45710 Novel hum
ADA76141 Human PRO
ADA18791 Human PRO
ADA61414 Homo sapi
ADA19199 Novel hum
AD227740 cDNA enco
ADA86219 Novel hum
ADB15783 Human PRO
ADA47569 Human PRO
ADA67364 Human PRO
ADB30371 cDNA enco
ADA85667 Novel hum
ADA96879 Human PRO
ADA79183 Human PRO
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ADB16524 Human PRO
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ADB14679 Human PRO
ADB18640 Novel hum
ADA93855 Human PRO
ADB19751 Novel hum
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ADA74317 Human PRO
ADB24550 Human PRO
ADA82074 Human PRO
ADA75037 Human PRO
ADA85115 Novel hum
ADA84563 Novel hum
ADB29819 cDNA enco
ADA80347 Human PRO
ADA75589 Human PRO
ADA46814 Human PRO
ADB25110 Human PRO
ADA93286 Human PRO
ADB26636 cDNA enco

QY 321 PheTrrProSerLeuProAlaAspLeuGlnAlaAlaTyrGluAsnProArgAspLysile 340
 Db 984 TTTCTGGCCATCTCTGCCAGCTGATCTGCAAGCTGCATACGAGAACCCAGATTAAGATT 1043
 QY 341 LeuValPheLysAspGluAsnPheTrrMetIleArgGlyTyrAlaValLeuProAspTyr 360
 Db 1044 CTGGTTTTAAAGATGAAGAACTCTCGATGATCAGAGATATGCTGCTGCCAGATTAT 1103
 QY 361 ProllysSerIleHisThrLeuGlyPheProGlyArgValLysLysIleAspAlaAlaVal 380
 Db 1104 CCCAAATCCATCCATACATAGTTTCCAGAGCTGTGAAGAAATAGATGACGCGTC 1163
 QY 381 CysAspLysThrThrArgLysThrTyrPheValGlyIleTyrCysTrrPheAsp 400
 Db 1164 TGTGATAGACCCCAAGAAACCTACTTCTTGTGGCATTTCTGCTGGAGTTTGTAT 1223
 QY 401 GluMetThrGlnThrMetAspLysGlyPheProGlnArgValLysHisPheProGly 420
 Db 1224 GAAATGACCCCAACCATGGACAAAGGATTCCCGCAGAGAGTGGTAAACACTTTCTCTGA 1283
 QY 421 IleSerIleArgValAspAlaAlaPheGlnTyrLysGlyPhePhePheSerArgGly 440
 Db 1284 ATCAGTATCCGTGTGTATGCTGCTTCCAGTACAAAGGATTCTTCTTTTTCAGCGGTGA 1343
 QY 441 SerLysGlnPheGluTyrAsnIleLysThrLysAsnIleThrArgIleMetArgThrAsn 460
 Db 1344 TCAAGCAATTTGAATACACATTAAGCAAGAAATATCCCGATCATGAGAACTAAT 1403
 QY 461 ThrTrrPheGlnCysLysGluProLysAsnSerSerPheGlyPheAspIleAsnLysGlu 480
 Db 1404 ACTTGGTTTCAATGCANAGAACCAAGAACTCTCATTTGGTTTGTATATCAACAAGAA 1463
 QY 481 LysAlaHisSerGlyGlyIleLysIleLeuTyrHisLysSerLeuSerLeuPheIlePhe 500
 Db 1464 AAAGCACATTCAGGAGGCATAAAGATATTGTATCATAGAGTTTAAAGCTTGTATTTT 1523
 QY 501 GlyIleValHisLeuLeuLysAsnThrSerIleTyrGln 513
 Db 1524 GGTATTGTTCATTCTGCTGAAACACACTTCTATTATCAAA 1562
 RESULT 3
 ACD66740
 ID ACD66740 standard; cDNA; 1542 BP.
 XX AC ACD66740;
 XX DT 17-SEP-2003 (first entry)
 XX DE Secreted polypeptide-related cDNA #31.
 XX Human; gene; ss; TANGO; INTERCEPT; secreted polypeptide; immune disorder;
 KW hormonal disorder; proliferative disorder; cancer; thyroid disorder;
 KW diabetes; multiple sclerosis; lupus; neurological disorder; anaemia;
 KW Alzheimer's disease; Parkinson's disease; cardiovascular disorder;
 KW myocardial infarction; congestive heart disease; blood platelet disorder;
 KW thrombocytopenia; blood vessel; atherosclerosis; vasculitis.
 XX OS Homo sapiens.
 XX PN US2003022279-A1.
 XX PD 30-JAN-2003.
 XX PF 12-JAN-2001; 2001US-00759130.
 XX PR 14-JUN-1999; 99US-00333159.
 PR 29-JUN-1999; 99US-00342364.
 PR 10-SEP-1999; 99US-00393996.
 PR 19-OCT-1999; 99US-00420707.
 PR 07-JAN-2000; 2000US-00479249.
 PR 27-APR-2000; 2000US-00559497.
 PR 24-MAY-2000; 2000US-00578063.
 PR 16-JUN-2000; 2000US-00596194.

23-JUN-2000; 2000US-00602871.
 30-JUN-2000; 2000US-00608452.
 (FRAS/) FRASER C C.
 (BARN/) BARNES T M.
 (SHAR/) SHARP J D.
 (KIRS/) KIRST S J.
 (MYER/) MYERS P S.
 (LEIB/) LEIBY K R.
 (HOLT/) HOLTZMAN D A.
 (MCCA/) MCCARTHY S A.
 (WRIG/) WRIGHTON N.
 (MACK/) MACKAY C R.
 (GOOD/) GOODEARL A D J.
 Fraser CC, Barnes TM, Sharp JD, Kirst SJ, Myers PS, Leiby KR,
 Holtzman DA, McCarthy SA, Wrighton N, Mackay CR, Goodearl ADJ;
 WPI; 2003-456290/43.
 P-PSDB; ABO32578.
 New nucleic acid molecule encoding a secreted protein (e.g. TANGO 202,
 TANGO 210 or INTERCEPT 217), useful for diagnosing, preventing or
 treating disorders such as cancer, diabetes or atherosclerosis, and in
 forensic biology.
 Claim 2; Fig 15A-15D; 482pp; English.
 The invention relates to secreted polypeptide-related proteins and
 nucleic acids (TANGO and INTERCEPT proteins and nucleic acids). The
 nucleic acids, proteins and antibodies specific to the proteins are
 useful in screening assays, predictive medicine (e.g. diagnostic assays,
 prognostic assays, monitoring clinical trials and pharmacogenetics) and
 prophylactic and therapeutic methods. The sequences are used in
 diagnosing, preventing or treating proliferative disorders (e.g.
 cancers), hormonal disorders (e.g. diabetes or thyroid disorders), immune
 disorders (e.g. multiple sclerosis or lupus), neurological disorders
 (e.g. Alzheimer's disease or Parkinson's disease), cardiovascular
 disorders (e.g. myocardial infarction or congestive heart disease), blood
 platelet disorders (e.g. thrombocytopenia or anaemia) and disorders
 involving blood vessels (e.g. atherosclerosis or vasculitis). The nucleic
 acids may also be used in chromosome mapping, tissue typing and forensic
 biology, and as surrogate markers. This sequence represents a secreted
 polypeptide-related cDNA of the invention. Note: The sequence data for
 this patent was obtained in electronic format directly from USPTO at
 seqdata.uspto.gov/sequence.html
 XX SQ Sequence 1542 BP; 447 A; 322 C; 334 G; 439 T; 0 U; 0 Other;

Alignment Scores:

Pred. No.: 1,49e-294 Length: 1542
 Score: 2752.00 Matches: 512
 Percent Similarity: 99.81% Conservative: 0
 Best Local Similarity: 99.81% Mismatches: 1
 Query Match: 99.60% Indels: 0
 Gaps: 0

US-10-729-807-10 (1-513) x ACD66740 (1-1542)

QY 1 MetLysArgLeuLeuLeuLeuLeuCysLeuPhePheIleThrPheSerSerAlaPheProLeu 20
 Db 1 ATGAAGCGCTTCTGCTTCTGTTTGTATTAACATTTCTCTGCAATTCCTCCCTTA 60
 QY 21 ValArgMetThrGluAsnGluGluAsnMetGlnLeuAlaGlnAlaTyrLeuAsnGlnPhe 40
 Db 61 GTCCGGATGACGGAATAATGAAGAAATATGCACTGGCTCAGGCATATCTCAACAGTTC 120
 QY 41 TyrSerLeuGluIleGluGlyAsnHisLeuValGlnSerLysAsnArgSerLeuIleAsp 60
 Db 121 TACTCTCTTGAATAGAGGGAATCATCTTGTTCAAAGCAAGAAATAGGAGTCTCATAGT 180
 QY 61 AspLysIleArgGluMetGlnAlaPhePheGlyLeuThrValThrGlyLysLeuAspSer 80

181	Db	GACAAAATTCGGGAAATGCAAGCAATTTTTTGGATTGACAGTGACCTGGAAACTGGACTCA	240
81	Qy	AsnThrLeuGluIleMetLysThrProArgCysGlyValProAspValGlyGlnTyrGly	100
241	Db	AACACCCTTGAGATCATGAAGACACCCAGGTTGCGGTGCTGATGTGGCCAGTATGCG	300
101	Qy	TyrThrLeuProGlyTyrArgLysIleAsnLeuThrTyrArgIleIleAsnTyrThrPro	120
301	Db	TACACCCTCCCTGGGTGGAGAAAATACAACTCCACTACAGATTAATAAACTATACTCCG	360
121	Qy	AspMetAlaArgAlaAlaValAspGluAlaIleGlnGluGlyLeuGluValTyrSerLys	140
361	Db	GATATGCGCAGAGCTGCTGTGGATGAGGCTATCCAAAGAGTTTAGAAGTGTGGAGCAA	420
141	Qy	ValThrProLeuLysPheThrLysIleSerLysGlyIleAlaAspIleMetIleAlaPhe	160
421	Db	GTCACTCCACTAAAATTCACCAAGATTCCAAAGGGGATTGCAGACATCATGATTCCTTT	480
161	Qy	ArgThrArgValHisGlyArgCysProArgTyrPheAspGlyProLeuGlyValLeuGly	180
481	Db	AGGACTCGAGTCCATGTGTGGTGTGCTCGCTATTTTGTATGTCCCTTGGGAGTCTTGGC	540
181	Qy	HisAlaPheProProGlyProGlyLeuGlyClyAspThrHisPheAspGluAspGluAsn	200
541	Db	CATGCCCTTCTCTCTGTGTCGGGTCTGGGTGGTGACACTATTGTGATGAGGATGAAAC	600
201	Qy	TrpThrLysAspGlyAlaGlyPheAsnLeuPheLeuValAlaAlaHisGluPheGlyHis	220
601	Db	TGGACCAAGATGGAGCAGGATTCAACTGTTCCTGTGGCTGCTCATGAATTGGTCAT	660
221	Qy	AlaLeuGlyLeuSerHisSerAsnAspGlnThrAlaLeuMetPheProAsnTyrValSer	240
661	Db	GCACTGGGGTCTCTCACTCCAAATGATCAACAGCCTTGATGTTCCCAAATATATGTCTCC	720
241	Qy	LeuAspProArgLysTyrProLeuSerGlnAspAspileasnglyIleGlnSerIleTyr	260
721	Db	CTGATCCCCAGAAAATACCCACTTCTCAGAGATGATATCAATGGAATCCAGTCCATCTAT	780
261	Qy	GlyGlyLeuProLysValProAlaLysProLysGluProThrIleProHisAlaCysAsp	280
781	Db	GGAGGTCGCTAAGGTACCTGTGAAGCAAGGNAACCATATACCCCATGCTGTGCAC	840
281	Qy	ProAspLeuThrPheAspAlaIleThrThrPheArgArgGluValMetPheLysGly	300
841	Db	CCTGACTGACTTTTGACGCTATCACAACTTTCGCGAGAGAAGTAATGTCTTTAAAGGC	900
301	Qy	ArgHisIleThrProArgIleTyrTyrAspIleThrAspValGluPheGluLeuIleAlaSer	320
901	Db	AGGCACCTATGGAGGATCTATATGATATCACGGATGTTGAGTTGAAATTAATTGCTTCA	960
321	Qy	PheTrpProSerLeuProAlaAspLeuGlnAlaAlaTyrGluAsnProArgAspLysIle	340
961	Db	TTCTGGCCATCTGCGCAGCTGATCTGCAAGCTGCATACGAGAACCCACGAGATAAGATT	1020
341	Qy	LeuValPheLysAspGluAsnPheTrpMetIleArgGlyTyrAlaValLeuProAspTyr	360
1021	Db	CTGGTTTTTAAAGATGAAAACTTCTGATGATCAGAGGATATGCTGTCTTGGCCAGATTAT	1080
361	Qy	ProLysSerIleHisThrLeuGlyPheProGlyArgValLysIleAspAlaAlaVal	380
1081	Db	CCCAAAATCCATCCATACATTAGGTGTTTTCCAGGACGTGTGAAGAAAATAGATGCAAGC	1140
381	Qy	CysAspLysThrThrArgLysThrTyrThrPheValGlyIleTrpCysTrpArgPheAsp	400
1141	Db	TGTGATAGACCAACAGAAAACCTACTTCTTTGGGCAATTTGGTGCTCGAGGTTTGAT	1200
401	Qy	GluMetThrGlnThrMetAspLysGlyPheProGlnArgValValLysHisPheProGly	420
1201	Db	GAATGACCCAAACCATGGACAAAGGATTCCTCGCAGAGATGGTAAACACTTTCCTGGA	1260
421	Qy	IleSerIleArgValAspAlaAlaPheGlnTyrLysGlyPhePhePheSerArgGly	440
1261	Db	ATCAGTATCCGTGTGATGCTGCTTCCAGTACAAAGGATTTCTCTTTTTCAGCCGTGGA	1320

Qy	441	SerLysGlnPheGluTyrAsnIleLysThrLysAsnIleThrArgIleMetArgThrAsn	460
Db	1321	TCAAGCAATTTGTAATCAACATTAACACAAAGAAATATTATCCCGAATCATGAGAACTAAT	1380
Qy	461	ThrTrpPheGlnCysLysGluProLysAsnSerSerPheGlyPheAspIleAsnLysGlu	480
Db	1381	ACTTGGTTTCAATGCAAGAAGAACCAAGAACTCCTCATTTGGTTTGAATCAACAAGGAA	1440
Qy	481	LysAlaHisSerGlyGlyIleLysLysLeuTyrHisLysSerLeuSerLeuPheIlePhe	500
Db	1441	AAAGCACATTCCAGGAGGCATAAAGATATTGATATAAGAGTTTAACTGTGTTATTTT	1500
Qy	501	GlyTleValHisLeuLeuLysAsnThrSerIleTyrGln	513
Db	1501	GGTATTGTTTCATTGCTGTAAGAAACACTTCTATTATCAA	1539
RESULT 4			
ID	ADQ10208	standard; cDNA; 1542 BP.	
XX	ADQ10208;		
AC	ADQ10208;		
DT	09-SEP-2004	(first entry)	
XX	Human polynucleotide #31.		
DE			
XX	Human; gene; ss; cancer; obesity; gastritis; diarrhoea; haemorrhoid;		
KW	Ashma; anaemia; graft-versus-host reaction; allergic reaction;		
KW	cystic fibrosis; hypogonadism; cardiovascular disorder; arthritis;		
KW	osteoarthritis; arteriosclerosis; hypertension; bacterial infection;		
KW	psoriasis; diabetes mellitus; hepatitis; Alzheimer's disease;		
KW	Huntington's disease; Parkinson's disease; AIDS; tuberculosis;		
KW	viral infection; malaria; goiter; infertility; endometriosis;		
KW	muscular disorder.		
XX			
OS	Homo sapiens.		
XX			
PN	US2004121396-A1.		
XX			
PD	24-JUN-2004.		
XX			
PF	19-DEC-2003; 2003US-00741790.		
XX			
PR	14-JUN-1999; 99US-00333159.		
PR	29-JUN-1999; 99US-00342364.		
PR	10-SEP-1999; 99US-00393996.		
PR	19-OCT-1999; 99US-00420707.		
PR	07-JAN-2000; 2000US-00479249.		
PR	27-APR-2000; 2000US-00559497.		
PR	24-MAY-2000; 2000US-00578063.		
PR	16-JUN-2000; 2000US-00596194.		
PR	23-JUN-2000; 2000US-00602871.		
PR	30-JUN-2000; 2000US-00608452.		
PR	12-JAN-2001; 2001US-00759130.		
XX			
PA	(MILL-) MILLENNIUM PHARM INC.		
XX			
PI	Fraser CC, Barnes TM, Sharp JD, Kirst SJ, Myers PS, Leiby KR;		
PI	Holtzman DA, McCarthy SA, Wrighton N, Mackay CR, Goodearl AD;		
XX			
XX	WPI; 2004-479675/45.		
DR			
XX			
FT	New TANGO, INTERCEPT, and MANGO, useful in diagnosing, preventing, and		
PT	treating cancer, constipation, hemorrhoids, cystic fibrosis,		
PT	hypogonadism, psoriasis, hepatitis, Alzheimer's disease, AIDS,		
PT	tuberculosis, malaria, goiter, infertility.		
XX			
PS	Claim 2; SEQ ID NO 172; 483pp; English.		
XX			
CC	The invention relates to human polynucleotides and the polypeptides they		
CC	encode. The invention also relates to a host cell containing a		
CC	polynucleotide of the invention, an antibody which selectively binds with		

Qy	221	AlaLeuGlyLeuSerHisSerAsnAspGlnThrAlaLeuMetPheProAsnTyrValSer	240
Db	661	GCACGGGGCTCTCTCACTCCAATGATCAACAGCCTTGATGTTCACAAATTTATGTCTCC	720
Qy	241	LeuAspProArgLysTyrProLeuSerGlnAspAspIleAsnGlyIleGlnSerIleTyr	260
Db	721	CTGGATCCCAAGAAAAATACCCACATTTCTCAGGATGATATCAATGGAAATCCAGTCCATCTAT	780
Qy	261	GlyGlyLeuProLysValProAlaLysProLysGluProThrIleProHisAlaCysAsp	280
Db	781	GGAGGTCTGCCTAAGGTACCTGCTAAGCCAAAGAACCCACTATACCCCATGGCTGTGGAC	840
Qy	281	ProAspLeuThrPheAspAlaIleThrThrPheArgArgGluValMetPhePheLysGly	300
Db	841	CCTGACTTGACTTTTGACGCTATCACAACTTTTCGCAGAGAAGTAATGTCTTTTAAAGGC	900

[illegible]

Qy	321	PheTrpProSerLeuProAlaAspLeuGluAlaAlaTyrGluAsnProArgAspLysIle	340
Db	961	TTCTGGCCATCTCTGGCAGCTGATCTGCAAGTGCATACGAGAACCCAGAGATAAGATT	1020
Qy	341	LeuValPheIysAspGluAsnPheTrpMetIleArgGlyTyrAlaValLeuProAspTyr	360

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381	CCCAATCCCATCCATACATTAGGTTTTTCCAGACGCTGTGAAGAAATAGATGCAGCCGTC	1140
Db		
381	CysAspLysThrThrArgLysThrTyrPhePheValGlyIleTrpCysTirArgPheAsp	400
Qy		
1141	TGTGATAAGACCCACAGAAAACCTACTCTTTGTGGSCATTTGGTCTCGAGGTTTGAT	1200
Db		
401	GluMetThrGlnThrMetAspLysLysGlyPheProGlnArgValValLysHisPheProGly	420
Qy		
1201	GAATGACCCAAACCATGGGCAAAAGGATTCCTCCGACAGAGTGGTAAACAACTTTCTCTGGA	1260
Db		
421	IleSerIleArgValAspAlaAlaPheGlnTyrlsGlyPhePhePheSerArgGly	440
Qy		
1261	ATCAGTATCCGTGTGATGTGCTTTCCAGTACAAAGGATTCCTCTCTTTTCAGCCGCTGGA	1320
Db		
441	SerLysGlnPheGluTyraSnIleLysThrLysaSnIleThrArgIleMetArgThrAsn	460
Qy		

D6	1321	TCAAAGCAATTTGAAATACCAATATAGACAAAGAAATATATACCCGGAATACAGAGAACTAA	1350
Qy	461	ThrTrpPheGlnCysLysGluProLYAsnSerSerPheGlyPheAspIleAsnLYsGlu	480
D6	1381	ACTTGGTGTTCATTCGAAAGAACCAAGAACTCCTCATTTGGTTTGGATATCAACAAGGAA	1440
Qy	481	LysAlaHisSerGlyGlyIleLYsIleLeuTyHisLYsSerLeuSerLeuPheIlePhe	500
D6	1441	AAAGCACCATTGAGGAGCATAAAGAAATTTGTATCATTAAGAGTTTAAAGCTGTTTATTTTT	1500
Qy	501	GlyIleValHisLeuLeuLYsAsnThrSerIleTyGln	513
D6	1501	GGTATTGTTTCATTTCGTGAAAAACACTTCTATTATCAA	1539
RESULT 5			
AAS21339			
ID AAS21339 standard; cDNA; 1647 BP.			
XX			

XX	
XX	
DT	24-OCT-2001 (first entry)
XX	
XX	Human cDNA sequence encoding for PRO5992 polypeptide.
DE	
XX	
XX	Human secretory and transmembrane; PRO; mammalian; cancer; lung; breast;
KW	prostate; cervical; tumour necrosis factor-alpha; TNF-alpha cartilage;
KW	

XX
DE Human cDNA sequence encoding for PRO5992 polypeptide.

XX Human secretory and transmembrane; PRO; mammalian; cancer; lung; breast;
KW prostate; cervical; tumour necrosis factor-alpha; TNF-alpha; cartilage;
KW ear; proliferation; glucose; free fatty acid; skeletal muscle; adipocyte;


```
QY 241 LeuAspProArgLysTyrProLeuSerGlnAspAspIleAsnGlyIleGlnSerIleTyr 260
DB 744 CTGGATCCCAGAAAATACCCACTTCTCAGGATGATATCAATGAAATCCAGTCCATCTAT 803
QY 261 GlyGlyLeuProLysValProAlaLysProLysGluProThrIleProHisAlaCysAsp 280
DB 804 GGAGGCTCTGCTAAGGTACCTGCTAAGCCAAAGAACCCACTATACCCATGCTGTGAC 863
QY 281 ProAspLeuThrPheAspAlaIleThrPheArgArgGluValMetPhePheLysGly 300
DB 864 CCTGACTTCTGCTTTCAGCGTATCACAACCTTTCGCGAGAGAAGTAATGTTCTTTAAAGGC 923
QY 301 ArgHisLeuTrpArgIleTyrAspIleThrAspValGluPheGluLeuIleAlaSer 320
DB 924 AGGCACCTATGGAGGATCTATTATGATATCACGGATGTGAGTTTGAATTAATTTGCTTCA 983
QY 321 PheTrpProSerLeuProAlaAspLeuGlnAlaAlaTyrGluAsnProArgAspLysIle 340
DB 984 TTCTGGCCATCTCTGCCAGTCTGATCTGCAAGCTGCATACGAGAACCCAGAGATAAGATT 1043
QY 341 LeuValPheLysAspGluAsnPheTrpMetIleArgGlyTyrAlaValLeuProAspTyr 360
DB 1044 CTGGTTTTTAAAGATGAAAACCTTCTGGATGATCAGAGATATGCTGCTTGCAGATTAT 1103
QY 361 ProLysSerIleHisThrLeuGlyPheProGlyArgValLysLysIleAspAlaAlaVal 380
DB 1104 CCCAAATCCATCATCATATGATAGGTTTTCCAGGACGTGTGAAGAAAATAGATGAGCCGTC 1163
QY 381 CysAspLysThrThrArgLysThrTyrPhePheValGlyIleTyrCysTrpAlaGlyPheAsp 400
DB 1164 TGTGTAAGACCAACAGAAAACCTACTTCTTTGTGGGCATTTGGTCTGGAGTTTGTAT 1223
QY 401 GluMetThrGlnThrMetAspLysGlyPheProGlnArgValValLysHisPheProGly 420
DB 1224 GAAATGACCCCAACCATGGACAAAGGATTCGCGCAGAGAGTGGTAAACACTTTCCTGGA 1283
QY 421 IleSerIleArgValAspAlaAlaPheGlnTyrLysGlyPhePhePheSerArgGly 440
DB 1284 ATCAGTATCCGTGTGATGCTGCTTCCAGTACAAAGGATTTCTTTTTCAGCCCGGGA 1343
QY 441 SerLysGlnPheGluTyrAsnIleLysThrLysAsnIleThrArgIleMetArgThrAsn 460
DB 1344 TCAAGCAATTTGAATACACATTAAGACAAAGAAATATACCCGAATCATGAGAACTAAT 1403
QY 461 ThrTrpPheGlnCysLysGluProLysAsnSerSerPheGlyPheAspIleAsnLysGlu 480
DB 1404 ACTTGGTTTCAATGCAAGAAACCAAGAACTCCTCATTTGGTTTTTGATATCAACAGGAA 1463
QY 481 LysAlaHisSerGlyGlyIleLysIleLeuTyrHisLysSerLeuSerLeuPheIlePhe 500
DB 1464 AAAGCAATTCAGAGGACATAAAGATATGTATCAAGAGTTTAAGCTTGTATTATTTT 1523
QY 501 GlyIleValHisLeuLeuLysAsnThrSerIleTyrGln 513
DB 1524 GGTATTGTTCTTGTCTGAAAACACTTCTATTATCAAA 1562

RESULT 6
ACAO3698
ID ACAO3698 standard; cDNA; 1647 BP.
XX
AC ACAO3698;
XX
DT 23-MAY-2003 (first entry)
XX
DE cDNA encoding human PRO polypeptide #96.
XX
KW Human; PRO polypeptide; secreted and transmembrane protein;
KW tumour necrosis factor-alpha; TNF-alpha; blood; proliferation;
KW differentiation; chondrocyte; tumour; genetic disorder; cytosolic; gene;
KW ss.
XX
OS Homo sapiens.
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PR 08-NOV-2000; 200WO-US030952.
 PR 10-NOV-2000; 200WO-US030873.
 PR 01-DEC-2000; 200WO-US032678.
 PR 20-DEC-2000; 200WO-US0747259.
 PR 28-FEB-2001; 200WO-US034956.
 PR 28-FEB-2001; 200WO-US0796498.
 PR 01-MAR-2001; 200WO-US006520.
 PR 09-MAR-2001; 200WO-US006666.
 PR 14-MAR-2001; 200WO-US0082706.
 PR 22-MAR-2001; 200WO-US008689.
 PR 05-APR-2001; 200WO-US00816744.
 PR 10-MAY-2001; 200WO-US00828366.
 PR 10-MAY-2001; 200WO-US0854208.
 PR 18-MAY-2001; 200WO-US00854280.
 PR 25-MAY-2001; 200WO-US00860216.
 PR 25-MAY-2001; 200WO-US00866028.
 PR 25-MAY-2001; 200WO-US00866034.
 PR 01-JUN-2001; 200WO-US017092.
 PR 01-JUN-2001; 200WO-US0872035.
 PR 01-JUN-2001; 200WO-US017800.
 PR 05-JUN-2001; 200WO-US00874503.
 PR 14-JUN-2001; 200WO-US00862636.
 PR 19-JUN-2001; 200WO-US00886342.
 PR 20-JUN-2001; 200WO-US019692.
 PR 21-JUN-2001; 200WO-US00887879.
 PR 22-JUN-2001; 200WO-US020116.
 PR 29-JUN-2001; 200WO-US021066.
 PR 09-JUL-2001; 200WO-US021735.
 PR 18-JUL-2001; 200WO-US00908827.
 PR 06-AUG-2001; 200WO-US0924419.
 PR 09-AUG-2001; 200WO-US0927796.
 PR 16-AUG-2001; 200WO-US0931836.
 PR 19-DEC-2001; 200WO-US0028072.
 XX PA (GETH) GENENTECH INC.
 XX PI Baker KP, Beresini M, Deforge L, Desnoyers L, Filvaroff E, Gao W;
 PI Gerritsen ME, Goddard A, Godowski PJ, Gurney AL, Sherwood S;
 PI Smith V, Stewart TA, Tumas D, Watanabe CK, Wood WI, Zhang Z;
 XX WPI; 2003-332040/31.
 DR P-PSDB; ABU66665.
 XX
 PT New secreted and transmembrane PRO nucleic acids, useful for gene
 PT therapy, in chromosome and gene mapping, as chromosome markers, in tissue
 PT typing, and in chromosome identification.
 XX
 PS Claim 2; Fig 191; 660pp; English.
 XX
 CC The present invention relates to the isolation of novel human PRO
 CC polypeptides, and the polynucleotide sequences encoding them. The PRO
 CC polypeptides are secreted and transmembrane proteins. The PRO
 CC polypeptides are useful for detecting other PRO polypeptides, for linking
 CC bioactive molecules to cells expressing PRO polypeptides, for modulating
 CC biological activities of cells expressing PRO polypeptides, and for
 CC identifying agonists or antagonists. The PRO polypeptides are useful for
 CC for stimulating the release of tumour necrosis factor (TNF)-alpha from
 CC human blood, for stimulating the proliferation or differentiation of
 CC chondrocytes, and detecting the presence of tumours. The polynucleotide
 CC sequences encoding PRO polypeptides are useful as hybridisation probes,
 CC in chromosome and gene mapping, in the generation of antisense RNA and
 CC DNA, in the preparation of PRO polypeptides, for generating transgenic
 CC animals or knockout animals, for the genetic analysis of individuals with
 CC genetic disorders, and in gene therapy. ACA03603-ACA03877 represent cDNAs
 CC encoding the human PRO polypeptides of the invention. Note: The sequence
 CC data for this patent was obtained in electronic format directly from the
 CC USPTO web site at seqdata.uspto.gov/psipsDIDEntry.html
 XX
 SQ Sequence 1647 BP; 492 A; 341 C; 347 G; 467 T; 0 U; 0 Other;

Alignment Scores:
 Pred. No.: 1.64e-294 Length: 1647
 Score: 2752.00 Matches: 512

Percent Similarity: 99.81% Conservative: 0
 Best Local Similarity: 99.81% Mismatches: 1
 Query Match: 99.60% Indels: 0
 DB: 8 Gaps: 0
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 QY 1 MetLysArgLeuLeuLeuLeuCysLeuPhePheLeuThrPheSerSerAlaPheProLeu 20
 DB 24 ATGAAGCGCCTTCTGCTTCTGTTTTTGTCTTTATTAACATTTTCTCTGCAATTCCTCTTA 83
 QY 21 ValArgMetThrGluAsnGluGluAsnMetGlnLeuAlaGlnAlaTyrLeuAsnGlnPhe 40
 DB 84 GTCCGGATGACGGAATAATGAAGAAATATGCACTGGCTCAGCAATCTCAACAGTTC 143
 QY 41 TyrSerLeuGluIleGluGlyAsnHisLeuValGlnSerLysAsnArgSerLeuLeuAsp 60
 DB 144 TACTCTCTTGAATAGAAGGAATCATCTTGTTCAAAGCAAGATAGGAGTCTCATAGAT 203
 QY 61 AspLysIleArgGluMetGlnAlaPhePheGlyLeuThrValThrGlyLysLeuAspSer 80
 DB 204 GACAAATTCGGGAAATCAAGCATTTTTTGGATTGACAGTGACTGGAAACTGACTCA 263
 QY 81 AsnThrLeuGluIleMetLysThrProArgCysGlyValProAspValGlyGlnTyrGly 100
 DB 264 AACACCTTGAGATCATGAAGACCCAGGTGTGGGTGCTGATGTGGCCAGTATGGC 323
 QY 101 TyrThrLeuProGlyTyrPArgLysTyrAsnLeuThrTyrArgIleIleAsnTyrThrPro 120
 DB 324 TACACCTCCCTGGGTGGAGAAATACAACTCCTACAGATAATAAATCTATCTACTCCG 383
 QY 121 AspMetAlaArgAlaAlaValAspGluAlaIleGlnGluGlyLeuGluValTyrSerLys 140
 DB 384 GATATGGCACCAGCTGCTGTGGATGAGGCTATCCAAAGAGGTTTAAAGATGTGGAGCAAA 443
 QY 141 ValThrProLeuLysPheThrLysIleSerLysGlyIleAlaAspIleMetIleAlaPhe 160
 DB 444 GTCACTCCCACTAAATTCACCAAGATTTCAAGGGGATTCAGACATCATGATGCCCTTT 503
 QY 161 ArgThrArgValHisGlyArgCysProArgTyrPheAspGlyProLeuGlyValLeuGly 180
 DB 504 AGGACTCGAGTCCATGGTGGTGTCTCGCTATTTTGTATGGTCCCTTGGAGTGTCTGGC 563
 QY 181 HisAlaPheProGlyProGlyLeuGlyAspThrHisPheAspGluAspGluAsn 200
 DB 564 CATGCCCTTCTCTCCGTGGTCCGGTCTGGGTGTGACTCATTTTGTAGAGGATGAAAC 623
 QY 201 TrpThrLysAspGlyValAlaGlyPheAsnLeuValAlaAlaHisGluPheGlyHis 220
 DB 624 TGGACCAAGGATGGAGCAGGATTCAACTGTCTTGTGGCTGCTCATGAATTTGGTCAT 683
 QY 221 AlaLeuGlyLeuSerHisSerAsnAspGlnThrAlaLeuMetPheProAsnTyrValSer 240
 DB 684 GCACCTGGGGCTCTCTCACTCCAAATGATCAACAGCCTTGATGTTCCTCCAAATTTATGCTCC 743
 QY 241 LeuAspProArgLysTyrProLeuSerGlnAspAspIleAsnGlyIleGlnSerIleTyr 260
 DB 744 CTGGATCCCAAGAAATACCCACTTTCTCAGGATGATATCAATGGAATCCAGTCCATCAT 803
 QY 261 GlyGlyLeuProLysValProAlaLysProLysGluProThrIleProHisAlaCysAsp 280
 DB 804 GGAGGTCTGCTAAGGTACTTCTAAGCCAAAGGACCCACTATATCCCTGCTGTGAC 863
 QY 281 ProAspLeuThrPheAspAlaIleThrThrPheArgArgGluValMetPhePheLysGly 300
 DB 864 CTGACTTGACTTTTGAAGCTATCACAACTTTCCGAGAGAAGTAATGTTCTTTAAAGGC 923
 QY 301 ArgHisLeuTyrArgIleTyrTyrAspIleThrAspValGluPheGluLeuLeuAlaSer 320
 DB 924 AGGCACCTATGAGGATCTATTATGATATCAGGATGTGTGATTTGAATTAATTTGCTTCA 983
 QY 321 PheTrpProSerLeuProAlaAspLeuGlnAlaTyrGluAsnProArgAspLysIle 340

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Db      984  TTCTGCCCTCTCTGCCAGCTGATCTCAGCTGCATACAGAGACCCAGAGATAAGATT 1043
QY      341  LeuValPheLysAspGluAsnPheTrpMetIleArgGlyTyrAlaValLeuProAspTyr 360
Db      1044  CTGGTTTAAAGATGAAATCTTCTGATGATCAGAGGATATGCTGCTTGCAGATTAT 1103
QY      361  ProLysSerIleHisThrLeuGlyPheProGlyArgValLysLysIleAspAlaAlaVal 380
Db      1104  CCCAATCCCATCATCATAGTTTTCAGGACGTGTGAAGAAATAGATGAGCCGTC 1163
QY      381  CysAspLysThrThrArgLysThrTyrPhePheValGlyIleTrpCysTrpArgPheAsp 400
Db      1164  TGTGATAAGACCAACAGAAAACCTACTTCTTGTGGGCATTTGGTCTCGAGTTTGTAT 1223
QY      401  GluMetThrGlnThrMetAspLysGlyPheProGlnArgValLysHisPheProGly 420
Db      1224  GAAATGACCCAAACCATGGCAAAAGGATTCCTCCGACAGAGCTGTGAACACTTTCCTGGA 1283
QY      421  IleSerIleArgValAspAlaAlaPheGlnTyrLysGlyPhePhePheSerArgGly 440
Db      1284  ATCAGTATCCGTGTGTGATGCTGCTTCCAGTACAAAGGATCTCTTTTTCAGCCGTGGA 1343
QY      441  SerLysGlnPheGlnThrAsnIleLysThrLysAsnIleThrArgIleMetArgThrAsn 460
Db      1344  TCAAGCAATTTGAATACAACTTAAGACAAAGATATTACCCGAATCATGAGAACTAAT 1403
QY      461  ThrTrpPheGlnCysLysGluProLysAsnSerSerPheGlyPheAspIleAsnLysGlu 480
Db      1404  ACTTGGTTTCAATGCAAAAGACCAAGAACTCTCTCATTTGGTTTGTATATCAACAAGAA 1463
QY      481  LysAlaHisSerGlyGlyIleLysIleLysThrLysLysSerLysSerLeuSerLeuPheIlePhe 500
Db      1464  AAGACATCTCAGGAGGCAATGAATATGTATCATAAGATTTTAACTTGTATTTATTTT 1523
QY      501  GlyIleValHisLeuLeuLysAsnThrSerIleTyrGln 513
Db      1524  GGTATTGTTTATTTGCTGAAACACACTTCTATTATCA 1562

RESULT 7
ABX89236
ID      ABX89236 standard; cDNA; 1647 BP.
XX
AC      ABX89236;
XX
DT      13-MAY-2003 (first entry)
XX
DE      DNA encoding novel secreted and transmembrane protein PRO5992.
XX
KW      Human; PRO; hypertrophy of neonatal heart; angiogenesis; wound healing;
KW      cardiac insufficiency disorder; cancer; tumour; immune response;
KW      adrenal cortical capillary endothelial growth; c-fos induction;
KW      vascular endothelial growth factor inhibition; VEGF inhibition;
KW      endothelial cell growth inhibitor; T-lymphocytes stimulation;
KW      retinal neurons cell survival; rod photoreceptor cell survival;
KW      retinal disorder; retinitis pigmentosa; kidney disorder;
KW      mammalian kidney mesangial cell proliferation; Berger disease;
KW      dermatitis; herpeticiformis; Crohn's disease; chondrocyte proliferation;
KW      chondrocyte redifferentiation; sports injury; arthritis; gene; ss.
XX
OS      Homo sapiens.
XX
PN      US2003017563-A1.
XX
PD      23-JAN-2003.
XX
PF      07-MAY-2002; 2002US-00140808.
XX
PR      31-MAR-1997; 97WO-US005230.
PR      12-JUN-1998; 98WO-US012456.
PR      14-JUL-1998; 98WO-US014552.
PR      28-AUG-1998; 98WO-US017888.
PR      10-SEP-1998; 98WO-US018824.
PR      14-SEP-1998; 98WO-US019093.
PR      14-SEP-1998; 98WO-US019094.
PR      14-SEP-1998; 98WO-US019177.
PR      16-SEP-1998; 98WO-US019330.
PR      17-SEP-1998; 98WO-US019437.
PR      07-OCT-1998; 98WO-US021141.
PR      29-OCT-1998; 98WO-US022991.
PR      29-OCT-1998; 98WO-US022992.
PR      20-NOV-1998; 98WO-US024855.
PR      01-DEC-1998; 98WO-US025108.
PR      05-JAN-1999; 99WO-US000106.
PR      08-MAR-1999; 99WO-US005028.
PR      10-MAR-1999; 99WO-US005190.
PR      20-APR-1999; 99WO-US008615.
PR      14-MAY-1999; 99WO-US010733.
PR      02-JUN-1999; 99WO-US012252.
PR      01-SEP-1999; 99WO-US020111.
PR      08-SEP-1999; 99WO-US020594.
PR      13-SEP-1999; 99WO-US020944.
PR      15-SEP-1999; 99WO-US021090.
PR      05-OCT-1999; 99WO-US021547.
PR      29-NOV-1999; 99WO-US023089.
PR      30-NOV-1999; 99WO-US028214.
PR      30-NOV-1999; 99WO-US028313.
PR      01-DEC-1999; 99WO-US028409.
PR      01-DEC-1999; 99WO-US028301.
PR      02-DEC-1999; 99WO-US028634.
PR      02-DEC-1999; 99WO-US028551.
PR      02-DEC-1999; 99WO-US028564.
PR      02-DEC-1999; 99WO-US028565.
PR      16-DEC-1999; 99WO-US030095.
PR      20-DEC-1999; 99WO-US030911.
PR      20-DEC-1999; 99WO-US030999.
PR      22-DEC-1999; 99WO-US030720.
PR      30-DEC-1999; 99WO-US031243.
PR      30-DEC-1999; 99WO-US031274.
PR      05-JAN-2000; 2000WO-US000219.
PR      06-JAN-2000; 2000WO-US000277.
PR      06-JAN-2000; 2000WO-US000376.
PR      11-FEB-2000; 2000WO-US000365.
PR      18-FEB-2000; 2000WO-US000341.
PR      18-FEB-2000; 2000WO-US000432.
PR      22-FEB-2000; 2000WO-US000414.
PR      24-FEB-2000; 2000WO-US0004914.
PR      24-FEB-2000; 2000WO-US005004.
PR      01-MAR-2000; 2000WO-US005601.
PR      02-MAR-2000; 2000WO-US005746.
PR      02-MAR-2000; 2000WO-US005641.
PR      10-MAR-2000; 2000WO-US006319.
PR      15-MAR-2000; 2000WO-US006884.
PR      20-MAR-2000; 2000WO-US007377.
PR      21-MAR-2000; 2000WO-US007532.
PR      30-MAR-2000; 2000WO-US008439.
PR      17-MAY-2000; 2000WO-US013705.
PR      22-MAY-2000; 2000WO-US014042.
PR      30-MAY-2000; 2000WO-US014941.
PR      02-JUN-2000; 2000WO-US015264.
PR      28-JUL-2000; 2000WO-US020710.
PR      11-AUG-2000; 2000WO-US022031.
PR      23-AUG-2000; 2000WO-US023522.
PR      24-AUG-2000; 2000WO-US023328.
PR      08-NOV-2000; 2000WO-US030952.
PR      10-NOV-2000; 2000WO-US030873.
PR      01-DEC-2000; 2000WO-US032678.
PR      20-DEC-2000; 2000US-00747259.
PR      20-DEC-2000; 2000WO-US034956.
PR      28-FEB-2001; 2001US-00796498.
PR      28-FEB-2001; 2001WO-US006520.
PR      01-MAR-2001; 2001WO-US006666.
PR      09-MAR-2001; 2001US-00802706.
PR      14-MAR-2001; 2001US-00806689.
PR      22-MAR-2001; 2001US-00816744.
PR      05-APR-2001; 2001US-00828366.
PR      10-MAY-2001; 2001US-00854208.
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10-MAY-2001; 2001US-00854280.
 PR 18-MAY-2001; 2001US-00860216.
 PR 25-MAY-2001; 2001US-00866028.
 PR 25-MAY-2001; 2001US-00866034.
 PR 25-MAY-2001; 2001US-00866034.
 PR 01-JUN-2001; 2001US-00872035.
 PR 01-JUN-2001; 2001US-00872035.
 PR 05-JUN-2001; 2001US-00874503.
 PR 14-JUN-2001; 2001US-00882636.
 PR 19-JUN-2001; 2001US-00886342.
 PR 20-JUN-2001; 2001US-00891992.
 PR 21-JUN-2001; 2001US-00887879.
 PR 22-JUN-2001; 2001US-00892011.
 PR 29-JUN-2001; 2001US-00910666.
 PR 09-JUL-2001; 2001US-00921735.
 PR 18-JUL-2001; 2001US-00908827.
 PR 06-AUG-2001; 2001US-00924419.
 PR 09-AUG-2001; 2001US-00927796.
 PR 16-AUG-2001; 2001US-00931836.
 PR 19-DEC-2001; 2001US-00028072.
 XX
 (GETH) GENENTECH INC.
 PA
 Baker KP, Beresini M, Deforge L, Desnoyers L, Filvaroff E, Gao W;
 PI Gerritsen ME, Goddard A, Godowski PJ, Gurney AL, Sherwood S;
 PI Smith V, Stewart TA, Tumas D, Watanabe CK, Wood WI, Zhang Z;
 XX
 WPI: 2003-148238/14.
 DR P-PSDB; ABUS9746.
 XX
 Two hundred and seventy five nucleic acids encoding PRO polypeptides,
 PT useful for treating pericyte-associated tumors, diabetes and various bone
 PT and/or cartilage disorders, e.g. arthritis.
 XX
 Claim 2; Fig 191; 659pp; English.
 PS
 XX The invention describes an isolated human PRO polypeptide. The PRO
 CC polypeptides are useful in detecting PRO polypeptides in a sample, in
 CC linking a bioactive molecule to a cell expressing a PRO polypeptide, and
 CC in modulating at least one biological activity of a cell expressing a PRO
 CC polypeptide. PRO1312 stimulates hypertrophy of neonatal heart and is thus
 CC useful for treating cardiac insufficiency disorders. PRO1154 and PRO1186
 CC stimulate adrenal cortical capillary endothelial growth, and PRO536,
 CC PRO943, PRO828, PRO826, PRO1068 or PRO535, PRO826, PRO819, PRO1126,
 CC PRO1360 and PRO1387 induce c-fos in endothelial cells, and are thus
 CC useful for treating conditions or disorders where angiogenesis would be
 CC beneficial, e.g. wound healing and antagonist of this polypeptide are
 CC useful for treating cancerous tumours. PRO812 inhibits vascular
 CC endothelial growth factor (VEGF) stimulated proliferation of endothelial
 CC cells and is thus useful for inhibiting endothelial cell growth in
 CC mammals which would be beneficial in inhibiting tumour growth. PRO826,
 CC PRO1068, PRO1184, PRO1346 and PRO1375 stimulate proliferation of
 CC stimulated T-lymphocytes and are therapeutically useful for enhancing
 CC immune response. PRO828, PRO826, PRO1068 or PRO1132 enhance survival of
 CC retinal neurons cells (PRO1132 is also enhances survival/proliferation of
 CC rod photoreceptor cells) and therefore are useful for treating retinal
 CC disorders of injuries, e.g. retinitis pigmentosa, AMD. PRO819, PRO813
 CC and PRO1066 induce proliferation of mammalian kidney mesangial cells,
 CC and therefore are useful for treating kidney disorders associated with
 CC decreased mesangial cell function such as Berger disease or other
 CC nephropathies associated with dermatitis, herpetiformis or Crohn's
 CC disease. PRO1310, PRO844, PRO1312, PRO1192 and PRO1387 induce the
 CC proliferation and/or reifferentiation of chondrocytes in culture and are
 CC thus useful for treating sports injuries, and arthritis. This sequence
 CC encodes a novel human PRO protein
 XX
 SQ Sequence 1647 BP; 492 A; 341 C; 347 G; 467 T; 0 U; 0 Other;
 Alignment Scores:
 Pred. No.: 1.64e-294 Length: 1647
 Score: 2752.00 Matches: 512
 Percent Similarity: 99.81% Conservative: 0
 Best Local Similarity: 99.81% Mismatches: 1

Query Match: 99.60% Indels: 0
 DB: 8 Gaps: 0
 US-10-729-807-10 (1-513) x ABX89236 (1-1647)
 QY 1 MetLysArgLeuLeuLeuCysLeuPhePheIleThrPheSerSerAlaPheProLeu 20
 DB 24 ATGAAGCGCCCTCTGCTCTCTGTTTGTCTTTATAACATTTCTCTGCAATTCCTTA 83
 QY 21 ValArgMetThrGluAsnGluGluAsnMetGlnLeuAlaGlnAlaTyrIleuAsnGlnPhe 40
 DB 84 GTCCGGATGACGGAAATATCAAGAAATATGCAACTGGCTCAGGCATATCTCAACCGATTC 143
 QY 41 TyrSerLeuGluIleGluGluYasnHisLeuValGlnSerLysAsnArgSerIleuLeasp 60
 DB 144 TACTCTCTTGAATAGAAGGAATCATCTTGTTCAAACAGAAATAGGAGTCTCATAGAT 203
 QY 61 AspLysIleArgGluMetGlnAlaPhePheGlyLeuThrValThrGlyLysLeuAspSer 80
 DB 204 GACAAATTCGGAAATGCAAGCATTTTTCGATTGACAGTGCAGTGGAAACCTGACTCA 263
 QY 81 AsnThrLeuGluIleMetLysThrProArgCysGlyValProAspValGlyGlnTyrGly 100
 DB 264 AACACCTTGGATCATGAAGACACCCAGGTGTGGGTGCCTGATGTGGCCAGTATGCGC 323
 QY 101 TyrThrLeuProGlyTyrArgLysTyrAsnLeuThrTyrArgIleIleAsnTyrThrPro 120
 DB 324 TACACCTCTCCCTGGGTGGAGAAATACACCTCACCTACAGAAATATAAATATATCTCG 383
 QY 121 AspMetAlaArgAlaAlaValAspGluAlaIleGlnGluGlyLeuGluValTyrSerLys 140
 DB 384 GATATGGCAGCGCTGCTGTGGATGAGCTATCCAAAGAGGTTTAGAAGTGTGGAGCAA 443
 QY 141 ValThrProLeuLysPheThrLysIleSerLysGlyIleAlaAspIleMetIleAlaPhe 160
 DB 444 GTCACTCCACTAAAATTCACCAAGATTTCAAAGGGGATTCAGACATCATGATTCGCTTT 503
 QY 161 ArgThrArgValHisGlyArgCysProArgTyrPheAspGlyProLeuGlyValLeuGly 180
 DB 504 AGGATCCAGTCCATGCGGTGCTCTCGCTATTTTGATGGTCCCTGGGAGTGTGTGCG 563
 QY 181 HisAlaPheProGlyProGlyLeuGlyAspThrHisPheAspGluAspGluAsn 200
 DB 564 CATGCTTTCTCTCGGTCTCGGGTCTGGGTGGTGACACTCATTTTGATGAGATGAAAC 623
 QY 201 TrpThrLysAspGlyAlaGlyPheAsnLeuPheLeuValAlaAlaHisGlnPheGlyHis 220
 DB 624 TGGACCAAGGATGGAGCAGGATTCAACTGTTTCTTGTGGTCTCATGAATTTGCTCAT 683
 QY 221 AlaLeuGlyLeuSerHisSerAsnAspGlnThrAlaLeuMetPheProAsnTyrValSer 240
 DB 684 GCATGGGGCTCTCTCACTCAATGATCAACAGCCTTGATGTTCCCAAAATATGCTGCC 743
 QY 241 LeuAspProArgLysTyrProLeuSerGlnAspIleAsnGlyIleGlnSerIleTyr 260
 DB 744 CTGGATCCAGAAATACCCACTTCTCAGGATGATATCAATGGAATCCAGTCCATCTAT 803
 QY 261 GlyGlyLeuProLysValProAlaLysProLysGluProThrIleProHisAlaCysAsp 280
 DB 804 GGAGGTCTGCTTAAGGTACCTGCTAAAGCAAAGGAACCCACTATACCCCATGCTGTGAC 863
 QY 281 ProAspLeuThrPheAspAlaIleThrPheArgArgGluValMetPhePheLysGly 300
 DB 864 CTGACTTGACTTTTGACGCTATCACAACTTTCCGACAGAGTAATGTTCTTTAAAGGC 923
 QY 301 ArgHisLeuTyrArgIleTyrTyrAspIleThrAspValGluPheGluLeuIleAlaSer 320
 DB 924 AGGCACCTATGGAGATCTATTATGATATCAGGAATGTGAGTTTGAATTAATTCCTCA 983
 QY 321 PheTrpProSerLeuProAlaAspLeuGlnAlaIleTyrGluAsnProArgAspLysIle 340
 DB 984 TTCTGGCCATCTCTGCCAGTGTATCTGCAAGCTGCACAGAGAACCCCCAGAGATAAGATT 1043

01-JUN-2001; 2001US-00872035.
 01-JUN-2001; 2001WO-US017800.
 05-JUN-2001; 2001US-00874503.
 14-JUN-2001; 2001US-00882636.
 19-JUN-2001; 2001US-00886342.
 20-JUN-2001; 2001WO-US019692.
 21-JUN-2001; 2001US-00887879.
 22-JUN-2001; 2001WO-US020116.
 29-JUN-2001; 2001WO-US021066.
 09-JUL-2001; 2001WO-US021735.
 18-JUL-2001; 2001US-00908827.
 06-AUG-2001; 2001US-00924419.
 09-AUG-2001; 2001US-00927796.
 16-AUG-2001; 2001US-00931836.
 19-DEC-2001; 2001US-00028072.
 (GETH) GENENTECH INC.
 Baker KP, Beresini M, Deforge L, Desnoyers L, Filvaroff E, Gao W;
 Gerritsen ME, Goddard A, Godowski PJ, Gurney AL, Sherwood S;
 Smith V, Stewart TA, Tumas D, Watanabe CK, Wood WI, Zhang Z;
 WPI: 2003-466355/44.
 P-PSDB; ABO24936.
 New isolated nucleic acid encoding a PRO polypeptide, e.g. PRO1114 or
 PRO4978, useful in molecular biology, chromosome and gene mapping, in
 generating antisense RNA and DNA, and in gene therapy.
 Claim 2; Fig 191; 659pp; English.
 The invention relates to an isolated nucleic acid comprising at least 80%
 sequence identity to a PRO (secreted and transmembrane protein) cDNA
 comprising a nucleic acid (a) encoding a PRO polypeptide, or its
 extracellular domain (with or without its associated signal peptide),
 which comprises any of the 275 120-850 residue amino acid sequences,
 given in the specification; (b) comprising any of the 275 300-3500
 nucleotide sequences, given in the specification; or (c) comprising the
 full-length coding sequence of the nucleotide sequences given in the
 specification, or of the DNA deposited under any of the American Type
 Culture Collection (ATCC) Accession Numbers listed in the specification.
 Also included are a vector comprising the novel nucleic acid, a host cell
 comprising the vector, producing a PRO polypeptide, the isolated PRO
 polypeptides detailed above, a chimeric molecule comprising the PRO
 polypeptide of fused to a heterologous amino acid sequence, an anti-PRO
 antibody, detecting a PRO polypeptide in a sample suspected of containing
 the PRO polypeptide, linking a bioactive molecule to a cell expressing a
 PRO polypeptide, modulating at least one biological activity of a cell
 expressing a PRO polypeptide, stimulating the release of tumour necrosis
 factor-alpha (TNF-alpha) from human blood, (or proteoglycans from
 cartilage or cytokine from peripheral blood mononuclear cells (PBMC)),
 modulating the uptake of glucose or FFA by skeletal muscle cells or
 adipocyte cells, stimulating the proliferation or differentiation of
 chondrocyte cells (or proliferation of or gene expression in pericyte
 cells), stimulating the proliferation of inner ear utricular supporting
 cells (or of T-lymphocyte cells, or of endothelial cells), inhibiting the
 binding of A-peptide to factor VIIA, or differentiation of adipocyte
 cells, detecting the presence of a tumour in a mammal and an
 oligonucleotide probe derived from any of the nucleotide sequences given
 in the specification. The polynucleotide is useful in molecular biology,
 including uses as hybridisation probes, in chromosome and gene mapping,
 in generating antisense RNA and DNA, and in gene therapy. The
 polynucleotide may also be used in preparing PRO polypeptides by
 recombinant techniques, and in generating either transgenic animals or
 knock-out animals which, in turn, are useful in the development and
 screening of therapeutically useful reagents. The PRO polypeptide or the
 antibody is used in preparing a medicament for treating a condition
 responsive to the polypeptide or antibody, such as tumours, and in
 various diagnostic assays. The present sequence encodes a PRO polypeptide
 Sequence 1647 BP; 492 A; 341 C; 347 G; 467 T; 0 U; 0 Other;
 Alignment Scores:

Pred. No.:	1-64e-294	Length:	1647
Score:	2752.00	Matches:	512
Percent Similarity:	99.81%	Conservative:	0
Best Local Similarity:	99.81%	Mismatches:	1
Query Match:	99.60%	Indels:	0
DB:	8	Gaps:	0

US-10-729-807-10 (1-513) x ACD41890 (1-1647)

QY	1	MetLysArgLeuLeuLeuLeuCysLeuPhePheLeuThrPheSerSerAlaPheProLeu	20
DB	24	ATGAAGCGCTTCTGCTTCTGTTTGTCTTTATATAACATTTCTTCTGCTTTCCCTTA	83
QY	21	ValArgMetThrGluAsnGluGluMetGlnLeuAlaGlnAlaTyrLeuAsnGlnPhe	40
DB	84	GTCCGGATGACGGAATAATGAGAAATATGCAACTGGCTCAGGCATATCTCAACCAATTC	143
QY	41	TyrSerLeuGluLeuGluGlyAsnHisLeuValGlnSerLysAsnArgSerLeuLeuLeu	60
DB	144	TACTCTTGAATAGAGGGATCATCTTGTTCAAAGCAAGANTAGGAGTCTCATAGAT	203
QY	61	AspLysIleArgGluMetGlnAlaPhePheGlyLeuThrValThrGlyLysLeuAspSer	80
DB	204	GACAAATTCGGGAATGCAAGCATTTTGTGATTGACAGTGACTGGAACCTGGACTCA	263
QY	81	AsnThrLeuGluLeuMetLysThrProArgCysGlyValProAspValGlyGlnTyrGly	100
DB	264	AACACCCCTTGAGATCATGAAGACCCCGGTGTGGGTGCTGATGTGGGCCAGTATGGC	323
QY	101	TyrThrLeuProGlyTyrArgLysTyrAsnLeuThrTyrArgIleIleAsnTyrThrPro	120
DB	324	TACACCCCTCCCTGGTGGAGAAATAACAACCTCACCTACAGANTATATAACTTACTCG	383
QY	121	AspMetAlaArgAlaAlaValAspGluAlaIleGlnGluGlyLeuGluValTyrSerLys	140
DB	384	GATATGGCAGCAGCTGCTGTGGATGAGGTATCCCAAGAGGTTTGAAGTGTGGAGCAA	443
QY	141	ValThrProLeuLysPheThrLysIleSerLysGlyIleAlaAspIleMetIleAlaPhe	160
DB	444	GTCACTCCACATAAAATTCACCAAGATTTCAAGGGGATTCAGACATCATGATTGCTTT	503
QY	161	ArgThrArgValHisGlyArgCysProArgTyrPheAspGlyProLeuGlyValLeuGly	180
DB	504	AGGACTCAGTCCAGTCCAGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGG	563
QY	181	HisAlaPheProProGlyProGlyLeuGlyAspThrHisPheAspGluAspGluAsn	200
DB	564	CATGCTTTTCTCTCTGGTCCGGTCTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGT	623
QY	201	TrpThrLysAspGlyValGlyPheAsnLeuPheLeuValAlaAlaHisGluPheGlyHis	220
DB	624	TGGACCAAGGATGGAGAGGATTCAACTTGTGTGGTGGTGGTGGTGGTGGTGGTGGTGGT	683
QY	221	AlaLeuGlyLeuSerHisSerAsnAspGlnThrAlaLeuMetPheProAsnTyrValSer	240
DB	684	GCACCTGGGCTCTCTCATCCAAATGATCAACAGCTTGATGTTCCCAAAATATGTCCTCC	743
QY	241	LeuAspProArgLysTyrProLeuSerGlnAspIleAsnGlyIleGlnSerIleTyr	260
DB	744	CTGGATCCAGAAATACCCACTTCTCAGGATGATATCAATGGAATCCAGTCCATCTAT	803
QY	261	GlyGlyLeuProLysValProAlaLysProLysGluProThrIleProHisAlaCysAsp	280
DB	804	GGAGTCTGCTTAAGGTACCTGGCTTAAGCAAGAAACCCACTATATCCCCCATGCTGTGAC	863
QY	281	ProAspLeuThrPheAspAlaIleThrThrPheArgGluValMetPhePheLysGly	300
DB	864	CCTGACTGACTTTTGACGCTATCACAACTTTCGACAGAGGATATGTTCTTTAAAGGC	923
QY	301	ArgHisLeuTrpArgIleTyrTyrAspIleThrAspValGluPheGluLeuIleAlaSer	320
DB	924	AGGCACCTATGGAGGATCTATTATGATATACCGGATGTTGAGTTTGAATTAATTGCTTCA	983

QY	321	PheTTPProSerLeuProAlaAspLeuGlnAlaAlaTyrClnuAsnProArgAspLysIle	340	PR	17-SEP-1998;	98WO-US019437.
Db	984	TTCTGGCCATCTCTGCCAGCTGATCTGCAAGCTGCATACGAGAACCCCGAGATAAGATT	1043	PR	07-OCT-1998;	98WO-US021141.
QY	341	LeuValPheLysAspGluAsnPheTTPMetIleArgGlyTyrAlaValLeuProAspTyr	360	PR	23-OCT-1998;	98WO-US022991.
Db	1044	CTGGTTTTTAAGATGAACCTTCTGGATGATCAGGATATGCTGCTGCCAGATTAT	1103	PR	20-NOV-1998;	98WO-US024855.
QY	361	ProLysSerIleHisThrLeuGlyPheProGlyArgValLysLysIleAspAlaAlaVal	380	PR	01-DEC-1998;	98WO-US025108.
Db	1104	CCCAATCCATCCATACATTAGGTTTTCCAGGACGCTGTGAAGAAATAGATGCAGCCGTC	1163	PR	05-JAN-1999;	99WO-US000106.
QY	381	CysAspLysThrThrArgLysThrTyrPhePheValGlyIleTTPCysTTPArgPheAsp	400	PR	08-MAR-1999;	99WO-US005028.
Db	1164	TGTGATAAGACCAACCAAGAAACCTACTTCTTTGTGGGCATTTGGTCTGGAGTTTGAT	1223	PR	10-MAR-1999;	99WO-US005190.
QY	401	GluMetThrGlnThrMetAspLysGlyPheProGlnArgValLysHisPheProGly	420	PR	20-APR-1999;	99WO-US008615.
Db	1224	GAATGACCCCAACCATGGACAAAGGATTCGCCGACAGAGTGGTAAACACTTTCCTGGA	1283	PR	14-MAY-1999;	99WO-US010733.
QY	421	IleSerIleArgValAspAlaAlaPheGlnTyrLysGlyPhePhePheSerArgGly	440	PR	02-JUN-1999;	99WO-US012252.
Db	1284	ATCAGTATCGTGTGATGCTGCTTTCAGTACAAAGGATTTCTTTTTCAGCCGTGGA	1343	PR	01-SEP-1999;	99WO-US020111.
QY	441	SerLysGlnPheGluTyrAsnIleLysThrLysAsnIleThrArgIleMetArgThrAsn	460	PR	08-SEP-1999;	99WO-US020594.
Db	1344	TCAAAGCAATTTGAATCAACATTAAACAAAGAAATATCCCGAATCATGAGAACTAAT	1403	PR	13-SEP-1999;	99WO-US020944.
QY	461	ThrTTPPheGlnCysLysGluProLysAsnSerPheGlyPheAspIleAsnLysGlu	480	PR	15-SEP-1999;	99WO-US021090.
Db	1404	ACTGGTTTCAATCAAGAACCAACCAAGACCTCTCATTTGTTTGATATCAACAGGAA	1463	PR	05-SEP-1999;	99WO-US021547.
QY	481	LysAlaHisSerGlyGlyIleLysIleLeuTyrHisLysSerLeuSerLeuPheIlePhe	500	PR	29-NOV-1999;	99WO-US028214.
Db	1464	AAAGCACATTGAGGAGGCAAAAGATATTGATCATAAGAGTTTAAAGCTTGTTATTTT	1523	PR	30-NOV-1999;	99WO-US028313.
QY	501	GlyIleValHisLeuLysAsnThrSerIleTyrGln	513	PR	01-DEC-1999;	99WO-US028551.
Db	1524	GGTATTGTTTCAATGCTGAAACACACTTCTATTATCAAA	1562	PR	02-DEC-1999;	99WO-US028564.
RESULT 9				PR	02-DEC-1999;	99WO-US028565.
ACA04119				PR	16-DEC-1999;	99WO-US030095.
XX	ACA04119;			PR	20-DEC-1999;	99WO-US030399.
XX	ACA04119;			PR	30-DEC-1999;	99WO-US031243.
XX	27-MAY-2003 (first entry)			PR	05-JAN-2000;	2000WO-US000219.
XX	Human cDNA encoding a secreted/transmembrane protein, SEQ ID 191.			PR	06-JAN-2000;	2000WO-US000277.
XX	Human; ss; gene; secreted protein; transmembrane protein; PRO;			PR	11-FEB-2000;	2000WO-US003565.
KW	inflammatory disease; organ failure; atherosclerosis; cardiac injury;			PR	18-FEB-2000;	2000WO-US004341.
KW	infertility; birth defects; premature aging; AIDS; biosensor;			PR	22-FEB-2000;	2000WO-US004342.
KW	acquired immunodeficiency syndrome; cancer; diabetic complication;			PR	24-FEB-2000;	2000WO-US004344.
KW	bioreactor; tumour.			PR	24-FEB-2000;	2000WO-US005004.
OS	Homo sapiens.			PR	01-MAR-2000;	2000WO-US005601.
XX	US2003032155-A1.			PR	02-MAR-2000;	2000WO-US005746.
XX	13-FEB-2003.			PR	10-MAR-2000;	2000WO-US005841.
XX	03-MAY-2002; 2002US-00137865.			PR	15-MAR-2000;	2000WO-US006319.
XX	31-MAR-1997; 97WO-US005230.			PR	20-MAR-2000;	2000WO-US006884.
PR	12-JUN-1998; 98WO-US012456.			PR	21-MAR-2000;	2000WO-US007377.
PR	14-JUL-1998; 98WO-US014552.			PR	30-MAR-2000;	2000WO-US008439.
PR	28-AUG-1998; 98WO-US017888.			PR	17-MAY-2000;	2000WO-US013705.
PR	10-SEP-1998; 98WO-US018824.			PR	22-MAY-2000;	2000WO-US014042.
PR	14-SEP-1998; 98WO-US019093.			PR	30-MAY-2000;	2000WO-US014941.
PR	14-SEP-1998; 98WO-US019094.			PR	02-JUN-2000;	2000WO-US015264.
PR	14-SEP-1998; 98WO-US019177.			PR	28-JUL-2000;	2000WO-US020710.
PR	16-SEP-1998; 98WO-US019330.			PR	11-AUG-2000;	2000WO-US022031.
PR				PR	23-AUG-2000;	2000WO-US023522.
PR				PR	24-AUG-2000;	2000WO-US023328.
PR				PR	08-NOV-2000;	2000WO-US030392.
PR				PR	10-NOV-2000;	2000WO-US030873.
PR				PR	01-DEC-2000;	2000WO-US032678.
PR				PR	20-DEC-2000;	2000US-0074259.
PR				PR	20-DEC-2000;	2000WO-US034956.
PR				PR	28-FEB-2001;	2001US-00796498.
PR				PR	28-FEB-2001;	2001WO-US006520.
PR				PR	01-MAR-2001;	2001WO-US006666.
PR				PR	09-MAR-2001;	2001US-00802706.
PR				PR	14-MAR-2001;	2001US-00808689.
PR				PR	22-MAR-2001;	2001US-00816744.
PR				PR	05-APR-2001;	2001US-00828366.
PR				PR	10-MAY-2001;	2001US-00854208.
PR				PR	10-MAY-2001;	2001US-00854280.
PR				PR	18-MAY-2001;	2001US-00860216.
PR				PR	25-MAY-2001;	2001US-00866028.

Db	1044	CTGGTCTTTAAAGATGAAACCTCTCGATGATCAGAGGATATGCTGCTGTCAGATTAT	1103	PR	29-OCT-1998;	98WO-US022991.
				PR	29-OCT-1998;	98WO-US022992.
				PR	20-NOV-1998;	98WO-US024855.
QY	361	ProLysSerIleHisThrLeuGlyPheProGlyArgValLysLysLysLysLeuAspAlaVal	380	PR	01-DEC-1998;	98WO-US025108.
				PR	05-JAN-1999;	98WO-US000106.
Db	1104	CCCAATCCATCCATACATATAGTGTTCAGGACGTTGTAAGAAATAGATGCGAGCGTC	1163	PR	08-MAR-1999;	98WO-US005028.
				PR	10-MAR-1999;	98WO-US005190.
QY	381	CysAspLysThrThrArgLysThrThrPhePheValGlyIleTrpCysTrpArgPheAsp	400	PR	20-APR-1999;	98WO-US008615.
				PR	14-MAY-1999;	98WO-US010733.
Db	1164	TGTGATAAGACCAACAAAGAAACCTACTCTTTGTGGCCATTTGGTGCTGGAGGTTGAT	1223	PR	02-JUN-1999;	98WO-US012252.
				PR	01-SEP-1999;	98WO-US020111.
QY	401	GluMetThrGlnThrMetAspLysGlyPheProGlnArgValLysHisPheProGly	420	PR	08-SEP-1999;	98WO-US020594.
				PR	13-SEP-1999;	98WO-US020944.
Db	1224	GAATGACCCAAACCACTGGCAAGGATCCCGCAGAGTGGTAAACACATTTCTCTGGA	1283	PR	15-SEP-1999;	98WO-US021090.
				PR	15-SEP-1999;	98WO-US021547.
QY	421	IleSerIleArgValAspAlaAlaPheGlnTyrLysGlyPhePhePheSerArgGly	440	PR	05-OCT-1999;	98WO-US023089.
				PR	29-NOV-1999;	98WO-US028214.
Db	1284	ATCAGTATCCGTGTGATGCTGCTTTCCAGTACAAAGGATCTCTTTTCAGCCGTGA	1343	PR	30-NOV-1999;	98WO-US028313.
				PR	30-NOV-1999;	98WO-US028409.
QY	441	SerLysGlnPheGlnTyrAsnIleLysThrLysAsnIleThrArgIleMetArgThrAsn	460	PR	01-DEC-1999;	98WO-US028301.
				PR	01-DEC-1999;	98WO-US028634.
Db	1344	TCAAAGCAATTCGAATCAACATTAAGACAAAGATATTACCCGAATCATGAGAACTAAT	1403	PR	02-DEC-1999;	98WO-US028551.
				PR	02-DEC-1999;	98WO-US028564.
QY	461	ThrTrpPheGlnCysLysGluProLysAsnSerSerPheGlyPheAspIleAsnLysGlu	480	PR	02-DEC-1999;	98WO-US028565.
				PR	16-DEC-1999;	98WO-US030095.
Db	1404	ACTTGGTTTCATGCAAGAACCAAGAACTCTCATTTGGTTTGNATCAACAGGAA	1463	PR	20-DEC-1999;	98WO-US030911.
				PR	20-DEC-1999;	98WO-US030999.
QY	481	LysAlaHisSerGlyGlyIleLysIleLysIleLysSerLysSerLysSerLysPhePhe	500	PR	22-DEC-1999;	98WO-US030720.
				PR	30-DEC-1999;	98WO-US031243.
Db	1464	AAAGCATTTCAGGAGGCATAAAGATATTGATATCAAGAGTTTAAGCTTGTATTATTTT	1523	PR	30-DEC-1999;	98WO-US031274.
				PR	05-JAN-2000;	2000WO-US000219.
QY	501	GlyIleValHisLeuLeuLysAsnThrSerIleTyrGln	513	PR	06-JAN-2000;	2000WO-US000277.
				PR	06-JAN-2000;	2000WO-US000376.
Db	1524	GGTATTGTTTCATTGCTGTAAGAAACACTTCTATTATTCAA	1562	PR	11-FEB-2000;	2000WO-US003565.
				PR	18-FEB-2000;	2000WO-US004341.
RESULT 10				PR	22-FEB-2000;	2000WO-US004414.
ADA45710				PR	24-FEB-2000;	2000WO-US004914.
ID ADA45710 standard; cDNA; 1647 BP.				PR	24-FEB-2000;	2000WO-US005004.
XX AC ADA45710;				PR	01-MAR-2000;	2000WO-US005601.
XX DT				PR	02-MAR-2000;	2000WO-US005746.
XX DE				PR	02-MAR-2000;	2000WO-US005841.
XX KW				PR	10-MAR-2000;	2000WO-US006319.
XX KW				PR	15-MAR-2000;	2000WO-US006884.
XX KW				PR	20-MAR-2000;	2000WO-US007377.
XX KW				PR	21-MAR-2000;	2000WO-US007532.
XX KW				PR	30-MAR-2000;	2000WO-US008439.
XX KW				PR	17-MAY-2000;	2000WO-US013705.
XX KW				PR	22-MAY-2000;	2000WO-US014042.
XX KW				PR	30-MAY-2000;	2000WO-US014941.
XX KW				PR	02-JUN-2000;	2000WO-US015264.
XX KW				PR	28-JUL-2000;	2000WO-US020710.
XX KW				PR	11-AUG-2000;	2000WO-US022031.
XX KW				PR	23-AUG-2000;	2000WO-US023522.
XX OS				PR	24-AUG-2000;	2000WO-US023328.
XX XX				PR	08-NOV-2000;	2000WO-US030952.
XX XX				PR	10-NOV-2000;	2000WO-US030873.
XX PN				PR	01-DEC-2000;	2000WO-US032578.
XX PD				PR	20-DEC-2000;	2000US-00747259.
XX PF				PR	20-DEC-2000;	2000WO-US034956.
XX XX				PR	28-FEB-2001;	2001US-00796498.
XX XX				PR	28-FEB-2001;	2001WO-US006520.
XX XX				PR	01-MAR-2001;	2001WO-US006666.
XX XX				PR	09-MAR-2001;	2001US-00802706.
XX XX				PR	14-MAR-2001;	2001US-00808689.
XX XX				PR	22-MAR-2001;	2001US-00816744.
XX XX				PR	05-APR-2001;	2001US-00828366.
XX XX				PR	10-MAY-2001;	2001US-00854208.
XX XX				PR	10-MAY-2001;	2001US-00854280.
XX XX				PR	18-MAY-2001;	2001US-00860216.
XX XX				PR	25-MAY-2001;	2001US-00866028.
XX XX				PR	25-MAY-2001;	2001US-00866034.
XX XX				PR	25-MAY-2001;	2001WO-US017092.

Db 1104 CCCAATCCATCATACATTAGTGTTCACGAGCGTGTGAAGAAATAGATGCAGCGTC 1163
QY 381 CysAspLysThrThrArgLysThrThrPhePheValGlylleTrpCysTrpArgPheAsp 400
Db 1164 TGTGATAAGACCAACAGAAAACCTACTTCTTTGTGGCAATTTGGTCTGGAGTTTGAT 1223
QY 401 GluMetThrGlnThrMetAspLysGlyPheProGlnArgValValLysHisPheProGly 420
Db 1224 GAAATGCCCAACCAATGGCAAGAGATCCCGCAGAGATGGTAAACACTTTCCTCGGA 1283
QY 421 IleSerIleArgValAspAlaAlaPheGlnTrpLysGlyPhePhePheSerArgGly 440
Db 1284 ATCAGTATCGTGTGTGATGCTGCTTCCAGTACAAAGATTCCTTTTCAGCGTGGGA 1343
QY 441 SerLysGlnPheGluTrpAsnIleLysThrLysIleAsnIleThrArgIleMetArgThrAsn 460
Db 1344 TCAAGCAATTCGAATACAAACATTAACAAAGAAATATCCCGAATCATGAGAACTAAT 1403
QY 461 ThrTrpPheGlnCysLysGluProLysAsnSerSerPheGlyPheAspIleAsnLysGlu 480
Db 1404 ACTTGGTTTCAATGCAAGAACCAAGAACTCCTCATTTGGTTTGTATATCAACAAGAA 1463
QY 481 LysAlaHisSerGlyGlyIleLysIleLysIleLeuTrpHisLysSerLeuSerLeuPheIlePhe 500
Db 1464 AAGCACATTCAGGAGGCATAAAGATATTGTATCATAGAGTTTAACTTGTATTATTTT 1523
QY 501 GlyIleValHisLeuLeuLysAsnThrSerIleTrpGln 513
Db 1524 GGTATTGTTGCTGCTGAAACACACTTCTATTATCAAA 1562
RESULT 11
ADA76141
ID ADA76141 standard; cDNA; 1647 BP.
AC ADA76141;
XX XX 20-NOV-2003 (first entry)
XX XX Human PRO polynucleotide #96.
DE Human; gene; ss; PRO; secreted polypeptide; transmembrane polypeptide;
KW tumour necrosis factor-alpha; TNF-alpha; chondrocyte cell; tumour;
KW cancer; adrenal; lung; colon; breast; prostate; rectum; kidney; cervix;
KW liver; microvascular endothelial cell; glucose; EPA;
KW skeletal muscle cell; adipocyte cell; pericyte cell;
KW inner ear utricular supporting cell; T-lymphocyte cell;
KW endothelial cell tube formation; bone disorder; cartilage disorder;
KW sports injury; proteoglycan; articular cartilage defect; osteoarthritis;
KW rheumatoid arthritis; haemoglobin-associated disorder thalassaemia;
KW immune system cell infiltration.
OS Homo sapiens.
OS OS
XX XX US2003073212-A1.
XX XX 17-APR-2003.
XX PF 16-APR-2002; 2002US-00123903.
XX XX 31-MAR-1997; 97WO-US005230.
PR 12-JUN-1998; 98WO-US012456.
PR 14-JUL-1998; 98WO-US014552.
PR 28-AUG-1998; 98WO-US017888.
PR 10-SEP-1998; 98WO-US018824.
PR 14-SEP-1998; 98WO-US019093.
PR 14-SEP-1998; 98WO-US019177.
PR 16-SEP-1998; 98WO-US019330.
PR 17-SEP-1998; 98WO-US019437.
PR 07-OCT-1998; 98WO-US021141.
PR 29-OCT-1998; 98WO-US022991.
PR 29-OCT-1998; 98WO-US022992.
PR 20-NOV-1998; 98WO-US024855.
PR 01-DEC-1998; 98WO-US025108.
PR 05-JAN-1999; 98WO-US000106.
PR 08-MAR-1999; 98WO-US005028.
PR 10-MAR-1999; 98WO-US0005190.
PR 20-APR-1999; 98WO-US0008615.
PR 14-MAY-1999; 98WO-US010733.
PR 02-JUN-1999; 98WO-US012252.
PR 01-SEP-1999; 98WO-US020111.
PR 08-SEP-1999; 98WO-US020594.
PR 13-SEP-1999; 98WO-US020944.
PR 15-SEP-1999; 98WO-US021090.
PR 15-SEP-1999; 98WO-US021547.
PR 05-OCT-1999; 98WO-US023089.
PR 29-NOV-1999; 98WO-US028214.
PR 30-NOV-1999; 98WO-US028313.
PR 30-NOV-1999; 98WO-US028409.
PR 01-DEC-1999; 98WO-US028301.
PR 01-DEC-1999; 98WO-US028634.
PR 02-DEC-1999; 98WO-US028551.
PR 02-DEC-1999; 98WO-US028564.
PR 02-DEC-1999; 98WO-US028565.
PR 16-DEC-1999; 98WO-US030095.
PR 20-DEC-1999; 98WO-US030911.
PR 20-DEC-1999; 98WO-US030999.
PR 22-DEC-1999; 98WO-US030720.
PR 30-DEC-1999; 98WO-US031243.
PR 30-DEC-1999; 98WO-US031274.
PR 05-JAN-2000; 2000WO-US000219.
PR 06-JAN-2000; 2000WO-US000277.
PR 11-FEB-2000; 2000WO-US000376.
PR 18-FEB-2000; 2000WO-US004341.
PR 18-FEB-2000; 2000WO-US004342.
PR 22-FEB-2000; 2000WO-US004414.
PR 24-FEB-2000; 2000WO-US004914.
PR 24-FEB-2000; 2000WO-US005004.
PR 01-MAR-2000; 2000WO-US005601.
PR 02-MAR-2000; 2000WO-US005746.
PR 02-MAR-2000; 2000WO-US005841.
PR 10-MAR-2000; 2000WO-US006319.
PR 15-MAR-2000; 2000WO-US006884.
PR 20-MAR-2000; 2000WO-US007377.
PR 21-MAR-2000; 2000WO-US007532.
PR 30-MAR-2000; 2000WO-US008439.
PR 17-MAY-2000; 2000WO-US013705.
PR 22-MAY-2000; 2000WO-US014042.
PR 30-MAY-2000; 2000WO-US014941.
PR 02-JUN-2000; 2000WO-US015264.
PR 28-JUL-2000; 2000WO-US020710.
PR 11-AUG-2000; 2000WO-US022031.
PR 23-AUG-2000; 2000WO-US023522.
PR 24-AUG-2000; 2000WO-US023328.
PR 08-NOV-2000; 2000WO-US030952.
PR 10-NOV-2000; 2000WO-US030873.
PR 01-DEC-2000; 2000WO-US032678.
PR 20-DEC-2000; 2000US-0074259.
PR 28-DEC-2000; 2000WO-US034956.
PR 28-FEB-2001; 2001US-00796498.
PR 28-FEB-2001; 2001WO-US006520.
PR 01-MAR-2001; 2001WO-US006666.
PR 09-MAR-2001; 2001US-00802706.
PR 14-MAR-2001; 2001US-00808689.
PR 22-MAR-2001; 2001US-00816744.
PR 05-APR-2001; 2001US-00828366.
PR 10-MAY-2001; 2001US-00854208.
PR 10-MAY-2001; 2001US-00854280.
PR 18-MAY-2001; 2001US-00860216.
PR 25-MAY-2001; 2001US-00866028.
PR 25-MAY-2001; 2001US-00866034.
PR 25-MAY-2001; 2001WO-US017092.
PR 01-JUN-2001; 2001US-00872035.
PR 01-JUN-2001; 2001WO-US017800.
PR 05-JUN-2001; 2001US-00874503.

PR 14-JUN-2001; 2001US-00882636.
 PR 19-JUN-2001; 2001US-00886342.
 PR 20-JUN-2001; 2001WO-US019692.
 PR 21-JUN-2001; 2001US-00887879.
 PR 22-JUN-2001; 2001WO-US020116.
 PR 29-JUN-2001; 2001WO-US021066.
 PR 09-JUL-2001; 2001WO-US021735.
 PR 18-JUL-2001; 2001US-00908827.
 PR 06-AUG-2001; 2001US-00924419.
 PR 09-AUG-2001; 2001US-00927796.
 PR 16-AUG-2001; 2001US-00931836.
 PR 19-DEC-2001; 2001US-00028072.
 XX
 PA (GETH) GENENTECH INC.
 XX
 PI Baker KP, Beresini M, Deforge L, Desnoyers L, Filvaroff E, Gao W;
 PI Gerritsen ME, Goddard A, Godowski PJ, Gurney AL, Sherwood S;
 PI Smith V, Stewart TA, Tumas D, Watanabe CK, Wood WI, Zhang Z;
 XX
 DR WPI; 2003-687639/65.
 DR P-PSDB; ADA76142.
 XX
 PT New isolated nucleic acid encoding a secreted and transmembrane
 PT polypeptide, designated e.g. PRO1114 or PRO4978, useful in chromosome and
 PT gene mapping, in generating antisense RNA and DNA, and in gene therapy.
 XX
 PS Claim 2; Fig 191; 659pp; English.
 XX
 CC The invention relates to isolated human PRO polypeptides (secreted and
 CC transmembrane polypeptides) and the polynucleotides encoding them. The
 CC invention also relates to an antibody which specifically binds to a PRO
 CC polypeptide, a method for stimulating the release of tumour necrosis
 CC factor-alpha (TNF-alpha) from human blood, a method for stimulating the
 CC proliferation or differentiation of chondrocyte cells and a method for
 CC detecting the presence of a tumour in a mammal (e.g. adrenal, lung,
 CC colon, breast, prostate, rectal, kidney, cervical and liver tumours). The
 CC polynucleotides are useful in molecular biology, including uses as
 CC hybridisation probes, in chromosome and gene mapping, in generating
 CC antisense RNA and DNA and in gene therapy. The polynucleotides may also
 CC be used in preparing PRO polypeptides by recombinant techniques and in
 CC generating either transgenic animals or knock-out animals which are
 CC useful in the development and screening of therapeutically useful
 CC reagents. The PRO polypeptides or antibodies are used in preparing a
 CC medicament for treating a condition responsive to the polypeptides or
 CC antibodies, such as tumours, for stimulating and inhibiting proliferation
 CC of human microvascular endothelial cells, for modulating the uptake of
 CC glucose or FFA by skeletal muscle cells or adipocyte cells, for
 CC stimulating differentiation of adipocyte cells, for stimulating
 CC the proliferation of or gene expression in pericyte cells, for stimulating
 CC the proliferation of inner ear utricular supporting cells or T-lymphocyte
 CC cells, for inducing endothelial cell tube formation and for treating
 CC various bone and/or cartilage disorders such as sports injuries and
 CC arthritis. PRO polypeptides which stimulate the release of proteoglycans
 CC from cartilage are useful for treating sports-related joint problems,
 CC articular cartilage defects, osteoarthritis and rheumatoid arthritis. PRO
 CC polypeptides are also useful for treating various mammalian haemoglobin-
 CC associated disorders such as various thalassemias and conditions which
 CC may benefit from enhanced local immune system cell infiltration. This
 CC sequence represents a human PRO polynucleotide of the invention. Note:
 CC The sequence data for this patent is also available in electronic format
 CC from USPTO at seqdata.uspto.gov/sequence.html.
 XX
 SQ Sequence 1647 BP; 492 A; 341 C; 347 G; 467 T; 0 U; 0 Other;
 Alignment Scores:
 Pred. No.: 1,646-294 Length: 1647
 Score: 2752.00 Matches: 512
 Percent Similarity: 99.81% Conservative: 0
 Best Local Similarity: 99.81% Mismatches: 1
 Query Match: 99.60% Indels: 0
 DB: 9 Gaps: 0
 US-10-729-807-10 (1-513) x ADA76141 (1-1647)

QY 1 MetLysArgLeuLeuLeuLeuCysLeuPhePhePheLeuThrPheSerSerAlaPheProLeu 20
 DB 24 ATGAAGCGCTTCTGCTTCTGTTTTGTTCTTATAACATTTTCTCTGCAATTCCTTTA 83
 QY 21 ValArgMetThrGluAsnGluGluAsnMetGlnLeuAlaGlnAlaTyrLeuAsnGlnPhe 40
 DB 84 GTCCGGATGACGGAATAATGAGAAAATATGCNACTGGCTCAGCATATCTCAACAGTTC 143
 QY 41 TyrSerLeuGluIleGluGlyAsnHisLeuValGlnSerLysAsnArgSerLeuIleAsp 60
 DB 144 TACTCTCTGAAATAGAAAGGAATCATCTGTGTTCAAGCAAGAAATAGGAGTCTCATAGT 203
 QY 61 AspLysIleArgGluMetGlnAlaPhePheGlyLeuThrValThrGlyLysLeuAspSer 80
 DB 204 GACAAAATTCGGGAAATCAAGCATTTTTTGGATTGACAGTGAAGTGAAGTGAAGTGA 263
 QY 81 AsnThrLeuGluIleMetLysThrProArgCysGlyValProAspValGlyGlnTyrGly 100
 DB 264 AACACCTTTGAGATCATGAGACACCCAGGTGTGGGTGCTGTAATGGGCCAGTATGGC 323
 QY 101 TyrThrLeuProGlyTyrArgLysTyrAsnLeuThrTyrArgIleIleAsnTyrThrPro 120
 DB 324 TACACCTTCCTGGGTGGAGAAAATACAACTCCTCAGTACAGAAATATAAATATACTCG 383
 QY 121 AspMetAlaArgAlaAlaValAspGluAlaIleGlnGluGlyLeuGluValTrpSerLys 140
 DB 384 GATATGGCAGCAGCTGCTGTGGATGAGGTATCCAAAGAGGTTTAGAAGTGTGGAGCAAA 443
 QY 141 ValThrProLeuLysPheThrLysIleSerLysGlyIleAlaAspIleMetIleAlaPhe 160
 DB 444 GTCACTCCACTAAATTCACCAAGATTCAAAGGGGATTCAGACATCATGATTCCTTT 503
 QY 161 ArgThrArgValHisGlyArgCysProArgTyrPheAspGlyProLeuGlyValLeuGly 180
 DB 504 AGGACTCGAGTCCATGCTGCTGCTCTGCTATTTTGTATGTCCTTGGAGTGCTTGGC 563
 QY 181 HisAlaPheProGlyProGlyLeuGlyGlyAspThrHisPheAspGluAspGluAsn 200
 DB 564 CATGCTTTCTCTGCTGGTCCGGGTCTGGGTGGTGGTGGTGGTGGTGGTGGTGGTGG 623
 QY 201 TrpThrLysAspGlyAlaGlyPheAsnLeuPheLeuValAlaAlaHisGluPheGlyHis 220
 DB 624 TGGACCAAGATGAGCAGGATTCAACTTGTTCTTGTGGCTGCTCATGAATTTGGTCTAT 683
 QY 221 AlaLeuGlyLeuSerHisSerAsnAspGlnThrAlaLeuMetPheProAsnTyrValSer 240
 DB 684 GCACCTGGGCTCTCTCACTCCCAATGATCAACAGCCTTGTATGTTCCCAAAATATGCTCC 743
 QY 241 LeuAspProArgLysTyrProLeuSerGlnAspIleAsnGlyIleGlnSerIleTyr 260
 DB 744 CTGATCCCAAGAAATACCCACTTTCTCAGGATGATATCAATGGAATCCAGTCCATCTAT 803
 QY 261 GlyGlyLeuProLysValProAlaLysProLysGluProThrIleProHisAlaCysAsp 280
 DB 804 GGAGTCTGCTTAGTACCTGCTTAAGCCAAAGAACCCACTATACCCCATGCTGCTGAC 863
 QY 281 ProAspLeuThrPheAspAlaIleThrThrPheArgArgGluValMetPhePheLysGly 300
 DB 864 CTTGACTTGACTTTTGGCTCATCAACTTTCCGACAGAGAAATGATGTTCTTTAAAGGC 923
 QY 301 ArgHisIleThrArgIleTyrTyrAspIleThrAspValGluPheGluLeuIleAlaSer 320
 DB 924 AGGCACCTATGGAGGATCTATTATGATATCAAGATGTTGAGTTGAATTAATTTGCTTCA 983
 QY 321 PheTrpProSerLeuProAlaAspLeuGlnAlaAlaTyrGluAsnProArgAspLysIle 340
 DB 984 TTCGGCCATCTCTGCCAGCTGATCTGCAAGCTCATACAGAGAACCCAGAGATAAGATT 1043
 QY 341 LeuValPheLysAspGluAsnPheTrpMetIleArgGlyTyrAlaValLeuProAspTyr 360
 DB 1044 CTGGTTTTAAAGATGAAACTTCTGGATGATCAGAGGATATGCTGCTTCCAGATAT 1103

RESULT 12

PR 20-JUN-2001; 2001WO-US019692.
 PR 21-JUN-2001; 2001US-00887879.
 PR 22-JUN-2001; 2001WO-US020116.
 PR 29-JUN-2001; 2001WO-US021066.
 PR 09-JUL-2001; 2001WO-US021735.
 PR 18-JUL-2001; 2001US-00908827.
 PR 06-AUG-2001; 2001US-00924419.
 PR 09-AUG-2001; 2001US-00927796.
 PR 16-AUG-2001; 2001US-00931836.
 PR 19-DEC-2001; 2001US-00028072.
 XX (GETH) GENENTECH INC.
 XX
 PI Baker KP, Beresini M, DeForge L, Desnoyers L, Filvaroff E, Gao W;
 PI Gerritsen ME, Goddard A, Godowski PJ, Gurney AL, Sherwood S;
 PI Smith V, Stewart TA, Tumas D, Watanabe CK, Wood WI, Zhang Z;
 XX
 DR WPI; 2003-521854/49.
 DR P-PSDB; ADA18792.
 XX

PT New PRO nucleic acid, useful for preparing a composition for treating
 PT e.g., tumors.
 XX

PS Claim 2; Fig 191; 660pp; English.
 XX

CC The invention relates to isolated human PRO polypeptides (secreted and
 CC transmembrane polypeptides) and the polynucleotides encoding them. The
 CC invention also relates to an antibody which specifically binds to a PRO
 CC polypeptide, a method for stimulating the release of tumour necrosis
 CC factor-alpha (TNF-alpha) from human blood, a method for stimulating the
 CC proliferation or differentiation of chondrocyte cells and a method for
 CC detecting the presence of a tumour in a mammal (e.g. lung, colon, breast,
 CC prostate, rectal, cervical and liver tumours). The polynucleotides are
 CC useful in molecular biology, including uses as hybridisation probes, in
 CC chromosome and gene mapping, in generating antisense RNA and DNA and in
 CC gene therapy. The polynucleotides may also be used in preparing PRO
 CC polypeptides by recombinant techniques and in generating either
 CC transgenic animals or knock-out animals which are useful in the
 CC development and screening of therapeutically useful reagents. The PRO
 CC polypeptides or antibodies are used in preparing a medicament for
 CC treating a condition responsive to the polypeptides or antibodies, such
 CC as tumours, for modulating the uptake of glucose or FFA by adipocyte
 CC cells, for stimulating the proliferation of or gene expression in
 CC pericyte cells, for stimulating the release of proteoglycans from
 CC cartilage, for stimulating the proliferation of inner ear utricular
 CC supporting cells, for stimulating the release of cytokines from PBMC
 CC cells, for inhibiting the binding of A-peptide to factor VIIA, for
 CC inhibiting the differentiation of adipocyte cells and for stimulating the
 CC proliferation of endothelial cells. This sequence represents a human PRO
 CC polynucleotide of the invention. Note: The sequence data for this patent
 CC is also available in electronic format from USPTO at
 CC seqdata.uspto.gov/sequence.html.
 XX

SQ Sequence 1647 BP; 492 A; 341 C; 347 G; 467 T; 0 U; 0 Other;

Alignment Scores:

Pred. No.:	1-64e-294	Length:	1647
Score:	2752.00	Matches:	512
Percent Similarity:	99.81%	Conservative:	0
Best Local Similarity:	99.81%	Mismatches:	1
Query Match:	99.60%	Indels:	0
DB:	9	Gaps:	0

US-10-729-807-10 (1-513) x ADA18791 (1-1647)

Qy 1 MetLysArgLeuLeuLeuLeuCysLeuPhePheIleThrPheSerSerAlaPheProLeu 20
 Db
 24 ATGAAGCGCCTCTGCTTCTGTTTGTCTTTTATTAACATTTCTTCGCAATTCCTTCA 83
 Qy 21 ValArgMetThrGluAsnGluGluAsnMetGlnLeuAlaGlnAlaTyrLeuAsnGlnPhe 40
 Db
 84 GTCCGGATGACGGAAATGAAGAAATATGCAACTGGCTCAGGCATATCTCAACCAAGTTC 143

Qy 41 TyrSerLeuGluIleGluGlyAsnHisLeuValGlnSerLysAsnArgSerLeuIleAsp 60
 Db 144 TACTCTCTTGAATAAGAGGAATCATCTTGTTCAAAGCAAGATAGAGAGTCTCATAGAT 203
 Qy 61 AspLysIleArgGluMetGlnAlaPhePheGlyLeuThrValThrGlyLysLeuAspSer 80
 Db 204 GACAAAATTCGGAAATGCAAGCATTTTGTGATGACAGTGACTGGAACCTGACTCA 263
 Qy 81 AsnThrLeuGluIleMetLysThrProArgCysGlyValProAspValGlyGlnTyrGly 100
 Db 264 AACACCTTGTAGATCATGAAGACACCCAGGTGTGGGTGCTGTGATGTGGCGAGTATGCG 323
 Qy 101 TyrThrLeuProGlyTyrArgLysTyrAsnLeuThrTyrArgIleIleAsnTyrThrPro 120
 Db 324 TACACCTCTCCCTGGGTGGAGAAATACAACTCACCTACAGAAATAATAAATTAATCTCCG 383
 Qy 121 AspMetAlaArgAlaValAspGluAlaIleGlnGluGlyLeuGluValTyrSerLys 140
 Db 384 GATATGGCAGCAGCTGCTGTGGATGAGGCTATCCAAAGAGGTTTAGAAGATGTGGAGCAAA 443
 Qy 141 ValThrProLeuLysPheThrLysIleSerLysGlyIleAlaAspIleMetIleAlaPhe 160
 Db 444 GTCACTCCACTAAAATTCACCAAGATTTCAAAGGGGATTCAGACATCATGATTCGCTTT 503
 Qy 161 ArgThrArgValHisGlyArgCysProArgTyrPheAspGlyProLeuGlyValLeuGly 180
 Db 504 AGGACTCGAGTCCATGTCGGTGTCTCGCTATTTTGTATGGTCCCTTGGAGTGTCTGGC 563
 Qy 181 HisAlaPheProGlyProGlyLeuGlyGlyAspThrHisPheAspGluAspGluAsn 200
 Db 564 CATGCTTTCTCTCTGCTGGTCTGGTGTGACACTCATTTTGTATGAGGATGAAAC 623
 Qy 201 TrpThrLysAspGlyAlaGlyPheAsnLeuPheLeuValAlaAlaHisGluPheGlyHis 220
 Db 624 TGGACCAAGATGGAGCAGGATTCAACTGTCTTGTGTGGCTGTCTCATGAATTTGGTCA 683
 Qy 221 AlaLeuGlyLeuSerHisSerAsnAspGlnThrAlaLeuMetPheProAsnTyrValSer 240
 Db 684 GCATGGGGGCTCTCTCACTCCAATGATCAACAGGCTTGATGTCCCAAAATATGTCTCC 743
 Qy 241 LeuAspProArgLysTyrProLeuSerGlnAspIleAsnGlyIleGlnSerIleTyr 260
 Db 744 CTGGATCCCAAGAAATACCCACTTCTCAGGATGATATCAATGGAATCCAGTCCATCTAT 803
 Qy 261 GlyGlyLeuProLysValProAlaLysProLysGluProThrIleProHisAlaCysAsp 280
 Db 804 GGAGGTCTGCTTAAGGTACCTGCTAAGCCAAAGGAACCCACTATACCCCATGCCGTGAC 863
 Qy 281 ProAspLeuThrPheAspAlaIleThrThrPheArgArgGluValMetPhePheLysGly 300
 Db 864 CTTGACTTGACTTTTGGCGCTATCACAACTTCCGAGAGAGTAATGTCTTTTAAAGGC 923
 Qy 301 ArgHisLeuTrpArgIleTyrTyrAspIleThrAspValGluPheGluLeuIleAlaSer 320
 Db 924 AGGCACCTATGAGGATCTATTATGATATACGGATGTGTAGTTGATTAATTAATTCCTCA 983
 Qy 321 PheTrpProSerLeuProAlaAspLeuGlnAlaLysTyrGluAsnProArgAspLysIle 340
 Db 984 TTCGGCCATCTCTGCCAGCTGATCTGCAAGCTGCATCAGAGAACCCAGAGATAAGATT 1043
 Qy 341 LeuValPheLysAspGluAsnPheTrpMetIleArgGlyTyrAlaValLeuProAspTyr 360
 Db 1044 CTGGTTTTTAAAGATGAATAAACTTCTGGATGATCAGAGGATATGCTGTCTGCCAGATTAT 1103
 Qy 361 ProLysSerIleHisThrLeuGlyPheProGlyArgValLysLysIleAspAlaAlaVal 380
 Db 1104 CCCAAATCCATCCATACATTAGGTTCACGAGCGTGTGAGAGAAATAGATGCGCGCTC 1163
 Qy 381 CysAspLysThrThrArgLysThrThrPhePheValGlyIleTyrCysTrpArgPheAsp 400
 Db 1164 TGTGATAAGACCAAGAAAAACCTACTCTTTTGGGCATTTGTGTGTGGAGGTTTGTAT 1223
 Qy 401 GluMetThrGlnThrMetAspLysGlyPheProGlnArgValValLysHisPheProGly 420

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Db      1224  GAAATGACCAACCAATGGCAAGAGATTCCCGCAGAGAGTGTAAACACTTCTCTGGA 1283
QY      421  IleSerIleArgValAspAlaAlaPheGlnTyrLysGlyPhePhePheSerArgGly 440
Db      1284  ATCAGTATCCGTGTTGATGCTGCTTCCAGTACAAAGGATTCTCTTTTCAGCCGTGGA 1343
QY      441  SerLysGlnPheGlnTyrAsnIleLysThrLysAsnIleThrArgIleMetArgThrAsn 460
Db      1344  TCAAGCAATTTGAATACACATTAAGACAAGAATATTATCCCGAATCATGAGAACTAAT 1403
QY      461  ThrTrpPheGlnCysLysGluProLysAsnSerSerPheGlyPheAspIleAsnLysGlu 480
Db      1404  ACTTGGTTTCATGCAAGAACCAAGAACTCTCTATGTTTGTATATACACAGAA 1463
QY      481  LysAlaHisSerGlyGlyIleLysIleLeuTyrHisLysSerLeuSerLeuPheIlePhe 500
Db      1464  AAAGCACATTTCAGGAGGCATAAAGATATTGTATCATTAAGAGTTTAAGCTTGTTATTTT 1523
QY      501  GlyIleValHisLeuLeuLysAsnThrSerIleTyrGln 513
Db      1524  GGTATTGTTTCATTGCTGAAACAACTTCTATTATCA 1562

RESULT 13
ADA61414
ID  ADA61414 standard; cDNA; 1647 BP.
XX
AC  ADA61414;
XX
DT  20-NOV-2003 (first entry)
XX
DE  Homo sapiens.
XX
KW  Human; secreted and transmembrane protein; PRO; gene; ss;
KW  Tumour necrosis factor alpha release; TNF-alpha release;
KW  glucose uptake modulator; FFA uptake modulator;
KW  cell proliferation stimulator; cell differentiation stimulator;
KW  cell differentiation inhibitor; cytokine release stimulator; tumour;
KW  lung tumour; colon tumour; breast tumour; prostate tumour; rectal tumour;
KW  cervical tumour; liver tumour; chromosome mapping; gene mapping;
KW  gene therapy; chromosome identification; chromosome marker.
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KW glucose uptake modulator; FFA uptake modulator;
KW cell proliferation stimulator; cell differentiation stimulator;
KW cell differentiation inhibitor; cytokin.
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GenCore version 5.1.6
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TITLE		Mammalia; Eutheria; Primates; Carnivora; Homini; Hominidae; Homo.				
JOURNAL		Holmgren, B., Kihlen, M., Wood, T. and Ekblom, J.				
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Qy	201	TrpThrLysAspGlyAlaGlyPheAsnLeuPheLeuValAlaHisGluPheGlyHis	220
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Qy	241	LeuAspProArgLysTyrProLeuSexGlnAspIleAsnGlyIleGlnSerIleTyr	260
Db	744	CTGGATCCAGAAATACCCACTTCTCAGGATGATATCAATGGAATCCAGTCCATCTAT	803
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Db	804	GGAGGTCTGCCTTAAGGTACCTGCTAAGCAAGGAACCCACTATACCCCATGCTGTGAC	863
Qy	281	ProAspLeuThrPheAspAlaIleThrThrPheArgArgGluValMetPhePheLysGly	300
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Qy	301	ArgHisLeuTrpArgIleTyrZAspIleThrAspValGluPheGluLeuIleAlaSer	320
Db	924	AGGCACCTATGAGGATCTATATGATATCAGGATGTTGAGTTGAATTAATGCTTCA	983
Qy	321	PheTrpProSerLeuProAlaAspLeuGlnAlaTyZGluAsnProArgAspLysIle	340
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 ACCESSION AY358752.1 GI:37182622
 VERSION FLI_CDNA.
 KEYWORDS Homo sapiens (human)
 SOURCE
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 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 REFERENCE 1 (bases 1 to 1647)
 AUTHORS Clark,H.F., Gurney,A.L., Abaya,E., Baker,K., Baldwin,D., Brush,J.,
 Chen,J., Chow,B., Chui,C., Crowley,C., Currell,B., Deuel,B.,
 Dowd,P., Eaton,D., Foster,J., Grimaldi,C., Gu,Q., Hass,P.E.,
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 Xie,M.H., Yansura,D., Yi,S., Yu,G., Yuan,J., Zhang,M., Zhang,Z.,
 Goddard,A., Wood,W.I. and Godowski,P.
 The Secreted Protein Discovery Initiative (SPDI), a Large-Scale
 Effort to Identify Novel Human Secreted and Transmembrane Proteins:
 A Bioinformatics Assessment
 Genomes Res. 13 (10), 2265-2270 (2003)

JOURNAL
 PUBMED 12975309
 REFERENCE 2 (bases 1 to 1647)
 AUTHORS Clark,H.F.
 TITLE Direct Submission
 JOURNAL
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gene
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Submitted (01-AUG-2003) Department of Bioinformatics, Genentech,
 Inc., 1 DNA Way, South San Francisco, CA 94080, USA

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ORIGIN

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US-10-729-807-10 (1-513) x AY358752 (1-1647)

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Qy	21	ValArgMetThrGluAenGluGluAenMetGlnLeuAlaGlnAlaTyrLeuAenGlnPhe	40
Db	84	GTCGGATGACGGAATAAGAAATATGCACTGGCTCAGGCATATCTCAACAGTTC	143
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Qy	201	TrpThrLysAspGlyAlaGlyPheAsnLeuPheLeuValAlaAlaHisGluPheGlyHis	220
Db	624	TGGACCAAGATGGAGCAGGATTCACATTTGTTCTTGTGGTCTCATGAATTTGTTGAT	683
Qy	221	AlaLeuGlyLeuSerHisSerAsnAspGlnThrAlaLeuMetPheProAsnTyrValSer	240
Db	684	GCACTGGGGCTCTCTCACTCCCAATGATCAACAGGCTTGATGTTCCCAAAATATGTCCTC	743

Qy	241	LeuAspProArgLysTyrProLeuSerGlnAspAspIleAsnGlyIleGlnSerIleTyr	260
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Qy	281	ProAspLeuThrPheAspAlaIleThrThrPheArgArgGluValMetPhePheLysGly	300
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Qy	301	ArgHisLeuTyrArgIleTyrTyrAspIleThrAspValGluPheGluLeuIleAlaSer	320
Db	924	AGGCACCTATGGAGGATCTATTATGATATCACGGATGTTGAGTTTGAATTAATGCTTCA	983
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Db	1164	TGTGATAAGACCAACAGAAAACCTACTTCTTTGTGGGCATTTGGTGCTGGAGTTTGAT	1223
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Qy	441	SerLysGlnPheGluTyrAsnIleLysThrLysAsnIleThrArgIleMetArgThrAsn	460
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Qy	501	GlyIleValHisLeuLeuLysAsnThrSerIleTyrGln	513
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RESULT 4

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DEFINITION	AF195192			
ACCESSION	AF195192.1	GI:11066089		
VERSION				
KEYWORDS	Homo sapiens (human)			
SOURCE	Homo sapiens			
ORGANISM	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.			
REFERENCE	1 (bases 1 to 1655)			
AUTHORS	Benoit de Coignac, A., Elson, G., Magistrelli, G., Jeannin, P., Delneste, Y., Aubry, J. P., Berthier, O., Bonnefoy, J. Y. and Gauchat, J. F.			
TITLE	Cloning of a Novel Matrix Metalloproteinase Homologous to			

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AUTHORS	Benoit de Coignac, A., Elson, G., Magistrelli, G., Jeannin, P., Delneste, Y., Aubry, J.P., Berthier, O., Bonnefoy, J.Y. and Gauchat, J.F.	QY	181	HisAlaPheProProGlyProGlyLeuGlyGlyArgThrHisPheAspGluAspGluAsn	200
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JOURNAL	Submitted (15-OCT-1999) Molecular Biology, Pierre-Fabre, 5, Avenue Napoleon III, Saint Julien en Genevois, 74 74164, France	QY	201	TrrThrLysAspGlyAlaGlyPheAsnLeuPheLeuValAlaAlaHisGluPheGlyHis	220
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QY 120 ProAspMetAlaArgAlaValAspGluAlaIleGlnGluGlyLeuGluValTyrSer 139
DB 1495 CCGGATATGACAGCTGCTGTGGATGAGGCTATCCAAAGAGGTTTAGAAGTGTGGAGC 1436

QY 140 LysValThrProLeuLysPheThrLysIleSerLysGlyIleAlaAspIleMetIleAla 159
DB 1435 AAAGTCACTCCACATAAATTCACCAAGATTTCAAAGGGATTCAGACATCATGATGCC 1376

QY 160 PheArgThrArgValHisGlyArgCysProArgTyrPheAspGlyProLeuGlyValLeu 179
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DB 1255 AACTGGACCAAGGATGGAGCAGGATTCACCTGTGTTCTGTGGCTGCTCATGAATTTGGT 1196

QY 220 HisAlaLeuGlyLeuSerHisSerAsnAspGlnThrAlaLeuMetPheProAsnTyrVal 239
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QY 240 SerLeuAspProArgLysTyrProLeuSerGlnAspAspIleAsnGlyIleGlnSerIle 259
DB 1135 TCCCTGGATCCAGAAATACCCACTTTCTCAGGATGATATCAATGGAAATCCAGTCCATC 1076

QY 260 TyrGlyGlyLeuProLysValProAlaLysProLysGluProThrIleProHisAlaCys 279
DB 1075 TATGAGGTCTGCTTAAGTACTCTGTAAGCAAGAACCCACTATACCCCATCCCTGT 1016

QY 280 AspProAspLeuThrPheAspAlaIleThrPheArgArgGluValMetPhePheLys 299
DB 1015 GACCTGACTTGTACCTTTTGACGCTATCAACTTCCGAGAGAAATGATGTTCTTTAA 956

QY 300 GlyArgHisLeuTrpArgIleTyrTyrAspIleThrAspValGluPheGluLeuIleAla 319
DB 955 GGCAGGCACCTATGAGGATCTATTATGATATCAGGATGTTGATTTGAATTAATGCT 896

QY 320 SerPheTrpProSerLeuProAlaAspLeuGlnAlaIleTyrGluAsnProArgAspLys 339
DB 895 TCATTCGCGCATCTCTGACCTGATCTGCAAGTGCATACAGAACCCAGAGATAAG 836

QY 340 IleLeuValPheLysAspGluAsnPheTrpMetIleArgGlyTyrAlaValLeuProAsp 359
DB 835 ATTCTGGTTTAAAGATGAAACTTCTGGATGATCAGAGGATATGCTGTCTTGGCAGAT 776

QY 360 TyrProLysSerIleHisThrLeuGlyPheProGly-ArgValLysLysIleAspAlaAl 379
DB 775 TATCCCAATCCATCCATACATAGGTTCAGGACCGTGTCAAGAAATAGATGCAGC 716

QY 379 aValCysAspLysThrArgLysThrTyrPhePheValGlyIleTyrCysTrpArgPh 399
DB 715 CGTCTGTGATAAGACCAACCAAGAAACCTACTTCTTTGTGGCATTTGGTCTGGAGTT 656

QY 399 eAspGluMetThrGlnThrMetAspLysGlyPheProGlnArgValValLysHisPhePr 419
DB 655 TGATGAATGACCCAAACCATGACAAAGATTCCCGCAGAGAGTGTAAACACATTTC 596

QY 419 oGlyIleSerIleArgValAspAlaAlaPheGlnTyrLysGlyPhePhePheSerAr 439
DB 595 TGGAAATCAGTATCCGTGTTGATGCTCTTCCAGTACAAAGGATTCCTCTTTTCAGCCG 536

QY 439 gGlySerLysGlnPheGluTyrAsnIleLysThrLysAsnIleThrArgIleMetArgth 459
DB 535 TGGATCAAGCAATTTGAATACAACTTAAGACAAAGATATTACCCGAATCATGAGAAC 476

QY 459 rAsnThrTrpPheGlnCysLysGluProLysAsnSerSerPheGlyPheAspIleAsnLy 479
DB 475 TAATACTTGGTTCATATGCAAGAACCAAGAACTCTCTCATTTGGTTTGTATCAACAA 416

QY 479 sGluLysAlaHisSerGlyGlyIleLysIleLeuTyrHisLysSerLeuSerLeuPheIl 499
DB 415 GGAAGAGACATTCAGAGGCATAAAGATATTGTATCATAGAGTTTAAGCTGTTTAT 356

QY 499 ePheGlyIleValHisLeuLeuLysAsnThrSerIleTyrGln 513
DB 355 TTTTGGTATTGTTCAATTGCTGAAAAACACTTCTATTATCAAA 313

RESULT 8

AX249967 1488 bp DNA linear PAT 28-SEP-2001
LOCUS Sequence 3 from Patent WO0166766.
DEFINITION AX249967
ACCESSION AX249967.1 GI:15864453
VERSION
KEYWORDS Homo sapiens (human)
SOURCE
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1
AUTHORS Fajardo, M.D., Smith, R. and Moss, P.
TITLE A matrix metalloproteinase (mmp-25)
JOURNAL Patent: WO 0166766-A 3 13-SEP-2001;
DARWIN MOLECULAR CORPORATION (US)
FEATURES
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ORIGIN

Alignment Scores:
Pred. No.: 1,44e-230 Length: 1488
Score: 2433.50 Matches: 463
Percent Similarity: 90.84% Conservatives: 3
Best Local Similarity: 90.25% Mismatches: 4
Query Match: 88.07% Indels: 43
DB: 6 Gaps: 1

US-10-729-807-10 (1-513) x AX249967 (1-1488)

QY 1 MetLysArgLeuLeuLeuLeuLeuLeuLeuLeuLeuLeuLeuLeuLeuLeuLeuLeuLeu 20
DB 53 ATGAAGCGCCTCTGCTTCTGTTTGTCTTTTATTAACATTTCTTCTGCTATTCCTTTA 112

QY 21 ValArgMetThrGluAsnGluGluAsnMetGlnLeuAlaGlnAlaTyrLeuAsnGlnPhe 40
DB 113 GTCCCGATGATGGAATAATGAAGAAATGTGCAACTGGCTCAGGCATATCTCAACAGTTC 172

QY	401	GluMetThrGlnThrMetAspLysGlyPheProGlnArgValValLysHisPheProGly	420
Db	1124	GAATGACCCAAACCATGGACAAAGGGTTCCTCCGACAGAGTGGTAAACACTTTCCTGGA	1183
QY	421	IleSerIleArgValAspAlaAlaPheGlnTyrIleLysGlyPhePheSerArgGly	440
Db	1184	ATCAGTATCCGTGTGATGCTGCTTCCAGTACAAAGGATTCCTCTTTTCAGCCGTTGA	1243
QY	441	SerLysGlnPheGluTyrAsnIleLysThrLysAsnIleThrArgIleMetArgThrAsn	460
Db	1244	TCAACGCAATTGTAATACGACATTAAGACAAAGAATATACCCGAATCATGAAGAACTAAT	1303
QY	461	ThrTrpPheGlnCysLysGluProLysAsnSerSerPheGlyPheAspIleAsnLysGlu	480
Db	1304	ACTTGGTTTCAATGCAAAAGAACCAAGAACTCCTCATTTGGTTTGTATATCAACAGGAA	1363
QY	481	LysAlaHisSerGlyGlyIleLysIleLeuTyrHisLysSerLeuSerLeuPheIlePhe	500
Db	1364	AAGCATTTCAGGAGGCAATAAGATATTGTATCATAGAGTTTAAGCTTGTTATTTT	1423
QY	501	GlyIleValHisLeuLeuLysAsnThrSerIleTyrGln	513
Db	1424	GGTATTGTTCAATTGCTGAATAACACTTCTATTATCA	1462
RESULT 9			
LOCUS	AF281673	1667 bp mRNA linear	MAM 08-JAN-2001
DEFINITION	Tupaia belangeri matrix metalloproteinase-27 mRNA, complete cds.		
ACCESSION	AF281673		
VERSION	AF281673.1	GI:12006363	
KEYWORDS			
SOURCE	Tupaia belangeri (northern tree shrew)		
ORGANISM	Tupaia belangeri		
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Scandentia; Tupalidae; Tupaiidae.		
AUTHORS	1 (bases 1 to 1667)		
TITLE	Guggenheim, J.A., To, C.H. and Frost, M.R.		
JOURNAL	Molecular cloning of a novel matrix metalloproteinase (MMP-27) from		
AUTHORS	Unpublished		
TITLE	2 (bases 1 to 1667)		
JOURNAL	Submitted (23-JUN-2000) Department of Optometry & Vision Sciences, Cardiff University, King Edward VII Avenue, Cardiff, Wales CF10 3NB, UK		
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ORIGIN			
Alignment Scores:			
Prod. No.:	6.03e-222	Length:	1667
Score:	2347.00	Matches:	434

Percent Similarity:	90.43%		Conservative:	29
Best Local Similarity:	84.77%		Mismatches:	49
Query Match:	84.94%		Indels:	0
DB:	4		Gaps:	0

US-10-729-807-10 (1-513) x F281673 (1-1667)

Qy	1	MeLysArgLeuLeuLeuLeuCysLeuPhePheIleThrPheSerSerAlapheProLeu	20
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Qy	21	ValArgMetThrGluAsnGluGluAsnMetGlnLeuAlaGlnAlaIatYrLeuAsnGlnPhe	40
Db	154	GACCAAAGATGGAAAATGAAGAACAATGCAGCTGGCTCAGCGGTATCTCAACAGTTC	213
Qy	41	TyrSerLeuGluIleGluGlyAsnHisLeuValGlnSerIysAsnArgSerLeulleasp	60
Db	214	TACTCTCTTGAANTAGAAGGAGGCATCTCGTTCAAGCAAAACCGGGAGTCTCTTAGAC	273
Qy	61	AspIysIleArgGluMetGlnAlaPhePheGlyLeuThrValIthrGlyIysLeuAspSer	80
Db	274	GGCAAAATTCGGAAAAATGCAAGCGTTTTTGGATTGACAGTGNATGGAACGCTGGATTCA	333
Qy	81	AsnThrLeuGluIleMetLysThrProArgCysGlyValProaspValGlyGlnTyrGly	100
Db	334	AACACTCTTGAGATCATGAACACCAGGTGTGGGTGCCTGATGGGTCAGTATGCG	393
Qy	101	TyrThrLeuProGlyTyrArgLysTyrAsnLeuThrTyrArgIleIleAsnTyrThrPro	120
Db	394	TACACTCTCCCTGGGTGGAGAAATAACAACCTCACATACAGAATAATGAACATACACTCCA	453
Qy	121	AspMetAlaArgAlaAlaValAspGluAlaIleGlnGluLeuGluValTrpSerIys	140
Db	454	GATATGGCAAGCGGATGTCGATGAGGCCATCCAAAAGCTTTGGAGTATGGAGTAG	513
Qy	141	ValThrProLeuIysPheThrLysIleSerIysGlyIleAlaAspIleMetIleAlaPhe	160
Db	514	GTACTCGCTCACATTCAACCAAGATTTCAAGGGGATTGCAGACATCATGATGGCTTC	573
Qy	161	ArgThrArgValHisGlyArgCysProArgTyrPheAspGlyProLeuGlyValLeuGly	180
Db	574	AGGACTCGAGTCCATGGTGGGTGCTCTGTTATTTCGATGGCCCTTTGGGAGTCTTGGC	633
Qy	181	HisAlaPheProGlyProGlyLeuGlyGlyAspThrHisPheAspGluAspGluAsn	200
Db	634	CATGCTTTTCTCTCTGGTCTGGGTCTGGSTGGTGACACTCACITTGATGAGGATGAAAC	693
Qy	201	TrpThrIysAspGlyAlaGlyPheAsnLeuPheLeuValAlaHisGluPheGlyHis	220
Db	694	TGGACCAAGGATACAGCAGGATTCAGTTTGTCTTGTGGCTGCTCATGAATTTGGTCAC	753
Qy	221	AlaLeuGlyLeuSerHisSerAsnAspGlnThrAlaLeuMetPheProAsnTyrValSer	240
Db	754	GCCTCTGGGGCTCTCTCATTCCAAATGATCAGACAGCCTTGATGTTCCAAATATGTCTCC	813
Qy	241	LeuAspProArgLysTyrProLeuSerGlnAspAspIleAsnGlyIleGlnSerIleTyr	260
Db	814	CTGGATCTCTAGCAATAACCACTTTCTCAGGATGATATCGATGGAATCCAAATCCATATAT	873
Qy	261	GlyGlyLeuProLysValProAlaLysProIysGluProThrIleProHisAlaCysAsp	280
Db	874	GGAGGTCTACCTTACCACACCTTTCTAAGCAAAAGGACCCAAAATACCCCATGCTGTGAC	933
Qy	281	ProAspLeuThrPheAspAlaIleThrThrPheArgArgGluValMetPhePheLysGly	300
Db	934	CCTGACTTCACCTTTGACGCTATCACCACATCCGCAGAGAAGTAATGTCTTTAAAGGC	993
Qy	301	ArgHisLeuTrpArgIleTyrTyrAspIleThrAspValGluPheGluLeuIleAlaSer	320
Db	994	AGGCACCTGTGGAGGATCTATCATGATATCAACGACGTGGAAATTTGAATTAATGTCTCA	1053
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CDS
ORIGIN
Alignment Scores:
Pred. No.: 9,41e-134 Length: 833
Score: 1451.00 Matches: 267
Percent Similarity: 99.26% Conservativeness: 1
Best Local Similarity: 98.89% Mismatches: 2
Query Match: 52.52% Indels: 0
DB: 6 Gaps: 0

US-10-729-807-10 (1-513) x AX249965 (1-833)
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Qy 264 ProlystValProAlaIleProLysGluProThrIleProHisAlaCysAspProAspLeu 283
Db 61 CCTAAGGACCTGTAAAGCAAGAACCCACTATACCCATGCTGTGACCTGACTG 120
Qy 284 ThrPheAspAlaIleThrPheArgGluValMetPhePheLysGlyArgHisLeu 303
Db 121 ACTTTTGACGCTATCACAACTTCCGACAGAGTAATGTTCTTTAAAGGAGGACCTA 180
Qy 304 TrpArgIleTyrTyrAspIleThrAspValGluPheGluLeuIleAlaSerPheTrpPro 323
Db 181 TGGAGGATCTATTATGATATCAGGAGTGTGATTTGAATTAATGCTTCATCTGGCCA 240
Qy 324 SerLeuProAlaAspLeuGlnAlaAlaTyrGluAsnProArgAspLysIleLeuValPhe 343
Db 241 TCTCTGCCAGCTGATCTCAAGCTGATACAGGACCCAGAGATTAAGATTCGTGTTTT 300
Qy 344 LysAspGluAsnPheTrpMetIleArgGlyTyrAlaValLeuProAspTyrProLysSer 363
Db 301 AAAGATGAAACTTCTGGATGATCAGAGATATGCTGTCTGCCAGATTAATCCCAATCC 360
Qy 364 IleHisThrLeuGlyPheProGlyValLysLysIleAspAlaValCysAspLys 383
Db 361 ATCCATACATAGGTTTCCAGAGCTGTGAAGAAATAGATGACGCGCTCTGTGATAAG 420
Qy 384 ThrThrArgLysThrTyrPhePheValGlyIleTrpCysTrpArgPheAspGluMetThr 403
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Qy 464 GlnCysLysGluProLysAsnSerSerPheGlyPheAspIleAsnLysGlyLysAlaHis 483
Db 661 CAATGCAAGAAACCAAGAACTCTCTATTTGGTTTGTATATCAAGGAAAGACACAT 720
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721 TCAGGAGGCATAAGATATTTGATATCAAGAGTTTAAGCTTGTATTTTGGTATGTT 780
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781 CATTTGCTGAAACACTTCTATTTATCAA 810

RESULT 12
LOCUS AY183143 1479 bp mRNA linear MAM 01-SEP-2003
DEFINITION Canis familiaris stromelysin 1 (MMP3) mRNA, complete cds.
ACCESSION AY183143
VERSION AY183143.1 GI:34391861
KEYWORDS
SOURCE Canis familiaris (dog)
ORGANISM Canis familiaris
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.
REFERENCE 1 (bases 1 to 1479)
AUTHORS Sorensen,K.C., Balkin,R.G., Kitchell,B.E., Siegel,A.M. and
Schaeffer,D.
TITLE Isolation, Characterization and Expression of Stromelysin-1 (MMP3)
in Canine Tumors
JOURNAL Unpublished
REFERENCE 2 (bases 1 to 1479)
AUTHORS Sorensen,K.C., Balkin,R.G. and Kitchell,B.E.
TITLE Direct Submission
JOURNAL Submitted (18-NOV-2002) Veterinary Clinical Medicine, University of
Illinois at Urbana-Champaign, 1008 W. Hazelwood Dr., Urbana, IL
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ORIGIN
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Score: 1286.50 Matches: 254
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Best Local Similarity: 52.92% Mismatches: 140
Query Match: 46.56% Indels: 17
DB: 4 Gaps: 8

US-10-729-807-10 (1-513) x AY183143 (1-1479)
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Qy 21 ValArgMetThrGluAsnGlu---GluAsnMetGlnLeuAlaGlnAlaTyrIleAsnGln 39
Db 85 GACAGAGCTGCAGAGGATGAGAACCAACATGGAACACTCCAGCACTACCTAGAAAAC 144
Qy 40 PheTyrSerLeuGluIleGluGlyAsnHisLeuValGlnSerLysAsnArgSerLeuIle 59

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Db	1120	AAAGGAACCTCAGTTCGGGCCATTAGAGGAAATGAGGTACAAGCTGGTTACCCAAGAAGC	1179
Qy	364	IleHisThrLeuGlyPheProGlyArgGValLysIleAspAlaValCysAspLys	383
Db	1180	ATCCACACCCTGGTTCCTTCAACCAAGAAAAAATTCATGTGTCATTTCTGTATAAG	1239
Qy	384	ThrThrArgLysThrTyrPhePheValGlyIleTyrCysTirpArgPheAspGluMetThr	403
Db	1240	GAAGGGAAGAAAAACATCTCTTTGTGGAAGACAAATACTGGAGGTTTGATGAGAGAGA	1299
Qy	404	GlnThrMetAspLysGlyPheProGlnArgValValLysHisPheProGlyIleSerIle	423
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Db	1360	AAGATCATGCTGTGTTTTGAAGCATTTTGGGTTCATTATCTTCAGTGGATCTTCACG	1419
Qy	444	PheGlnTyrAsnIleLysThrLysAsnIleThrArgIleMetArgThrAsnThrTirpPhe	463
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RESULT 14			
AR380629			
LOCUS			
DEFINITION Sequence 1174 from patent US 6607879.			
ACCESSION AR380629			
VERSION AR380629.1 GI:40088263			
KEYWORDS			
SOURCE			
ORGANISM			
REFERENCE			
AUTHORS			
TITLE			
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AUTHORS			
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AUTHORS			
TITLE			

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Db 121 TACTACGACCTCGAAAAGATGTGAACAGCTTTTGTAGGAGAAAGGACAGTGGTCTCGTT 180
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QY 80 SerAsnThrLeuGluIleMetLysThrProArgCysGlyValProAspValGlyGlnTyr 99
Db 241 TCCGACACTCTGGAGGTGATGCGCAAGCCAGGTGTGGAGTTCCTGACGTGGTCACTTC 300
QY 100 GlyTyrThrLeuProGly-----TrpArgLysTyrAsnLeuThrTyrArgIleIle 116
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QY 117 AsnTyrThrProAspMetAlaArgAlaValAspGluAlaIleGlnGluGlyLeuGlu 136
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Db 478 ATGATCTCTTTGACGTAGAGAAACATGGAGACTTTTACCT-----TTTGATGACCT 531
QY 176 LeuGlyValLeuGlyHisAlaPheProGlyProGlyLeuGlyGlyAspThrHisPhe 195
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QY 196 AspGluAspGluAsnTrpThrLysAspGlyAlaGlyPheAsnLeuPheLeuValAlaA 215
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QY 216 HisGluPheGlyHisAlaLeuGlyLeuSerHisSerAsnAspGlnThrAlaLeuMetPhe 235
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RESULT 15
AX402358
LOCUS AX402358
DEFINITION Sequence 12 from Patent WO0196606.
ACCESSION AX402358
VERSION AX402358.1 GI:21387395
KEYWORDS Homo sapiens (human)
SOURCE Homo sapiens
ORGANISM Homo sapiens
REFERENCE 1
AUTHORS Yamamoto,H., Kroes,R. and Moskal,J.R.
TITLE Identification of genes and compounds for treatment of cancer
JOURNAL Patent: WO 0196606-A 12 20-DEC-2001;
NXVIS Neurotherapies, Inc. (US)
FEATURES
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        1..1434
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        /mol_type="unassigned DNA"
        /db_xref="taxon:9606"

ORIGIN

Alignment Scores:
Pred. No.: 6.08e-114 Length: 1434
Score: 1254.00 Matches: 247
Percent Similarity: 66.04% Conservative: 70
Best Local Similarity: 51.46% Mismatches: 145
Query Match: 45.39% Indels: 18
DB: 6 Gaps: 9

US-10-729-807-10 (1-513) x AX402358 (1-1434)
QY 1 MetLysArgLeuLeuLeuLeuCysLeuPhePheIleThrPheSerSerAlaPheProLeu 20
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QY 21 ValArgMetThrGluAsnGluGlu---AsnMetGlnLeuAlaGlnAlaTyrLeuAsnGln 39
Db 61 GATGGAGCTGCAAGGGTGGAGCACACCAAGTGAACCTTGTTCAGAAATATCTAGAAAC 120
QY 40 PheTyrSerLeuGluIleGluGlyAsnHisLeuValGlnSerLysAsnArgSerLeuIle 59
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QY 60 AspAspLysIleArgGluMetGlnAlaPhePheGlyLeuThrValThrGlyLysLeuAsp 79
Db 181 GTTAAAAAATCCGAGAAATCAGAAAGTTCCTTGAATTTGGAGGTGACGGGGAAGCTGGAC 240
QY 80 SerAsnThrLeuGluIleMetLysThrProArgCysGlyValProAspValGlyGlnTyr 99
Db 241 TCCGACACTCTGGAGGTGATGCGCAAGCCAGGTGTGGAGTTCCTGACGTGGTCACTTC 300
QY 100 GlyTyrThrLeuProGly-----TrpArgLysTyrAsnLeuThrTyrArgIleIle 116
Db 301 ---AGAACCTTCTCGCATCCCGAAGTGGAGAAACCCACCTTACATACAGGATTGTG 357
QY 117 AsnTyrThrProAspMetAlaArgAlaValAspGluAlaIleGlnGluGlyLeuGlu 136

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Db 358 AATTATACACCAGATTTCACAAAGATGCTGTTGATTCCTGCTGTGAGAAAGCTCTGAAA 417
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Db 418 GTCTGGAGAGAGTGACTCCACTCACATTCTCAGGCTGTATGAAGAGAGGCTGATATA 477
QY 157 MetIleAlaPheArgThrArgValHisGlyArg--CysProArgTyrPheAspGlyPro 175
Db 478 ATGATCTCTTTTGGCAGTAGAGACATGGAGACTTTTACCT-----TTTGATGGACCT 531
QY 176 LeuGlyValLeuGlyHisAlaPheProGlyProGlyLeuGlyGlyAspThrHisPhe 195
Db 532 GGAATGCTTTTGGCCCATGCTATGCTCCCTGGCCAGGGATTAAATGAGATGCCACTTT 591
QY 196 AspGluAspGluAsnTrpThrLysAspGlyAlaGlyPheAsnLeuPheLeuValAlaAla 215
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QY 236 ProAsnTyrValSerLeu---AspProArgLysTyrProLeuSerGlnAspAspIleAsn 254
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Db 892 GCTGTCAGCACTCTGAGGGGAGAAATCCTGATCTTTAAAGACAGGCACTTTTGGCGCAA 951
QY 307 TyrTyrAspIleThrAspValGluPheGluLeuIleAlaSerPheTrpProSerLeuPro 326
Db 952 TCCCTCAGGAAGCTTGAACCTGAATTGCAATTGATCTCTCATTTTGGCCATCTCTCCT 1011
QY 327 AlaAspLeuGlnAlaAlaTyrGlu---AsnProArgAspLysIleLeuValPheLysAsp 345
Db 1012 TCAGCGGTGATGCCGCAATATGAGTTACTACGAGGACCTCGTTTTCATTTTAAAGGA 1071
QY 346 GluAsnPheTrpMetIleArgGlyTyrAlaValLeuProAspTyrProLysSerIleHis 365
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QY 366 ThrLeuGlyPheProGlyArgValLysIleAspAlaAlaValCysAspLysThrThr 385
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QY 386 ArgLysThrTyrPhePheValGlyIleTrpCysTrpArgPheAspGluMetThrGlnThr 405
Db 1192 AACAAACATATTTCTTTGAGAGCAAAATCTCGAGATTGATGAGAGAGAAATCC 1251
QY 406 MetAspLysGlyPheProGlnArgValLysHisPheProGlyIleSerIleArgVal 425
Db 1252 ATGGAGCCAGGCTTTCCCAAGCAAAATAGCTGAAGACTTTCCAGGGATTGACTCAAGATT 1311
QY 426 AspAlaAlaPheGlnTyrLysGlyPhePhePheSerArgGlySerLysGlnPheGlu 445
Db 1312 GATGCTGTTTGAAGAAATTTGGGTCTTTTATTTTCTTTACTGGATCTTCACAGTTGGAG 1371
QY 446 TyrAsnIleLysThrLysAsnIleThrArgIleMetArgThrAsnThrTrpPheGlnCys 465
Db 1372 TTGACCCCAATGCCAAGAAAGTGACACACACTTTGAAGAGTAAACAGCTGGCTTAATTGT 1431

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: November 15, 2004, 20:52:31 ; Search time 27 seconds
(without alignments)
1828.118 Million cell updates/sec

Title: US-10-729-807-10

Perfect score: 2763

Sequence: 1 MKRLLLCLEFFITFSSAFPL.....SLSLFIFGVHLKNTSIYQ 513

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : PIR 79:*

1: pir1:*

2: pir2:*

3: pir3:*

4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1271.5	46.0	478	1 KCRBS1	stromelysin 1 (EC
2	1250	45.2	477	1 KCHUS1	stromelysin 1 (EC
3	1243.5	45.0	476	1 JC6505	stromelysin 2 (EC
4	1234	44.7	476	1 KCHUS2	stromelysin 2 (EC
5	1233	44.6	477	1 KMSS1	stromelysin 1 (EC
6	1205	43.6	469	1 KCPGI	interstitial colla
7	1198.5	43.4	476	1 KRTS2	stromelysin 2 (EC
8	1177.5	42.6	469	1 KCB01	interstitial colla
9	1170.5	42.4	468	1 KCB01	interstitial colla
10	1169	42.3	475	1 KRTIH	stromelysin 1 (EC
11	1161.5	42.0	469	1 KCHUI	interstitial colla
12	1161	42.0	467	1 KCHUI	interstitial colla
13	1141	41.3	471	2 A53711	stromelysin 1 (EC
14	1133	41.0	470	2 A49499	neutrophil colla
15	1126	40.8	466	2 A23685	collagenase 3 (EC
16	1117	40.4	472	2 S29243	interstitial colla
17	1020.5	36.9	462	2 A24241	interstitial colla
18	1002.5	36.3	484	2 JC5743	macrophage elastase
19	798	28.9	384	2 I51267	stromelysin 1 (EC
20	797	28.8	660	1 A28153	collagenase (EC 3
21	790	28.6	662	2 A24246	gelatinase A (EC 3
22	790	28.6	662	2 S34780	gelatinase A (EC 3
23	783	28.3	662	2 S70365	gelatinase A (EC 3
24	769.5	27.9	663	1 S46492	gelatinase A (EC 3
25	715.5	25.9	669	2 I38029	gelatinase A (EC 3
26	713	25.8	582	2 I38028	matrix metallopro
27	698	25.3	582	2 I84471	matrix metallopro
28	667	24.1	582	2 I48673	matrix metallopro
29	626.5	22.7	712	1 I46031	gelatinase B (EC 3

ALIGNMENTS

RESULT 1

KCRBS1

stromelysin 1 (EC 3.4.24.17) precursor - rabbit

N:Alternate names: collagenase activating protein; matrix metalloproteinase 3 (MMP3); pro

C:Species: Oryctolagus cuniculus (domestic rabbit)

C>Date: 30-Sep-1992 #sequence_revision 30-Sep-1992 #text_change 09-Jul-2004

C:Accession: A37306; A29157

R:Finl, M.E.; Karmilowicz, M.J.; Ruby, P.L.; Beeman, A.M.; Borges, K.A.; Brinckerhoff, C.

Arthritis Rheum. 30, 1254-1264, 1987

A:Title: Cloning of a complementary DNA for rabbit proactivator. A metalloproteinase tha

ed with collagenase.

A:Reference number: A37306; MUID:88077214; PMID:2825726

A:Accession: A37306

A:Molecule type: mRNA

A:Residues: 1-478 <PIN>

A:Cross-references: UNIPROT:P28863; GB:M25664; NID:G165709; PIDN:AAA31467.1; PID:G165710

R:Whitham, S.E.; Murphy, G.; Angel, P.; Rahmsdorf, H.J.; Smith, B.J.; Lyons, A.; Harris,

Biochem. J. 240, 913-916, 1986

A:Title: Comparison of human stromelysin and collagenase by cloning and sequence analysis

A:Reference number: A90336; MUID:87156645; PMID:3030290

A:Accession: A29157

A:Status: nucleic acid sequence not shown; not compared with conceptual translation

A:Molecule type: mRNA

A:Residues: 1-82,'D',84-127,'K',129-167,'GNS', <WHI>

C:Comment: This enzyme degrades various extracellular matrix proteins, including fibron

C:Comment: Stromelysin 1 hydrolyzes peptide bonds in plasminogen to yield a fragment with

C:Comment: Stromelysin 1 activates its proenzyme after cleavage(s) within the activation

C:Comment: Stromelysin is found in glycosylated and unglycosylated forms, both of whi

C:Function:

A:Description: endopeptidase preferentially hydrolyzing peptide bonds on the carboxyl sid

C:Superfamily: interstitial collagenase; hemopexin repeat homology; matrix metalloprotei

C:Keywords: calcium; extracellular matrix; fibroblast; glycoprotein; hydrolase; metallo

F:1-17/Domain: signal sequence #status predicted <SG>

F:18-478/Product: prostromelysin 1 #status predicted <PRO>

F:18-100/Domain: activation peptide #status predicted <ACT>

F:61-265/Domain: matrix metalloproteinase homology <MMP>

F:91-98/Region: autoinhibitory

F:101-478/Product: stromelysin 1 #status predicted <MAT>

F:285-478/Domain: hemopexin repeat homology <PXN>

F:93,219,223,229/Binding site: zinc, catalytic (Cys, His, His) (inhibited) #status p

F:121/Binding site: carbohydrate (Asn) (covalent) #status predicted

F:219,223,229/Binding site: zinc, catalytic (His) (active) #status predicted

F:220/Active site: Glu #status predicted

F:291-478/Disulfide bonds: #status predicted

Query Match 46.0%; Score 1271.5; DB 1; Length 478;

Best Local Similarity 51.9%; Pred. No. 2.3e-95;

Matches 250; Conservative 75; Mismatches 136; Indels 21; Gaps 9;

Qy 1 MKRLLLCLEFFITFSSAFPLVRMTENE--NMQLAQYLNQFYSLTEGHNHLSVSKNRS 58

Db 1 MKTLPTLLLCVALCSAYPLDGASRDATTNMDLLQYLENYNLEKDVQFVKRKDSSP 60

A,Molecule type: protein
A,Residues: 18-29<P100-108 <LAR>
R,R,Koklitis, P.A.; Murphy, G.; Sutton, C.; Angal, S.
Biochem. J. 276, 217-221, 1991
A,Title: Purification of recombinant human prostromelysin
A,Reference number: S15427; MUID:91248150; PMID:2039471
A,Accession: S15427
A,Status: preliminary
A,Molecule type: protein
A,Residues: 18-23 <BIO>
R,Linen, H.R.; Ugwu, F.; Bini, A.; Collen, D.
Biochemistry 37, 4699-4702, 1998
A,Title: Generation of an angiotensin-like fragment from
A,Reference number: A58612; MUID:9548733; PMID:9548733
A,Contents: annotation
R,Becker, J.W.
submitted to the Brookhaven Protein Data Bank, February
A,Reference number: A68466; PDB:1HFS
A,Contents: annotation; X-ray crystallography, 1.70 ang.
R,Becker, J.W.; Marcy, A.I.; Rokosz, L.L.; Axel, M.G.;
Protein Sci. 4, 1966-1976, 1995
A,Title: Stromelysin-1: three-dimensional structure of
A,Reference number: A58814; MUID:96117647; PMID:8535233
A,Contents: annotation; X-ray crystallography, 1.70 ang.
R,Marcy, A.I.; Eiberger, L.L.; Harrison, R.; Chan, H.K.
Biochemistry 30, 6476-6483, 1991
A,Title: Human fibroblast stromelysin catalytic domain:
A,Reference number: A39589; MUID:91274298; PMID:1647201
A,Contents: annotation
R,Becker, J.W.
submitted to the Brookhaven Protein Data Bank, August 1
A,Reference number: A66637; PDB:1ISM

RESULT 2
KCHUS1
stromelysin 1 (EC 3.4.24.17) precursor [validated] - human
N;Alternate names: angioctatin-converting enzyme; collagenase activating protein; matrix
C;Species: Homo sapiens (man)
C;Date: 30-Sep-1992 #sequence_revision 08-May-1998 #text_change 09-Jul-2004
C;Accession: A32156; C29157; A28399; A60964; S15427
R;Saus, J.; Quinones, S.; Otani, Y.; Nagase, H.; Harris Jr., E.D.; Kurkinen, M.
J. Biol. Chem. 263, 6742-6745, 1988
A;Title: The complete primary structure of human matrix metalloproteinase-3. Identity wi
A;Reference number: A32156; PMID:88198243; PMID:3360803

A:Reference number: A67284; PDB:2SRT
A:Contents: annotation; conformation by (1)H-NMR, residues
R;Gooley, P.R.; Johnson, B.A.; Marcy, A.I.; Cuca, G.C.; Sa-
Biochemistry 32, 13098-14008, 1993
A:Title: Secondary structure and zinc ligation of human re-
A:Reference number: A58815; MUID:94059987; PMID:8241164
A:Contents: annotation; conformation by (1)H-NMR
C:Comment: Stromelysin 1 activates its proenzyme after cle-
C:Comment: Prostromelysin is found in glycosylated and ung-
C:Genetics:
A:Gene: GDB:MMP3; STM1; STM11
A:Cross-references: GDB:120727; OMIM:185250
A:Map position: 11q23-11q23
C:Function:
A:Description: endopeptidase preferentially hydrolyzing pep-
A:Note: degrades various extracellular matrix proteins, in-
plasminogen to yield a fragment with angiotensin activity
C:Superfamily: interstitial collagenase; hemopexin repeat
C:Keywords: calcium; extracellular matrix; fibroblast; gly-
P:1-17/Domain: signal sequence #status predicted <SIG>
P:18-477/Product: prostromelysin 1 #status experimental <P>
P:18-99/Domain: activation peptide #status experimental <A>
P:160-264/Domain: matrix metalloproteinase homology <MMP>
P:100-477/Product: stromelysin 1 #status experimental <MAT>
P:284-477/Domain: hemopexin repeat homology <PN>
P:92,218,222,228/Binding site: zinc, catalytic (Cys, His,
P:120/Binding site: carbohydrate (Asn) (covalent) #status
P:218,222,228/Binding site: zinc, catalytic (His) (active)
P:219/Active site: Glu #status predicted
P:290-477/hisulfide bonds: #status predicted

A,Cross-references: GB:U78045; NID:gl688257; PIDN:AA36942.1.1; PID:gl688259
A,Cross-references: GB:U78045; NID:gl688257; PIDN:AA36942.1.1; PID:gl688259
A>Note: part of the sequence, including the amino end of the proenzyme, was confirmed by
R;Lark, M.W.; Walakovits, L.A.; Shah, T.K.; Vanmiddlesworth, J.; Cameron, P.M.; Lin, T.Y.
Connect. Tissue Res. 25, 49-65, 1990
A,Title: Production and purification of prostromelysin and procollagenase from IL-1 beta
A,Reference number: A60964; MUID:91059606; PMID:2173990
A,Accession: A60964

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Db      1  MKSLPIILLLCVAVCSAYPLDGAAGDTSNNLYQKYLENYDLKDVQKQVVRKDSGPV 60
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QY      117  NYTPDMARAAVDAIBAQGLEVSWKVTPLKFTKTSKGIADIMIAPIRTRVHGRCPRY-FDGP 175
Db      120  NYTPDLPKDAVDAVEKALKVWEVTLTFSRLYEGADIMISFAVREHG--DFYPDPGP 177
QY      176  LGVLGHAFPPGGLGGDTHFEDENWTKGAGNLFVAAHFGHAGLGLSHNDQATLMF 235
Db      178  GNSLAHAYAPGPGINGDAHDDDEQMTKDTGTGNLFVAAHFGHAGLGLSHSANTALMY 237
QY      236  PNVVSL-DRPKYPLSODDINGIISYG-----GLPKVPK--PKETIPIHACDPLTFD 286
Db      238  PLYHSLTDLTRFLSODDINGISLYGPPDPSPETPLVPTPEPPPGTTPANCDPALSFD 297
QY      287  AITTFREVMFFKGRHLWRIYYIDTVEFEELIASFWPSPADLQAAVE-NPRDKILVFKD 345
Db      298  AVSTLRGEILFKDRHFWKSLRKLPELHLISSFWPSPGVDAAYEVTSKDLVIFKG 357
QY      346  ENFMWIRGAVLDPDYKPSIHTLFGPGRVKKIDAACVCKTKRKYFFVGVGWCWFDEMTQT 405
Db      358  NOFWAIRGNEVAGYPRGIHTLFGPPTVRKIDAAISDKKKNKYFFVGVGWCWFDEKRS 417
QY      406  MDKGFQPVVVKHPPGISIRVDAFAQYKGFPPFSGSKQFENYKTKNITRIMTNTWFOC 465
Db      418  MBPGPKQIAEDPPGIDSKIDAVEFEFGFYFTGSSQLEFDPNAKKVTHLTKNSWLNC 477

RESULT 3
JC6505
stromelysin 2 (EC 3.4.24.22) precursor - mouse
N:Alternate names: matrix metalloproteinase 10
C:Species: Mus musculus (house mouse)
C>Date: 16-Oct-1998 #sequence_revision 16-Oct-1998 #text_change 09-Jul-2004
C:Accession: J06505
R:Madlener, M.; Werner, S.
Gene 202, 75-81, 1997
A:Title: cDNA cloning and expression of the gene encoding murine stromelysin-2 (MMP-10).
A:Reference number: J06505; MUID:98087420; PMID:9427548
A:Accession: J06505
A:Molecule type: mRNA
A:Residues: 1-476 <MAD>
A:Cross-references: UNIPROT:O5123; GB:Y13185; NID:92791311; PIDN:CAA73641.1; PID:927913
C:Comment: This enzyme degrades various extracellular matrix proteins, including fibronectin.
C:Genetics:
A:Gene: MMP-10
C:Superfamily: interstitial collagenase; hemopexin repeat homology; matrix metalloproteinase
C:Keywords: calcium; extracellular matrix; fibroblast; glycoprotein; hydrolase; metalloproteinase
F:18-476/Product: prostromelysin 2 #status predicted <PRO>
F:18-99/Domain: activation peptide #status predicted <ACT>
F:60-264/Domain: matrix metalloproteinase homology <MMP>
F:90-97/Region: autoinhibitory
F:100-476/Product: stromelysin 2 #status predicted <MAT>
F:120-476/Domain: hemopexin repeat homology <PXN>
F:120/Binding site: zinc, catalytic (Cys, His, His) (inhibited) #status predicted
F:218,222,228/Binding site: zinc, catalytic (His) (active) #status predicted
F:219/Active site: Glu #status predicted
F:289-476/Disulfide bonds: #status predicted

Query Match 45.0%; Score 1243.5; DB 1; Length 476;
Best Local Similarity 50.8%; Pred. No. 4.3e-93;
Matches 244; Conservative 77; Mismatches 140; Indels 19; Gaps 9;

QY      1  MKRLILCLFITTSAPPL-VRMTENEENMOLAQVLYNQVSLIEGHNHVLQSKNRLI 59
Db      1  MEPLAILALLSLPCISAVPLHGAVTQGHPSMDLAQQYLEKYNFKNKQKIFKRDSSPV 60
QY      60  DDKIREMQAFGLVTGKLDNTLEIMKTRCGVDPVQGYTILPG---WRKYNLTVRII 116

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Db      61  VKKIREMQKFLGLEMTGKLDNTLMELMHKPRCGVDPVGGFS-TTPGSPKWKSHITVRII 119
QY      117  NYTPDMARAAVDAIBAQGLEVSWKVTPLKFTKTSKGIADIMIAPIRTRVHGRCPRY-FDGP 175
Db      120  NYTPDLPRQSVDAIEKALKVWEVTLTFSRISGEADIMISFAVGEHG--DFYPDPGP 177
QY      176  LGVLGHAFPPGGLGGDTHFEDENWTKGAGNLFVAAHFGHAGLGLSHNDQATLMF 235
Db      178  GNSLAHAYAPGPGFYGDVHFDDEKWTLPASGTLNLFVAAHFGHAGLGLSHSDDKESIMY 237
QY      236  PNV-LSLDRPKYPLSODDINGIISYG-----LPKVPKPKETIPIHACDPLTFD 286
Db      238  PVTFRSTSPANFHLSDQDIEGISOGLYAGFSSDATVVPVLSVSPR-PETPDKCDPALSFD 296
QY      287  AITTFREVMFFKGRHLWRIYYIDTVEFEELIASFWPSPADLQAAVE-NPRDKILVFKD 345
Db      297  SVSTLRGEVLFFKDRYFWRSHWNPEPEHLISAFWPTLPSPDLDAAAYEAHNTOSVLIKFG 356
QY      346  ENFMWIRGAVLDPDYKPSIHTLFGPGRVKKIDAACVCKTKRKYFFVGVGWCWFDEMTQT 405
Db      357  SQFWAVRGNEVQAGYKGIHTLFGPPTVKKIDAAVEKEKKKYFFVGVGWCWFDETRHV 416
QY      406  MDKGFQPVVVKHPPGISIRVDAFAQYKGFPPFSGSKQFENYKTKNITRIMTNTWFOC 465
Db      417  MDKGFPRQITDDFPGLIEPQVDVLFHEFGFYFPRGSSQFEEDFNARTVTHLTKNSWLLC 476

RESULT 4
KCHUS2
stromelysin 2 (EC 3.4.24.22) precursor [validated] - human
N:Alternate names: matrix metalloproteinase 10 (MMP10); transin-2
C:Species: Homo sapiens (man)
C>Date: 30-Sep-1992 #sequence_revision 30-Sep-1992 #text_change 09-Jul-2004
C:Accession: A28816; A47496
R:Muller, D.; Quantin, B.; Geanel, M.C.; Millon-Collard, R.; Abecassis, J.; Breathnach, J.;
Biochem. J. 253, 187-192, 1988
A:Title: The collagenase gene family in humans consists of at least four members.
A:Reference number: A90339; MUID:8839885; PMID:2844164
A:Accession: A28816
A:Molecule type: mRNA
A:Residues: 1-476 <MUL>
A:Cross-references: UNIPROT:P09238; EMBL:X07820; NID:936628; PIDN:CAA30679.1; PID:936629
A:Note: mRNA for this protein was detected in several human tumors
R:Windsor, L.J.; Grenett, H.; Birkedal-Hansen, B.; Bodden, M.K.; Engler, J.A.; Birkedal-
J. Biol. Chem. 268, 17341-17347, 1993
A:Title: Cell type-specific regulation of SL-1 and SL-2 genes. Induction of the SL-2 gene
A:Reference number: A47496; MUID:93352520; PMID:8349617
A:Accession: A47496
A:Molecule type: protein
A:Residues: 17-33 <WIN>
C:Comment: This enzyme degrades various extracellular matrix proteins, including fibronectin.
C:Genetics:
A:Gene: GDB:MMP10; STWY2
A:Cross-references: GDB:120392; OMIM:185260
A:Map position: 11q22.3-11q23
C:Superfamily: interstitial collagenase; hemopexin repeat homology; matrix metalloproteinase
C:Keywords: calcium; extracellular matrix; fibroblast; glycoprotein; hydrolase; metalloproteinase
F:11-16/Domain: signal sequence #status predicted <SIG>
F:17-476/Product: prostromelysin 2 #status experimental <PRO>
F:17-98/Domain: activation peptide #status predicted <ACT>
F:59-263/Domain: matrix metalloproteinase homology <MMP>
F:89-96/Region: autoinhibitory
F:99-476/Product: stromelysin 2 #status predicted <MAT>
F:99-476/Domain: hemopexin repeat homology <PXN>
F:91,217,221,227/Binding site: zinc, catalytic (Cys, His, His) (inhibited) #status predicted
F:119/Binding site: carboxydrate (Asn) (covalent) #status predicted
F:217,221,227/Binding site: zinc, catalytic (His) (active) #status predicted
F:218/Active site: Glu #status predicted
F:289-476/Disulfide bonds: #status predicted

Query Match 44.7%; Score 1234; DB 1; Length 476;
Best Local Similarity 51.4%; Pred. No. 2.5e-92;

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C:Superfamily: interstitial collagenase; hemopexin repeat homology; matrix metalloproteinase; extracellular matrix; fibroblast; glycoprotein; hydrolase; metalloproteinase; signal sequence #status predicted <SIG>
F;1-17/Domain: signal sequence #status predicted <SIG>
F;18-477/Product: prostromelysin 1 #status predicted <PRO>
F;18-99/Domain: activation peptide #status predicted <ACT>
F;60-264/Domain: matrix metalloproteinase homology <MMP>
F;90-97/Region: autoinhibitory
F;100-477/Product: stromelysin 1 #status predicted <MAT>
F;284-477/Domain: hemopexin repeat homology <PXN>
F;92,218,222,228/Binding site: zinc, catalytic (Cys, His, His) #status predicted
F;218,222,228/Binding site: zinc, catalytic (His) (active) #status predicted
F;219/Active site: Glu #status predicted
F;290-477/Disulfide bonds: #status predicted

Query Match 44.6%; Score 1233; DB 1; Length 477;
Best Local Similarity 51.0%; Pred. No. 3e-92;
Matches 245; Conservative 72; Mismatches 145; Indels 18; Gaps 9;

QY 1 MKRLLLCLFFITFSSAPFLVRMTENEE-NMOLAQAYLNQFYSLEIEGHNHVSQKNSLI 59
DB 1 MKGLPVLLMLCVVSSYPLHDSARDGAGWELLQKYLENYGLAKDVQKFIKKDSSLI 60
QY 60 DDKIREMQAFGLTVTKLDSNTLEIMKTGRCGVPDVGQYGLPG--WRKYNLTYYII 116
DB 61 VKKIQEMQKFLGLEMTKGLDSNTMELMHKPRCGVPDVGGSF--TFPGSPKWRKSHITRIIV 119
QY 117 NYTPDMARAANDAIQGLVSWKVTPLKFTKISKGIADIMIAFRTVHGR-CPRYFDGP 175
DB 120 NYTPDLPRQVDSALEKALKVWEVTLTFSRISGEADIMISFAVGEHGFVFP--FDGP 177
QY 176 LGVLGHAFPPGPGGLGGDTHFDEENWTKDGAGFNLFVAHFEHGHALGLSHNSDQALMF 235
DB 178 GTVLAHAYAPGPGINGDAHFDDEDDERWTEVTGTLFLVAHGLHSLGLYHSAKAEALMY 237
QY 236 PNY-VSLDPRKPLSQDDINGIQSIYQ-----GLPKVPAPKPK-EPTIPHACDPLTFD 286
DB 238 PVYKSTDLGRFHLSDQDDVGIQSLYGTPTTASPDVLPVPTKNSLEPETSPMCSTLTFD 297
QY 287 AITTFREVPFPGKRLHRIYDITDVEFELIASFWSLPADLOAAYE-NPRDKILVFKD 345
DB 298 AVSTRGEVLFPKDRHWRKSLRTPPEFYLLISFWSLPSMDAAAYEVNTRDTVFIK 357
QY 346 ENFWIRGYAVLPDPYKSIHTLPGFRVKKIDAAVCDTKTKTKTYFFVGIWCRFDEMOT 405
DB 358 NQFWAIRGHEELAGYKPSIHTLGLPATVKKIDAAISNKEKTKTYFFVDEKWDKQKS 417
QY 406 MDKGFPPQVVKHFGIGIRVDAAYQYKGFPPFSRSGSKQFYNIKTKNITRMNTWFOC 465
DB 418 MEPGPRKIARDFFGVDSRVDVAFVFAFGFLYFFSGSSQLEEDPNAKKVTILKSNWFNC 477

RESULT 6
KCPGI
Interstitial collagenase (EC 3.4.24.7) precursor [validated] - pig
N:Alternate names: fibroblast collagenase; matrix metalloproteinase 1 (MMP1); tissue co
C:Species: Sus scrofa domestica (domestic pig)
C:Date: 30-Sep-1992 #sequence_revision 30-Sep-1992 #text_change 09-Jul-2004
C:Accession: S15986; S13597
R:Richards, C.D.; Rafferty, J.A.; Reynolds, J.J.; Saklatvala, J.
Matrix 11, 161-167, 1991
A:Title: Porcine collagenase from synovial fibroblasts: cDNA sequence and modulation of
A:Reference number: S15986; MUID:91333421; PMID:1651440
A:Accession: S15986
A:Status: not compared with conceptual translation
A:Molecule type: mRNA
A:Residues: 1-469 <RIC>
A:Cross-references: UNIPROT:P21692
A:Note: part of the sequence, including the amino end of the proenzyme, was confirmed
R:Clarke, N.J.; O'Hare, M.C.; Cawston, T.E.; Harper, G.P.
Nucleic Acids Res. 18, 6703, 1990
A:Title: Nucleotide sequence of a cDNA for porcine type I collagenase, obtained by PCR
A:Reference number: S13597; MUID:91067477; PMID:2174547
A:Accession: S13597

Matches 244; Conservative 77; Mismatches 136; Indels 18; Gaps 8;

QY 4 LLLLLCLFFITFSSAPFLVRMTENEE-NMOLAQAYLNQFYSLEIEGHNHVSQKNSLI 62
DB 7 LVLLCLL---PVCAYPLSGAAKEEDSKDLAQYLEKYNLEKDVQKF-RRKDSNLIVKK 62
QY 63 IREMQAFGLTVTKLDSNTLEIMKTGRCGVPDVGQY--TLPGWRKYNLTYYIIINYP 120
DB 63 IQGMQKFLGLEMTKGLDSNTLEIMKTGRCGVPDVGQY--TLPGWRKYNLTYYIIINYP 122
QY 121 DMARAANDAIQGLVSWKVTPLKFTKISKGIADIMIAFRTVHGR-CPRYFDGPGLVGL 180
DB 123 DLPRDAVDSAIKALKVWEVTLTFSRLYEGADIMISFAVGEHGF-YSPFGPHSLA 191
QY 181 HAPPPGGLGGDTHFDEENWTKDGAGFNLFVAHFEHGHALGLSHNSDQALMFNYS 240
DB 182 HATPPGGLYGDTHFDDDEKWTEDASCTNLFVAHGLHSLGLFHSANTEALMPLYSN 241
QY 241 L-DPRKPLSQDDINGIQSIYGLPKVPAPKPKPT-----IPHACDPLTFDAITTF 291
DB 242 FTLEAQRHLSDQDDVGIQSLYGTPTTASPDVLPVPTKNSLEPETSPMCSTLTFD 301
QY 292 RREVMFKGRHLRIYDITDVEFELIASFWSLPADLOAAYE-NPRDKILVFKDENFWM 350
DB 302 RGEYLFKDRYFWRSHWNPEPEPHLLISAFWPSLPSVLDRAAYEVNSRDTVFIKGNFWA 361
QY 351 IRGVAVLDPYKPSIHTLPGFRVKKIDAAVCDTKTKTKTYFFVGIWCRFDEMOTMOKGF 410
DB 362 IRGNEVQAGYRGHTLGLFPPTIRKIDAAVSDKKEKTKTYFAADKYKWRFDENSQMEQGF 421
QY 411 PORVVKHFGIGIRVDAAYQYKGFPPFSRSGSKQFYNIKTKNITRMNTWFOC 465
DB 422 PLLIADDFGVEPKVDVLAQFGFFYFFSGSQFEPDPNARMVTILKSNLWLC 476

RESULT 5
KCMSS1
stromelysin 1 (EC 3.4.24.17) precursor - mouse
N:Alternate names: collagenase activating protein; matrix metalloproteinase 3 (MMP3); p
C:Species: Mus musculus (house mouse)
C:Date: 30-Sep-1992 #sequence_revision 30-Sep-1993 #text_change 09-Jul-2004
C:Accession: JCI1476; S18867; B32963; S33139
R:Hammani, K.; Henriot, P.; Eeckhout, Y.
Gene 120, 321-322, 1992
A:Title: Cloning and sequencing of a cDNA encoding mouse stromelysin 1.
A:Reference number: JCI1476; MUID:93013057; PMID:1398148
A:Accession: JCI1476
A:Molecule type: mRNA
A:Residues: 1-477 <HAM>
A:Cross-references: UNIPROT:P28862; EMBL:X66402; NID:G296167; PID:G2961
A:Note: it is uncertain whether Met-1 is the initiator or whether translation is initia
R:Li, F.; Strange, R.; Saurer, S.; Niemann, H.; Friis, R.R.
submitted to the EMBL Data Library, August 1991
A:Reference number: S18867
A:Accession: S18867
A:Molecule type: mRNA
A:Residues: 'MK', 1-477 <HIF>
A:Cross-references: EMBL:X631162; NID:G54871; PID:CAA44860.1; PID:G54872
R:Brenner, C.A.; Adler, R.R.; Rappolee, D.A.; Pedersen, R.A.; Werb, Z.
Genes Dev. 3, 848-859, 1989
A:Title: Genes for extracellular matrix-degrading metalloproteinases and their inhibitor
A:Reference number: A32963; MUID:89306621; PMID:2744464
A:Accession: B32963
A:Status: nucleic acid sequence not shown; not compared with conceptual translation
A:Molecule type: mRNA
A:Residues: 415-467, 'T', 469 <BRE>
A:Experimental source: clone EMS-2
C:Comment: Stromelysin 1 activates its proenzyme after cleavage(s) within the activation
C:Comment: This enzyme degrades various extracellular matrix proteins, including fibron
C:Comment: Stromelysin 1 hydrolyzes peptide bonds in plasminogen to yield a fragment wi
C:Comment: Prostromelysin is found in glycosylated and unglycosylated forms, both of whi
C:Function:
A:Description: endopeptidase preferentially hydrolyzing peptide bonds on the carboxyl s

[illegible]

Tue Nov 16 16:10:23 2004

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356 GSQFNAVRNEVOAGVPKRIHLGFPPTVKIDAAVFEKKEKKTYFFVGDKYWRFDTRQ 415
405 TMDKGFQPVVHFFPGISIRVDAAFQYKGFPPFSRGSQFEXYNIKTNTIRMTNTRWFQ 464
416 LMDKGFRLITDDFGLEPQVDALHAFGFFYFCGSGQFEPDPNARTVTHTLKSNWLL 475
465 C 465
476 C 476

RESULT 8
KCRBI
interstitial collagenase (EC 3.4.24.7) precursor - bovine
N;Alternate names: fibroblast collagenase; matrix metalloproteinase 1 (MMP1); tissue col
C;Species: Bos primigenius taurus (cattle)
C;Date: 30-Sep-1992 #sequence_revision 30-Sep-1992 #text_change 09-Jul-2004
C;Accession: S14654; S20336; S14655
R;Tamura, M.; Shimokawa, H.; Sasaki, S.
submitted to the EMBL Data Library, March 1991
A;Reference number: S14654
A;Accession: S14654
A;Molecule type: mRNA
A;Residues: 1-469 <TAM>
A;Cross-references: UNIPROT:P28053; EMBL:X50256; NID:Q259; PIDN:CAAA1210.1; PID:Q260
R;Sudbeck, B.D.; Jeffrey, J.J.; Welgus, H.G.; Mecham, R.P.; McCourt, D.; Parks, W.C.
Arch. Biochem. Biophys. 293, 370-376, 1992
A;Title: Purification and characterization of bovine interstitial collagenase and tissue
A;Reference number: S20336; MUID:92161820; PMID:1311165
A;Accession: S20336
A;Molecule type: protein
A;Residues: 19-21, 'FP', 24-29, 'L', 31-34, 'LL', 37-39, 'F', 96-105, 'NPR', 109-112, 'D', 114-125 <
C;Comment: This enzyme cleaves collagens of types I, II, and III at a Gly-Ile site in th
C;Comment: Procollagenase can be activated without removal of the activation peptide. Su
tion peptide by other proteinases.
C;Comment: Procollagenase is found in glycosylated and unglycosylated forms, both of whi
C;Description: hydrolyzes collagens, in particular types I, II, III, and X, serpins, and
C;Superfamily: interstitial collagenase; hemopexin repeat homology; matrix metalloprote
C;Keywords: calcium; extracellular matrix; fibroblast; glycoprotein; hydrolase; metallo
F;1-18/Domain: signal sequence #status predicted <SIG>
F;19-469/Product: procollagenase #status predicted <PRO>
F;19-99/Domain: activation peptide #status predicted <ACT>
F;60-261/Domain: matrix metalloproteinase homology <MMP>
F;90-97/Region: autoinhibitory
F;100-469/Product: interstitial collagenase #status predicted <MAT>
F;272-466/Domain: hemopexin repeat homology <PXN>
F;92,216,222,228/Binding site: zinc, catalytic (Cys, His, His) (inhibited) #status
F;120,143/Binding site: carboxylate (Asn) (covalent) #status predicted
F;218,222,228/Binding site: zinc, catalytic (His) (active) #status predicted
F;219/Active site: Glu #status predicted
F;278-466/Disulfide bonds: #status predicted

Query Match 42.6%; Score 1177.5; DB 1; Length 469;
Best Local Similarity 50.2%; Pred. No. 9.7e-88;
Matches 238; Conservative 74; Mismatches 149; Indels 13; Gaps 9;

QY 1 MKRL-LLLCLFFITSSAPFLVRMTENERNMQALYLNQFYSLBIEGHLVQSNRSLI 59
DB 1 MRLPLLLLLLWGTGSHGFPATSETQEQDVETVKVLYNLYNSNGKVRQRNGGLI 60
QY 60 DKIREMQAFGLTVTKGLDSNTLEMTKPRCGVDPVGYGYTLPG---WRKYNLTYRII 116
DB 61 TEKLKMQKFFGLRVTKGPDATFLNMQKPRCGVDPVAPVLT-PKSKSWENTNLTYLE 119
QY 117 NYPEDMARAAVDEAIOGLEVWSKVTPLKFTKISKIGIADIMIAFRTRVHRCRPFYDGPL 176
DB 120 NYPEDLUSRADVDQAIKAKQLNSNVTLFTTKVSEQADIMISF-VRGDHRDNPDPGPG 178
QY 177 GVILGHAFPPGKGLGGTHFDEENWTQKAGFNLFVVAHEFGHALGLSHNDQTALMPF 236
DB 179 GNLAHAFQGAGIGGDAHFDDDEWWTSNFQDYNLYRVAHEFGHSLGHAHSTDIGALMYP 238

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RESULT 9

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KCRBI
interstitial collagenase (EC 3.4.24.7) precursor - rabbit
N;Alternate names: fibroblast collagenase; matrix metalloproteinase 1 (MMP1); tissue col
C;Species: Oryctolagus cuniculus (domestic rabbit)
C;Date: 30-Sep-1992 #sequence_revision 30-Sep-1992 #text_change 09-Jul-2004
C;Accession: A27500; B27500; I46694
R;Finii, M.E.; Plucinska, I.M.; Mayer, A.S.; Gross, R.H.; Brinckerhoff, C.E.
Biochemistry 26, 6156-6165, 1987
A;Title: A gene for rabbit synovial cell collagenase: member of a family of metallopro
A;Reference number: A27500; MUID:88077876; PMID:2825772
A;Accession: A27500
A;Molecule type: mRNA
A;Residues: 1-468 <FTN>
A;Cross-references: UNIPROT:P13943; GB:M19240
A;Accession: B27500
A;Molecule type: DNA
A;Residues: 1-391,399-468 <PI2>
A;Cross-references: GB:M17820
A;Note: the location of the intron between exons 7 and 8 is approximate
R;Finii, M.E.; Austin, S.D.; Holt, P.T.; Ruby, P.L.; Gross, R.H.; White, H.D.; Brincker
Coll. Relat. Res. 6, 239-248, 1986
A;Title: Homology between exon-containing portions of rabbit genomic clones for synovia
A;Reference number: I46694; MUID:87029174; PMID:3021384
A;Accession: I46694
A;Status: translated from GB/EMBL/DBJ
A;Molecule type: mRNA
A;Residues: 449-468 <PI3>
A;Cross-references: GB:M25663; NID:G53121; PIDN:AAA31203.1; PID:G531212
C;Comment: This enzyme cleaves collagens of types I, II, and III at a Gly-Ile site in t
C;Comment: Procollagenase can be activated without removal of the activation peptide. S
tion peptide by other proteinases.
C;Comment: Procollagenase is found in glycosylated and unglycosylated forms, both of whi
C;Genetics:
A;Introns: 34/3, 116/2; 166/1; 208/1; 260/1; 299/2; 344/1; 398/1; 433/1
C;Function:
A;Description: hydrolyzes collagens, in particular types I, II, III, and X, serpins, an
C;Superfamily: interstitial collagenase; hemopexin repeat homology; matrix metalloproce
C;Keywords: calcium; extracellular matrix; fibroblast; glycoprotein; hydrolase; metallo
F;1-18/Domain: signal sequence #status predicted <SIG>
F;19-469/Product: procollagenase #status predicted <PRO>
F;19-98/Domain: activation peptide #status predicted <ACT>
F;59-260/Domain: matrix metalloproteinase homology <MMP>
F;89-96/Region: autoinhibitory
F;99-468/Product: interstitial collagenase #status predicted <MAT>
F;271-465/Domain: hemopexin repeat homology <PXN>
F;91,217,221,227/Binding site: zinc, catalytic (Cys, His, His) (inhibited) #status
F;119,142/Binding site: carboxylate (Asn) (covalent) #status predicted
F;217,221,227/Binding site: zinc, catalytic (His) (active) #status predicted
F;218/Active site: Glu #status predicted
F;277-465/Disulfide bonds: #status predicted

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Query Match 42.4%; Score 1170.5; DB 1; Length 468;
Best Local Similarity 50.4%; Pred. No. 3.6e-87;
Matches 237; Conservative 77; Mismatches 141; Indels 15; Gaps 10;

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QY 5 LLILCLPITTSASPFLVMTENEMNQLAQVLNQFYSLIEIENHNLVQSNNRSLIDDKIR 64
||| ||| ||| ||| : | : | : | : | : | : | : | : | : | :
Dd 6 LLLLLLGVGSHGFPAASETO-EQDVEMVKYLENYLNKDWKRKPQRKGNGLAVEKLK 64
||| ||| ||| ||| : | : | : | : | : | : | : | : | : | :
QY 65 EMQAFFGLTVTGKLDNTLEIMTKPRCGVPDVGQCYT--LPGRWKYNLTYYRIINTPDM 122
:||| ||| ||| ||| ||| : | : | : | : | : | : | : | : | : | :
Dd 65 QMQEFFGLKVTKEDPATLKMMKKPRCGVPDVAQFVLTPEGNPRWEQTHLYRIENTPD 124
:||| ||| ||| ||| ||| : | : | : | : | : | : | : | : | : | :
QY 123 ARAAVDAIOEGLEVSWKVTPLKETIKISGIADIAMIARFRVHGRCPRYFDGPLGVLGHA 182
:||| ||| ||| ||| ||| : | : | : | : | : | : | : | : | : | :
Dd 125 SRADVNAIEKAFLMSNVTELTFTKVSQGADIMISF-VRGDHDRNSDFDGEGOLAJA 183
:||| ||| ||| ||| ||| : | : | : | : | : | : | : | : | : | :
QY 183 FPPGPGLGDTHDEDENWTKOGAGFNLFVAAHEFGHALGSLHSNDQTALMPNPYV-SL 241
:||| ||| ||| ||| ||| : | : | : | : | : | : | : | : | : | :
Dd 184 FQPGLIGGGVDHFDEDRTWTDKFNNYLRYVAAAHLSGLSHSHTDIGALMYPNYWFSG 243
:||| ||| ||| ||| ||| : | : | : | : | : | : | : | : | : | :
QY 242 DPRKYPSLODDINGIOSIYGCLPKVPAKPKPTTPHACDPDLTFDAITTFRRREVMPFKGR 301
:||| ||| ||| ||| ||| : | : | : | : | : | : | : | : | : | :
Dd 244 DVQ---LAQDIIDIQAIIYP-SONSPQVPGFPQPVKVCDSKLTJFDAITTRGEIMFFKOR 299
:||| ||| ||| ||| ||| : | : | : | : | : | : | : | : | : | :
QY 302 HLWRI--YYIDITVFELIASFWPSLPADLQAAVE-NPRDKILPFKDENVIRGVAVLP 358
:||| ||| ||| ||| ||| : | : | : | : | : | : | : | : | : | :
Dd 300 FYMRANPYX--SEVELNFISVFPHPLNGLQAAEVAHRDELIFPKGKNYWTVOQNELP 357
:||| ||| ||| ||| ||| : | : | : | : | : | : | : | : | : | :
QY 359 DYPKSTH-TLGPGRVKKIDAADCCKTRKTYYFFVGMWCRFDEMTQMDKGFQRPVRKH 417
:||| ||| ||| ||| ||| : | : | : | : | : | : | : | : | : | :
Dd 358 GYPKDIHSSFGFPSRNHNIDAASEEDTGTGYFFVANKYRWYDEYKRSMDAGYPMKIYD 417
:||| ||| ||| ||| ||| : | : | : | : | : | : | : | : | : | :
QY 418 PFGISRVDAAFOYKGFEPFSRGSQFEYNLIKTNITRMETNTWFQCKE 467
:||| ||| ||| ||| ||| : | : | : | : | : | : | : | : | : | :
Dd 418 PFIGNKVDVAFKOGFFYFHFGTRQYKFPDKRKRLTLQANSWFNCRK 467
:||| ||| ||| ||| ||| : | : | : | : | : | : | : | : | : | :
RESULT 10

KCRITH
stromelysin 1 (EC 3.4.24.17) precursor - rat
N;Alternate names: collagenase activating protein; matrix metalloproteinase 3 (MMP3); pr
C;Species: Rattus norvegicus (Norway rat)
C;Date: 13-Aug-1986 #sequence revision 13-Aug-1986 #text_change 09-Jul-2004
C;Accession: A00997; PS0150; S22767
R;Matrisian, L.M.; Glaichenhaus, N.; Gesnel, M.C.; Breathnach, R.
EMBO J. 4, 1435-1440, 1985
A;Title: Epidermal growth factor and oncogenes induce transcription of the same cellular
A;Reference number: A00997; PMID:85284930; PMID:3875482
A;Accession: A00997
A;Molecule type: mRNA
A;Residues: 1-475 <MA>
A;Cross-references: UNIPROT:P03957; GB:X02601; NID:g57460; PIDN:CAX26448.1; PID:g57461
R;Umenishi, F.; Yasumatsu, H.; Ashida, Y.; Yamauti, J.; Umeda, M.; Miyazaki, K.
J. Biochem. 108, 537-543, 1990
A;Title: Purification and properties of extracellular matrix-degrading metallo-proteinases
A;Reference number: PS0150; PMID:91154156; PMID:1963430
A;Molecule type: protein
A;Residues: 19-20,'X',22-28;'110-112','X',114-115,'X',117,'X',119;309-325 <UME>
R;Breathnach, R.; Matrisian, L.M.; Gesnel, M.C.; Staub, A.; Leroy, P.
Nucleic Acids Res. 15, 1139-1151, 1987
A;Title: Sequences coding for part of oncogene-induced transin are highly conserved in a
A;Reference number: A26403; PMID:87146421; PMID:3547333
A;Contents: annotation; introns
A;Note: Intron positions were determined by comparison of the previously reported cDNA s
R;Sanchez-Lopez, R.; Nicholson, R.; Gesnel, M.C.; Matrisian, L.M.; Breathnach, R.
J. Biol. Chem. 263, 11892-11899, 1988
A;Title: Structure-function relationships in the collagenase family member transin.
A;Reference number: S22767; PMID:88298869; PMID:2841336
A;Contents: annotation; active site; activation
A;Note: molecules with mutations in the autoinhibitory region showed a much increased te
A;Note: mutations of His-216, Glu-217, and His-226 inactivate the enzyme
R;Park, A.J.; Matrisian, L.M.; Kells, A.F.; Pearson, R.; Yuan, Z.; Navre, M.
J. Biol. Chem. 266, 1584-1590, 1991
A;Title: Mutational analysis of the transin (rat stromelysin) autoinhibitor region demor
A;Reference number: A43028; PMID:91107652; PMID:1988438
A;Contents: annotation; autoinhibitory region

A>Note: Arg-89 and Cys-92 are essential for maintaining latency
C:Comment: This enzyme degrades various extracellular matrix proteins, including fibronectin
C:Comment: Stromelysin 1 hydrolyzes peptide bonds in plasminogen to yield a fragment with latent fibrinolytic activity
C:Comment: Stromelysin 1 activates its proenzyme after cleavage(s) within the activation site
C:Comment: Prostromelysin is found in glycosylated and unglycosylated forms, both of which are essential for maintaining latency
C:Genetics: 33/3; 115/2; 165/1; 207/1; 262/1; 310/2; 355/1; 408/2; 443/1
A:Introns: 33/3; 115/2; 165/1; 207/1; 262/1; 310/2; 355/1; 408/2; 443/1
C:Function:
A:Description: endopeptidase preferentially hydrolyzing peptide bonds on the carboxyl side
C:Superfamily: interstitial collagenase; hemopexin repeat homology; matrix metalloproteinase
C:Keywords: calcium; extracellular matrix; fibroblast; glycoprotein; hydrolase; metalloproteinase
F:1-17/Domain: signal sequence #status predicted <SIG>
F:18-475/Product: prostromelysin 1 #status predicted <PRO>
F:18-97/Domain: activation peptide #status predicted <ACT>
F:58-262/Domain: matrix metalloproteinase homology <MMP>
F:88-95/Region: autoinhibitory
F:98-475/Product: stromelysin 1 #status predicted <MAT>
F:282-475/Domain: hemopexin repeat homology <PXN>
F:90,216,220,226/Binding site: zinc, catalytic (Cys, His, His) (inhibited) #status predicted
F:118/Binding site: carboxylate (Asn) (covalent) #status predicted
F:216,220,226/Binding site: zinc, catalytic (His) (active) #status predicted
F:217/Active site: Glu #status experimental
F:288-475/Disulfide bonds: #status predicted

Query Match 42.3%; Score 1169; DB 1; Length 475;
Best Local Similarity 49.1%; Pred. No. 4.8e-87;
Matches 235; Conservative 75; Mismatches 151; Indels 18; Gaps 8;

QY 1 MKRLLLCLFITPSSAPFLVRMTENEMQLAAYLNQFYLEIEGHLVQSKNRLSD 60
DB 1 MKGLPVLMLTAVCSSYPL-HGSEDAQMEVLQYLENYYLEKDVQFTKKDSSPVV 59
QY 61 DKIREMQAFLGTVTGKLDNTLEIMTKPRGVPDVGQGYTLPG---WRKYNLTIRIN 117
DB 60 KKIEMQKFLGLKMTGKLDNTLEIMTKPRGVPDVGQGYTLPG---WRKYNLTIRIN 118
QY 118 YTPDMARAANDAEIQEGLVSKVTPLKTKISKIGIADIMIAFRKRVHGR-CPRYFDG 176
DB 119 YTLDLPRESVDATLALRWEEVTPLTFSRISGEADIMISFAVEEHGDFTP--FDG 176
QY 177 GVLGHAPPGGLGDDTHFDENWTKDAGFNFLVAAHEFGHALGSHSNDOTALMPP 236
DB 177 MVLAAHAPGGTGDHAFDDDERWTDVGTNLFVAAHELGSLGLFHSANAALMYP 236
QY 237 NY-VSLDPRKXPLSQDDINGIQSYGGLPKVPAPKPEPTIPHACDPD-----LT 287
DB 237 VYKSTDLAPHLSDQDVGDLQSYGPTSPDVLVWPTKNSLDPELTPMCSALSFDA 296
QY 288 ITTFRVMPFKGRHLRIYYDITDVEFLIASFWPSLPADLQAAYE-NPRDKILVF 346
DB 297 VSTLRGVLFFKDRHFRKSLRTPPGFYLLISSFWPSLPNMDAAVEYTNDRTPIL 356
QY 347 NFWIRGYAVLPDYPKSIHILGPPGRVKKIDAAVCDKTRTKYTFVGLWCWFDM 406
DB 357 QIWAIRGHEELAGYPKSIHTLGLPETVQKIDAAISLKDQKTYFFVEDKFRF 416
QY 407 DKGPORVAKHFGCISLRVDAAFQYKGFPPFSRSGKQFEYNIKTIRMTWTWFO 465
DB 417 DPEPRKIAENFGIQTVDVAEFAFGFLYFFSGSSQLEFPDNPAGKVTILKSN 475

RESULT 11
KCHUI
N:Interstitial collagenase (EC 3.4.24.7) precursor [validated] - human
C:Species: Homo sapiens (man)
C:Date: 13-Aug-1986 #sequence revision 30-Sep-1992 #text change 09-Jul-2004
C:Accession: A37308; S22766; I56760; A00996; D29157; A44518; S06132; B0964; S10595; S53
R:Templeton, N.S.; Brown, P.D.; Levy, A.T.; Margulies, I.M.K.; Liotta, L.A.; Stetler-St
Cancer Res. 50, 5431-5437, 1990
A:Title: Cloning and characterization of human tumor cell interstitial collagenase.
A:Reference number: A37308; PMID:90352587; PMID:2167156
A:Accession: A37308

A.Status: preliminary
A.Molecule type: protein
A.Residues: 20-108 <SUZ>
R.R.Springman, E.B.; Angleton, E.L.; Birkedal-Hansen, H.; Van Wart, H.E.
Proc. Natl. Acad. Sci. U.S.A. 87, 364-368, 1990
A.Title: Multiple modes of activation of latent human fibroblast collagenase: evidence f
A.Reference number: A44517; MUID:90115977; PMID:2153297
A.Contents: annotation; disulfide bond; activation mechanism
F:Salowe, S.P.; Marcy, A.I.; Cuccia, G.C.; Smith, C.K.; Kopka, I.E.; Hagmann, W.K.; Hermes
Biochemistry 31, 4535-4540, 1992
A.Description: hydrolyzes collagens, in particular types I, II, III, and X, serpins, and
C:Superfamily: interstitial collagenase; hemopexin repeat homology; matrix metalloprote
C:Keywords: calcium; extracellular matrix; fibroblast; glycoprotein; hydrolase; metallo
F:1-19/Domain: signal sequence #status predicted <SIG>
F:20-469/Product: procollagenase #status experimental <PRO>
F:20-99/Domain: activation peptide #status experimental <ACT>
F:60-261/Domain: matrix metalloproteinase homology <MMP>
F:90-97/Region: autoinhibitory
F:100-469/Product: interstitial collagenase #status experimental <MAT>
F:272-466/Domain: hemopexin repeat homology <PNX>
F:92,218,222,228/Binding site: zinc, catalytic (Cys, His, His, His) (inhibited) #status
F:120,143/Binding site: carbohydrate (Asn) (covalent) #status predicted
F:218,222,228/Binding site: zinc, catalytic (His) (active) #status predicted
F:219/Active site: Glu #status predicted
F:269-270/Cleavage site: Pro-Ile (autolytic) #status experimental
F:278-466/Disulfide bonds: #status experimental

Query Match 42.0%; Score 1161.5; DB 1; Length 469;
Best Local Similarity 50.0%; Pred. No. 1, 9e-86;
Matches 234; Conservative 77; Mismatches 146; Indels 11; Gaps 8;

QY 5 LLLCLFFITPSSAPFLVRMTENBNMQALQAAYLNQFYSLIEGNHLVQSNNRSIIDDKIR 64
||| : | : || : || : || : || : || : || : || : || : || :
DB 7 LLLLLFWGVSHSPATLETQ-EQDVLDVGKYLEKYNLKNDRGQRVKRRNSGFVEKLK 65

QY 65 EMQAFLGLTVTKLDSNLTLEIMKTPCRGVDVGQGYT--LPGRWKYNLTTRIINYTPDM 122
||||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| :
DB 66 QMOEFFGLKVTKPDPAETLKVMQPRCGVPDVAQFVTUTEGNPREQHTLTRIENYTDEL 125
||||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| :

QY 123 ARAAVEDAIQGLEWWSKVTPLKFTEIKSGTIADTMIAFRTRVHGRCPPRYDFGPGLVLGHA 182
126 PRADVDAEKAQLMSNVTLPTFTKVSQGADIWISF-VRGDHSDNSPFDPGGCNLAHA 184

QY 183 FPGPGLGGDTHFDENDNTKGAGNFLFLVAAHFHGLGHSNDOTALMFNYV-SL 241
185 FQPGEIGGDAHFEDEDERWTNNFREYLHRVAAHELGHSLGSLSHDTDGALMYPSYTFSG 244

QY 242 DPRXYPLSODDIINGIOSLYGCLPKVBRAKEPTPHACDDPLTFDAITTFREVMVFKKR 301
245 DVQ---LAQQIDDIGIQAILY-GRSQNFPQIPGTQPKACDSKITFDAITTIGEWMFKDR 300

QY 302 HLMRIYYDTIDEPELIASFWPSLPADLOAQAE-NPRDKILVFKDENVFMRIrgvAVLPDY 360
301 FYMRTNIFYEVNELNFISVFWPOLPNGLEAAHYEFADRDEVFFFNGNKYWAWQGNLVHGY 360

QY 361 PKSTH-TLGPPGRVKKIDAADCRTTKTYTFVGIWCWFDEMCTMDKGRPQRVVXXPP 419
361 PKDIYSFGFPRTVKHIADAALSEENTGTYTFVANWKYRIDBKSMDDPGYPONTAHDP 420

QY 420 GISLRVDAAFQYGKFFFFSRGSKOPEYNIKNITRMINTTWFOCKE 467
||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| :

Db 421 GIGHKVDVAFMKDGFYFFHCTROYKFDPKTKRIITLQKANSWFNCRK 468

RESULT 12

KCHUN

neutrophil collagenase (EC 3.4.24.34) precursor [validated] - human

N;Alternate names: matrix metalloproteinase 8

C;Species: Homo sapiens (man)

C;Date: 30-Sep-1992 #sequence revision 30-Sep-1992 #text change 09-Jul-2004

C;Accession: A37073; A61175; B61175; A36230; S09680; S11026; S19576; S32527; S62

R;Hasty, K.A.; Pourmottabbed, T.F.; Goldberg, G.I.; Thompson, J.P.; Spiniella, D.G.; Steve

J. Biol. Chem. 265, 11421-11424, 1990

A;Title: Human neutrophil collagenase. A distinct gene product with homology to other ma

A;Reference number: A37073; MUID:90307647; PMID:2164002

A;Accession: A37073

A;Molecule type: mRNA

A;Residues: 1-467 <HAS>

A;Cross-references: UNIPROT:P22894; GB:J05556; NID:g180617; PIDN:AAA88021.1; PID:g180618

R;Devarajan, P.; Mookhtiar, K.; Van Wart, H.; Berliner, N.

Blood 77, 2731-2738, 1991

A;Title: Structure and expression of the cDNA encoding human neutrophil collagenase.

A;Reference number: A61175; MUID:91255696; PMID:1646048

A;Accession: A61175

A;Status: not compared with conceptual translation

A;Molecule type: protein

A;Residues: 1-31, 'I', '33-86, 'E', '88-467 <DEV>

A;Accession: B61175

A;Molecule type: protein

A;Residues: 263-264, 'X', '266-270, 'X', '272-273, 'X', '275, 'X', '277 <DE2>

R;Mallaya, S.K.; Mookhtiar, K.A.; Gao, Y.; Brew, K.; Dioszegi, M.; Birkedal-Hansen, H.; V

Biochemistry 29, 10628-10634, 1990

A;Title: Characterization of 58-kilodalton human neutrophil collagenase: comparison with

A;Reference number: A36230; MUID:91104978; PMID:2176876

A;Accession: A36230

A;Molecule type: protein

A;Residues: 'X', '86-87, 'X', '89-90, 'X', '92-97, 'X', '99-111, 'X', '113-120 <MAL>

R;Knaeuper, V.; Kraemer, S.; Reinke, H.; Tschesche, H.

Eur. J. Biochem. 189, 295-300, 1990

A;Title: Characterization and activation of procollagenase from human polymorphonuclear

A;Reference number: S09680; MUID:90249372; PMID:2159879

A;Accession: S09680

A;Molecule type: protein

A;Residues: 21-31, 'I', '33-39, 'I', '41-47, 'V', '49-53, 'I', '55-72, 'G', '74-86, 'E', '88-111, 'X', '113-1

A;Note: 67-lys was also found

R;Knaeuper, V.; Kraemer, S.; Reinke, H.; Tschesche, H.

Biol. Chem. Hoppe-Seyler 371, 733, 1990

A;Title: Corrigendum. Partial amino-acid sequence of human PMN leukocyte procollagenase.

A;Reference number: S11026; MUID:91000455; PMID:2169766

A;Note: original publication was Biol. Chem. Hoppe-Seyler 371(Suppl.), 295-304, 1990

A;Accession: S11026

A;Molecule type: protein

A;Residues: 21-31, 'I', '33-53, 'I', '55-72, 'G', '74-111, 'X', '113-140; 183-203, 'X', '205-209; 248-261

A;Note: 87-Glu was also found

R;Blaeser, J.; Knaeuper, V.; Osthus, A.; Reinke, H.; Tschesche, H.

Eur. J. Biochem. 202, 1223-1230, 1991

A;Title: Mercurial activation of human polymorphonuclear leucocyte procollagenase.

A;Reference number: S19576; MUID:92111500; PMID:1662606

A;Accession: S19576

A;Molecule type: protein

A;Residues: 69-103 <BL2>

R;Blaeser, J.; Triebel, S.; Reinke, H.; Tschesche, H.

FEBS Lett. 313, 59-61, 1992

A;Title: Formation of a covalent Hg-Cys-bond during mercurial activation of PMNL procoll

A;Reference number: S27225; MUID:93050220; PMID:1330697

A;Accession: S27225

A;Molecule type: protein

A;Residues: 68-103 <BLA>

R;Knaeuper, V.; Osthus, A.; DeClerck, Y.A.; Langley, K.E.; Blaeser, J.; Tschesche, H.

Biochem. J. 291, 847-854, 1993

A;Title: Fragmentation of human polymorphonuclear-leucocyte collagenase.

A;Reference number: S32527; MUID:93256897; PMID:8489511

A;Accession: S32527

A;Molecule type: protein

A;Residues: 100-112;263-276 <KN3>

R;Knaeuper, V.; Murphy, G.; Tschesche, H.

Eur. J. Biochem. 235, 187-191, 1996

A;Title: Activation of human neutrophil procollagenase by stromelysin 2.

A;Reference number: S62608; MUID:96202934; PMID:8631328

A;Accession: S62608

A;Molecule type: protein

A;Residues: 21-39, 'I', '41-47, 'V', '49-122 <KN4>

R;Stams, T.; Spurlino, J.C.; Smith, D.L.; Rubin, B.

submitted to the Brookhaven Protein Data Bank, January 1994

A;Reference number: A67078; PDB:1MNC

C;Contents: annotation; X-ray crystallography, 2.1 angstroms, residues 'G', '106-149, 'G', '1

R;Stams, T.; Spurlino, J.C.; Smith, D.L.; Wahl, R.C.; Ho, T.F.; Oronfleh, M.W.; Banks,

Nat. Struct. Biol. 1, 119-123, 1994

A;Title: Structure of human neutrophil collagenase reveals large S1' specificity pocket.

A;Reference number: A58274; MUID:95384762; PMID:7656015

C;Contents: annotation; X-ray crystallography, 2.1 angstroms, residues 'G', '106-149, 'G', '1

C;Comment: This protein is more highly glycosylated than interstitial collagenase and is

C;Genetics:

A;Gene: GDB:MMP8; CUG1

A;Cross-references: GDB:128173; OMIM:120355

A;Map position: 11q22.2-11q22.3

C;Function:

A;Description: hydrolyzes collagen types I, II, and III at Gly-Ile sites in collagenous

A;Note: Cleaves type I collagen most rapidly

C;Superfamily: interstitial collagenase; hemopexin repeat homology; matrix metalloprotei

F;1-20/Domain: signal sequence #status predicted <SIG>

F;21-467/Product: procollagenase #status predicted <PRO>

F;21-100/Domain: activation peptide #status experimental

F;59-262/Domain: matrix metalloproteinase homology <MMP>

F;89-96/Region: autoinhibitory

F;101-467/Product: neutrophil collagenase #status predicted <MAT>

F;273-464/Domain: hemopexin repeat homology <PN>

F;54,73,112,119,204,246/Binding site: carbohydrate (Asn) (covalent) #status predicted

F;73-74/Cleavage site: Asn-Val (autolytic) #status experimental

F;84-95/Cleavage site: Asp-Met (autolytic) #status experimental

F;91,217,221,227/Binding site: zinc, catalytic (Cys, His, His, His) (inhibited) #status

F;99-100/Cleavage site: Phe-Met (autolytic) #status experimental

F;167,169,182,195/Binding site: zinc, catalytic (His, Asp, His, His) #status experime

F;174,175,177,179,197,200/Binding site: calcium (Asp, Gly, Asn, Ile, Asp, Glu) #status e

F;217,221,227/Binding site: zinc, catalytic (His) (active) #status experimental

F;218/Active site: Glu #status predicted

F;262-263/Cleavage site: Gly-Leu (autolytic) #status experimental

F;279-464/Disulfide bonds: #status predicted

Query Match 42.0%; Score 1161; DB 1; Length 467;

Best Local Similarity 48.3%; Pred. No. 2.1e-86;

Matches 228; Conservative 71; Mismatches 157; Indels 16; Gaps 8;

QY 1 MKRLLLLCLFFITFSAPFLVRMTENEENWQLAQAYLNQFYSLTEGHNHVSQKNRSLID 60

Db 4 LKTLFLLLLHVVQISKAFP---VSSKKNKTKVDYLEKFLQPSNQVQSTRKNTNIV 60

QY 61 DKIREMQAFGLTVTKDLSNTLEIMKTPRCVPDVGQGYTL-----PCWRKYNLTYYII 116

Db 61 EKLKEMQRFGLNVTGKFNBEETLDMKKKPRCGVDSG--GFMLTPGNKWTNLTYYIR 118

QY 117 NYPDMAAAVDEAIOEGLEVMSKVTLKFTKISKIADIIMIAFRTRVHG-RCPRYFDGP 175

Db 119 NYTQLSAAEVRALKDFELWSVASPLIFTRISQGEADINIAFYQRDHGNSP--FDGP 176

QY 176 LGVLGHAPFPQGLGGDTHDFEDENWTKDGAFLNFLVAAHEFGHALGLSHNSDQALMF 235

Db 177 NGILAHAFQPGQGGDGAHFAETWNTSANYNLFVAAHEFGHSLAHSSDPGALMY 236

QY 236 PNYVSLDRKPYPLSQDDINGIQSYGLPKVPAPKPEPTIPHACDPDLTDAITFRREV 295

Db 237 PNYAFRETSNYSPLPQDDIDGQAIY-GLSSNPIQTPGTPSTKPCDPSLTFDAITLGEI 295

QY 296 MFRKGRHLWRIYYDITVEFELIASFPWSPADLQAAAYEN-PRDKILVFDKNFWMIRGY 354

Db 296 LFFKDRYFRRRHHPOLQRVEMNFI SLFWPSLPTGIQAAYEDFDRLIIFLKGNQYWALSGY 355

355 AVLEDPYKSIHITGLFGRVKKIDAAVCDKTKRTYFFVGLWCRFDEMOTQMDKGPQV 414
356 DILQGYPKDLSNYPSPSSQAIDAAVYRS--KTYEFVNDQFWRYNQRFMEPGYPKSI 413
357 VKEHFGISIRVDAFQYKGFPPSRGSKQFYNKTKNIRIMRTNFWOCK 466
358 SCAPPKIESKVDAAFOQEHFFHVSFGRYAFYAFLLIAQRTVRVAGKNWLNCR 465

RESULT 13
A53711
collagenase 3 (EC 3.4.24.-) - human
N;Alternate names: matrix metalloproteinase 13 (MMP13)
C;Species: Homo sapiens (man)
C;Date: 07-Jul-1995 #sequence_revision 07-Jul-1995 #text_change 09-Jul-2004
C;Accession: A53711
R;Freilje, J.M.P.; Diez-Itza, I.; Balbin, M.; Sanchez, L.M.; Blasco, R.; Toliivia, J.; Lopez, J. Biol. Chem. 269, 16766-16773, 1994
A;Title: Molecular cloning and expression of collagenase-3, a novel human matrix metalloproteinase
A;Reference number: A53711; MUID:94266894; PMID:8207000
A;Accession: A53711
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-471 <PRE>
A;Cross-references: UNIPROT:P45452; GB:X75308; NID:9516385; PIDN:CA53056.1; PID:G516386
C;Genetics:
A;Gene: GDB:MMP13; CLG3
A;Cross-references: GDB:373966; OMIM:600108
A;Map position: 11q22.2-11q22.3
C;Superfamily: interstitial collagenase; hemopexin repeat homology; matrix metalloproteinase
C;Keywords: hydrolase; metalloproteinase; zinc; zymogen
F:64-267/Domain: matrix metalloproteinase homology <MMP>
F:278-471/Domain: hemopexin repeat homology <PXN>
F:96,222,226,232/Binding site: zinc, catalytic (Cys, His, His) (inhibited) #status
F:222,226,232/Binding site: zinc, catalytic (His) (active) #status predicted
F:223/Active site: Glu #status predicted

Query Match 41.3%; Score 1141; DB 2; Length 471;
Best Local Similarity 49.8%; Pred. No. 9e-85;
Matches 222; Conservative 62; Mismatches 150; Indels 12; Gaps 8;

26 NEENMQLAQYLNQYF-SLEIEGHLVQSKNSLDDKIREMOAFPGTLVTGKLDNSTLE 84
32 SEEDLQFAERYLSYHPTNLAG--ILKENAASSWTERLREMQSFGLVETGKLDNDTLD 89
85 IMKTRCGVDPVGVQY--TLPGWRKYNLTIRIINYPDMARAAVDEAIOGLEVWSKV 141
90 VMKRCRCVDPVGVQYVPRITLK-WSKNLTIRIINYPDMTHSEVENAKFAKFWGSDV 148
142 TPLKFTKISKGIADIMAFRTRVHRCPRY-FDGLVLGHAFFPGPGGLGGDTHFEDEN 200
149 TPLNTRLDGDIADIMISFQIKHG--DFYDFGSGLLAHAFPPGPNYGGDAHFDDET 206
201 WTKDAGFNLFLVAHFEHGLSHNSDQATLMENPVVSLDPRKYPVLSQDDINGIOSYI 260
207 WTSKSGYNYLFLVAHFEHGLSHNSDQATLMENPVVSLDPRKYPVLSQDDINGIOSYI 266
261 GGLPKVPAKPKPTIIPACDPLTDAITTFRRVNFVFFGRHLWRIIYDITDVEFLIAS 320
267 GPGDEP-NPKHKPTDKCDPSLSDAITSLRGTIMFKDRFWRLHQVQVDAELFLTKS 325
321 FWPSLPADLQAAVFNPR-RKILVFKDENTFMIRGAYLVDYPKSIHTIGFPGVKKIDAA 379
326 FWPFLPNRIDAAYEHPHSHDLIFRGRKFWALNGYDILEGYPKSELGLPKVKKISAA 385
380 VCDKTRTKYFFYGIWCRFDEMOTQMDKGPQVVKHPPGISIRVDAAFQYKGFPPSR 439
386 VHFEDTGKTLFLFSGNQVRIYDDTNHMDKDYPLIEDEFGIGDKVDVAYEKNGIYFFN 445
440 GSKQFYNKTKNITRIMRTNFWOC 465
446 GPIQFEYSIWSNIRVWMPANSILWC 471

RESULT 14
A49499
metalloelastase HME (EC 3.4.24.-) - human
C;Species: Homo sapiens (man)
C;Date: 07-Apr-1994 #sequence_revision 18-Nov-1994 #text_change 09-Jul-2004
C;Accession: A49499
R;Shapiro, S.D.; Kobayashi, D.K.; Ley, T.J. J. Biol. Chem. 268, 23824-23829, 1993
A;Title: Cloning and characterization of a unique elastolytic metalloproteinase produced by a human fibroblast cell line
A;Reference number: A49499; MUID:94043200; PMID:8226919
A;Accession: A49499
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-470 <SHA>
A;Cross-references: UNIPROT:P39900; GB:L23808; NID:G435969
A;Experimental source: alveolar macrophage
A;Note: sequence extracted from NCBI backbone (NCBI:139457, NCBI:139458)
C;Genetics:
A;Gene: GDB:MMP12; HME
A;Cross-references: GDB:266582; OMIM:601046
A;Map position: 11q22.2-11q22.3
C;Superfamily: interstitial collagenase; hemopexin repeat homology; matrix metalloproteinase
C;Keywords: hydrolase; metalloproteinase; zinc; zymogen
F:60-263/Domain: matrix metalloproteinase homology <MMP>
F:276-470/Domain: hemopexin repeat homology <PXN>
F:92,218,222,228/Binding site: zinc, catalytic (Cys, His, His) (inhibited) #status
F:218,222,228/Binding site: zinc, catalytic (His) (active) #status predicted
F:219/Active site: Glu #status predicted

Query Match 41.0%; Score 1133; DB 2; Length 470;
Best Local Similarity 48.3%; Pred. No. 4e-84;
Matches 229; Conservative 77; Mismatches 152; Indels 16; Gaps 10;

3 RLLLCLEFFITFSAPFLVMTENENMQL-AQAYLQYFSLIEGHLVQSKNR--SL 58
2 KFLILLIQAATASGALPLNSTSLKNNVLFGRYLFYGLI--NKLPTKKYKSNL 59
59 IDDKIREMOAFPGTLVTGKLDNSTLEIMKTRCGVDPVGVQYTLPG---WRKNLTIRI 115
60 MKEKIQEMQHFLGLKVTGQDLSLEMMHAPRCGVPOVHHF-REMPGPGVWRKHVITRI 118
116 INYTPDMARAAVDEAIOGLEVWSKVTPKTKISKGIADIMAFRTRVHRCPRYFDPG 175
119 NNYTPDMNRDVEDYAIRKAFQVSNVTPKTKSKINTGMADILWVFARGAGDF-HAFDGK 177
176 LGVLGHAFPPGPGGLGGDTHFEDENWTKDAGFNLFLVAHFEHGLSHNSDQATLMF 235
178 GGLLAHAFPGSGIGGDAHFEDEFTWTHSGGTNLFITAVHIEHGLSHLSGSDPKVMF 237
236 ENYVSLDPRKYPVLSQDDINGIOSYIYGGPLKVPKPKP--TIPHACDPLTDAITTFPR 293
238 PTKYVDINTFRLSADDIRGQSLYGD-PKENQRLPNPNDSSEPALCDPNLSFDAVTVGN 296
294 EVMFFPKGRHLWRIIYDITDVEFLIASFWPSLPADLQAAVE-NPRDKILVFKDENFWMIR 352
297 KIFFKDFRFFLKVLSERPKTSVNLISLWPTLPSGIEAAYEIEARNQVFLFKDDKYLIS 356
353 GYAVLPDYPKSIHTIGFPGVKKIDAAVCDKTKRTYFFVGLWCRFDEMOTQMDKGPQ 412
357 NLRPEPNPKSIHTSGFNFVKKIDAAVFNPRFYRIYFFVDNQYWEYDERQWMDPGYPK 416
413 RVVKKIPPGISIRVDAAFQYKGFPPSRGSKQFYNKTKNITRIMRTNFWOC 465
417 LITKNFQIGPKIDAVFYKKNKYVFFQSGNQFVEYDFLLQRIITKILKSNWFGC 470

RESULT 15
A23685
interstitial collagenase (EC 3.4.24.7) precursor - rat (fragment)
N;Alternate names: matrix metalloproteinase 1 (MMP1); vertebrate collagenase
C;Species: Rattus norvegicus (Norway rat)

Search completed: November 15, 2004, 21:01:48
Job time : 28 secs

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Db	61	DKIREMQAFGLTVTGKLSNTLEIMKTPRCGVDVGYGYTLPGWRKYNLTIRIINYTP	120
QY	121	DMARAADVAIOEGLEVWSKVPLKFTKISGDIADIMIAFRTRVHGRCPRYFDGPGVLG	180
Db	121	DMARAADVAIOEGLEVWSKVPLKFTKISGDIADIMIAFRTRVHGRCPRYFDGPGVLG	180
QY	181	HAFPPGPGGLGGTHFDEDENTKDGAGFNLFLVAHEFGHALGSHNSDOTALMFFNYVS	240
Db	181	HAFPPGPGGLGGTHFDEDENTKDGAGFNLFLVAHEFGHALGSHNSDOTALMFFNYVS	240
QY	241	LDPKPYPLSODDINGIQSYGGLPKVPAPKKEPTIPHACDPDLTDAITTFREVVFFKG	300
Db	241	LDPKPYPLSODDINGIQSYGGLPKVPAPKKEPTIPHACDPDLTDAITTFREVVFFKG	300
QY	301	RHLWRIYDITDVEFELIASFWPSLPADLQAAAYENPRDKILVFKDENFWMIRGYAVLPDY	360
Db	301	RHLWRIYDITDVEFELIASFWPSLPADLQAAAYENPRDKILVFKDENFWMIRGYAVLPDY	360
QY	361	PKSIHTLGFPRGVKKIDAAVCDKTRKTYFFVGIWCRFDEMTQMDKGPQVRVVKHPPG	420
Db	361	PKSIHTLGFPRGVKKIDAAVCDKTRKTYFFVGIWCRFDEMTQMDKGPQVRVVKHPPG	420
QY	421	ISIRVDAAFQYKGFPPFSRSGSKQFEYNIKTNITRIMRTNFWOCKEKPKNSSFGDINKE	480
Db	421	ISIRVDAAFQYKGFPPFSRSGSKQFEYNIKTNITRIMRTNFWOCKEKPKNSSFGDINKE	480
QY	481	KAHSGGKILYHKSLSLFIQVHLLKNTSIYQ	513
Db	481	KAHSGGKILYHKSLSLFIQVHLLKNTSIYQ	513

RESULT 3

Q9H306	PRELIMINARY;	PRT;	513 AA.
ID	Q9H306		
AC	Q9H306;		
DT	01-MAR-2001 (TREMBlrel. 16, Created)		
DT	01-MAR-2001 (TREMBlrel. 16, Last sequence update)		
DT	01-MAR-2004 (TREMBlrel. 26, Last annotation update)		
DE	Matrix metalloprotease MMP-27.		
OS	Homo sapiens (Human).		
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
OC	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.		
OX	NCBI TaxID=9606;		
EN	[1]_		
RP	SEQUENCE FROM N.A.		
RA	Benoit de Coignac A., Elson G., Magistrelli G., Jeannin P.,		
RA	Delneste Y., Aubry J.P., Berthier O., Bonnefoy J.Y., Gauchat J.F.;		
RL	Submitted (OCT-1999) to the EMBL/GenBank/DBJ databases.		
DR	EMBL; AF195192; AAG28453.1;		
DR	HSSP; P08254; 1HV7.		
DR	MEROPS; M10.027;		
DR	Genew; HGNC:14250; MMP27.		
DR	GO; GO:0005578; C:extracellular matrix; IEA.		
DR	GO; GO:0004222; F:metalloendopeptidase activity; IEA.		
DR	GO; GO:0006508; P:proteolysis and peptidolysis; IEA.		
DR	InterPro; IPR000585; Hemopexin.		
DR	InterPro; IPR006026; Peptidase M.		
DR	InterPro; IPR001818; Pept_M10A_M12B.		
DR	InterPro; IPR006025; Pept_M_Zn_BS.		
DR	InterPro; IPR009070; PGHD-like.		
DR	Pfam; PF00045; Hemopexin; 4.		
DR	Pfam; PF00413; Peptidase M10; 1.		
DR	Pfam; PF03933; Peptidase M10_N; 1.		
DR	PRINTS; PR00138; MATRXIN.		
DR	SMART; SM00120; HX; 4.		
DR	SMART; SM00235; ZnMC; 1.		
DR	PROSITE; PS00546; CYSTEINE_SWITCH; 1.		
DR	PROSITE; PS00024; HEMOPEXIN; 1.		
DR	PROSITE; PS00142; ZINC_PROTEASE; UNKNOWN_1.		
KW	Metalloprotease; Protease.		
SQ	SEQUENCE 513 AA; 59023 MW; ED3C9B175C014683 CRC64;		

Db	61	DKIREMQAFGLTVTGKLSNTLEIMKTPRCGVDVGYGYTLPGWRKYNLTIRIINYTP	120
QY	121	DMARAADVAIOEGLEVWSKVPLKFTKISGDIADIMIAFRTRVHGRCPRYFDGPGVLG	180
Db	121	DMARAADVAIOEGLEVWSKVPLKFTKISGDIADIMIAFRTRVHGRCPRYFDGPGVLG	180
QY	181	HAFPPGPGGLGGTHFDEDENTKDGAGFNLFLVAHEFGHALGSHNSDOTALMFFNYVS	240
Db	181	HAFPPGPGGLGGTHFDEDENTKDGAGFNLFLVAHEFGHALGSHNSDOTALMFFNYVS	240
QY	241	LDPKPYPLSODDINGIQSYGGLPKVPAPKKEPTIPHACDPDLTDAITTFREVVFFKG	300
Db	241	LDPKPYPLSODDINGIQSYGGLPKVPAPKKEPTIPHACDPDLTDAITTFREVVFFKG	300
QY	301	RHLWRIYDITDVEFELIASFWPSLPADLQAAAYENPRDKILVFKDENFWMIRGYAVLPDY	360
Db	301	RHLWRIYDITDVEFELIASFWPSLPADLQAAAYENPRDKILVFKDENFWMIRGYAVLPDY	360
QY	361	PKSIHTLGFPRGVKKIDAAVCDKTRKTYFFVGIWCRFDEMTQMDKGPQVRVVKHPPG	420
Db	361	PKSIHTLGFPRGVKKIDAAVCDKTRKTYFFVGIWCRFDEMTQMDKGPQVRVVKHPPG	420
QY	421	ISIRVDAAFQYKGFPPFSRSGSKQFEYNIKTNITRIMRTNFWOCKEKPKNSSFGDINKE	480
Db	421	ISIRVDAAFQYKGFPPFSRSGSKQFEYNIKTNITRIMRTNFWOCKEKPKNSSFGDINKE	480
QY	481	KAHSGGKILYHKSLSLFIQVHLLKNTSIYQ	513
Db	481	KAHSGGKILYHKSLSLFIQVHLLKNTSIYQ	513

RESULT 2

AAQ89112	PRELIMINARY;	PRT;	513 AA.
ID	AAQ89112		
AC	AAQ89112;		
DT	02-MAR-2004 (TREMBlrel. 27, Created)		
DT	02-MAR-2004 (TREMBlrel. 27, Last sequence update)		
DT	02-MAR-2004 (TREMBlrel. 27, Last annotation update)		
DE	MMP27		
GN	UNQ2503.		
OS	Homo sapiens (Human).		
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
OC	Mammalia; Eutheria; Primata; Catarrhini; Hominidae; Homo.		
OX	NCBI TaxID=9606;		
EN	[1]		
RP	SEQUENCE FROM N.A.		
RX	PubMed=12975309;		
RA	Clark H.F., Gurney A.L., Abaya E., Baker K., Baldwin D., Brush J.,		
RA	Chen J., Chow B., Chui C., Crowley C., Currell B., Deuel B., Dowd P.,		
RA	Eaton D., Foster J., Grimaldi C., Gu Q., Hass P.E., Heldens S.,		
RA	Huang A., Kim H.S., Klimowski L., Jin Y., Johnson S., Lee J.,		
RA	Lewis L., Liao D., Mark M., Robbie E., Sanchez C., Schoenfeld J.,		
RA	Seshagiri S., Simmons L., Singh J., Smith V., Stinson J., Vagts A.,		
RA	Vandlen R., Watanabe C., Wileand D., Woods K., Xie M.H., Yansura D.,		
RA	Yi S., Yu G., Yuan J., Zhang M., Zhang Z., Goddard A., Wood W.I.,		
RA	Godowski P.;		
RT	"The Secreted Protein Discovery Initiative (SPDI), a Large-Scale		
RT	Effort to Identify Novel Human Secreted and Transmembrane Proteins: A		
RT	Bioinformatics Assessment."		
RL	Genome Res. 13:2265-2270 (2003).		
DR	EMBL; AY358752; AAQ89112.1;		
SQ	SEQUENCE 513 AA; 58994 MW; 1B1D556995553DCD CRC64;		
Query Match			
Best Local Similarity 99.8%; Score 2752; DB 2; Length 513;			
Matches 512; Conservative 0; Mismatches 1; Indels 0; Gaps 0;			
QY	1	MKRLLLCLFFITFSSAPFLVRVTENEENMQAAYLNQFYSLEIGNHLVQSKNRLSD	60
Db	1	MKRLLLCLFFITFSSAPFLVRVTENEENMQAAYLNQFYSLEIGNHLVQSKNRLSD	60
QY	61	DKIREMQAFGLTVTGKLSNTLEIMKTPRCGVDVGYGYTLPGWRKYNLTIRIINYTP	120

Query Match 98.8%; Score 2731; DB 2; Length 513;
 Best Local Similarity 99.0%; Pred. No. 4.5e-214;
 Matches 508; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 1 MKELLLCLFFITFSSAFPLVRMTENENMQLAQAYLNQFYSLEIEGNHVLVQSKNSLID 60
 DB 1 MKELLLCLFFITFSSAFPLVRMTENENMQLAQAYLNQFYSLEIEGNHVLVQSKNSLID 60

QY 61 DKIREMQAFGLTVTGLKLSNTLEIMKTPRCGVDVQGYTLPGWRKYNLTTRIINYTP 120
 DB 61 DKIREMQAFGLTVTGLKLSNTLEIMKTPRCGVDVQGYTLPGWRKYNLTTRIINYTP 120

QY 121 DMARAADVAIQBLEVWSKVTPKFTKISKGIADIMIAFRTRVHGRCPRYFDGPGVLG 180
 DB 121 DMARAADVAIQBLEVWSKVTPKFTKISKGIADIMIAFRTRVHGRCPRYFDGPGVLG 180

QY 181 HAPPPGGLGGDTHFDEDENTWKDAGFNLFLVAAHEFGHALGLSHSNDQTALMFNNYVS 240
 DB 181 HAPPPGGLGGDTHFDEDENTWKDAGFNLFLVAAHEFGHALGLSHSNDQTALMFNNYVS 240

QY 241 LDPKRYPLSQDDINGIQSYGGLPKVPAPKPEPTIPHACDPDLTDAITTFREVMFFKG 300
 DB 241 LDPKRYPLSQDDINGIQSYGGLPKVPAPKPEPTIPHACDPDLTDAITTFREVMFFKG 300

QY 361 PKSIHTLGPGRVKKIDAAVCDKTRTKTYFFVGIWCRWDEMTQTMKGFPPQVVKHFFG 420
 DB 361 PKSIHTLGPGRVKKIDAAVCDKTRTKTYFFVGIWCRWDEMTQTMKGFPPQVVKHFFG 420

QY 421 ISIRVDAAFQYKGFPPFSGSKOFEYNIKTNITRMTNTWFOCKEKNSSGFDINKE 480
 DB 421 ISIRVDAAFQYKGFPPFSGSKOFEYNIKTNITRMTNTWFOCKEKNSSGFDINKE 480

QY 481 KAHSGGKILYHKSLSLFIQVHLLKNTSIY 513
 DB 481 KAHSGGKILYHKSLSLFIQVHLLKNTSIY 513

RESULT 4
 Q9GKE1 PRELIMINARY; PRT; 512 AA.

ID Q9GKE1
 AC Q9GKE1;
 DT 01-MAR-2001 (Tremblrel. 16, Created)
 DT 01-MAR-2001 (Tremblrel. 16, Last sequence update)
 DT 01-MAR-2004 (Tremblrel. 26, Last annotation update)
 DE Matrix metalloproteinase-27.
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Scandentia; Tupaiidae; Tupaiidae; Tupaiidae;
 OC NCBI_TaxID=37347;
 RN [1]_TaxID=37347;
 RP SEQUENCE FROM N.A.
 RC TISSUE=Sciera;
 RA Guggenheim J.A., To C.H., Frost M.R.;
 RL Submitted (JUN-2000) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AF281673; AAG44844.1; -;
 DR HSSP; P03956; 1CGL.
 DR MEROPS; M10.027; -;
 DR GO; GO:0005578; C:extracellular matrix; IEA.
 DR GO; GO:0004222; F:metalloendopeptidase activity; IEA.
 DR GO; GO:0006508; P:proteolysis and peptidolysis; IEA.
 DR InterPro; IPR000585; Peptidase.
 DR InterPro; IPR006026; Peptidase M.
 DR InterPro; IPR001818; Pept M10A M12B.
 DR InterPro; IPR006025; Pept M Zn BS.
 DR InterPro; IPR009070; PGSD-like.
 DR Pfam; PF00045; Hemopexin; 4.
 DR Pfam; PF00413; Peptidase M10; 1.
 DR Pfam; PF03933; Peptidase M10_N; 1.
 DR PRINTS; PR00138; MATRINXIN.

DR SMART; SM00120; HX; 4.
 DR SMART; SM00235; ZMC; 1.
 DR PROSITE; PS00546; CYSTEINE_SWITCH; 1.
 DR PROSITE; PS00034; HEMOPEXIN; 1.
 DR PROSITE; PS00142; ZINC_PROTEASE; UNKNOWN 1.
 SQ SEQUENCE 512 AA; 5816 MW; 9CB089C4F807CEFF5 CRC64;

Query Match 84.9%; Score 2347; DB 2; Length 512;
 Best Local Similarity 84.8%; Pred. No. 9.8e-183;
 Matches 434; Conservative 29; Mismatches 49; Indels 0; Gaps 0;

QY 1 MKELLLCLFFITFSSAFPLVRMTENENMQLAQAYLNQFYSLEIEGNHVLVQSKNSLID 60
 DB 1 MKELLLCLFFITFSSAFPLVRMTENENMQLAQAYLNQFYSLEIEGNHVLVQSKNSLID 60

QY 61 DKIREMQAFGLTVTGLKLSNTLEIMKTPRCGVDVQGYTLPGWRKYNLTTRIINYTP 120
 DB 61 DKIREMQAFGLTVTGLKLSNTLEIMKTPRCGVDVQGYTLPGWRKYNLTTRIINYTP 120

QY 121 DMARAADVAIQBLEVWSKVTPKFTKISKGIADIMIAFRTRVHGRCPRYFDGPGVLG 180
 DB 121 DMARAADVAIQBLEVWSKVTPKFTKISKGIADIMIAFRTRVHGRCPRYFDGPGVLG 180

QY 181 HAPPPGGLGGDTHFDEDENTWKDAGFNLFLVAAHEFGHALGLSHSNDQTALMFNNYVS 240
 DB 181 HAPPPGGLGGDTHFDEDENTWKDAGFNLFLVAAHEFGHALGLSHSNDQTALMFNNYVS 240

QY 241 LDPKRYPLSQDDINGIQSYGGLPKVPAPKPEPTIPHACDPDLTDAITTFREVMFFKG 300
 DB 241 LDPKRYPLSQDDINGIQSYGGLPKVPAPKPEPTIPHACDPDLTDAITTFREVMFFKG 300

QY 301 RHLWRIYDITDVEFELIASFWPSLPADLQAAAYENPRDKILVFKDENFWIRGYAVLPDY 360
 DB 301 RHLWRIYDITDVEFELIASFWPSLPADLQAAAYENPRDKILVFKDENFWIRGYAVLPDY 360

QY 361 PKSIHTLGPGRVKKIDAAVCDKTRTKTYFFVGIWCRWDEMTQTMKGFPPQVVKHFFG 420
 DB 361 PKSIHTLGPGRVKKIDAAVCDKTRTKTYFFVGIWCRWDEMTQTMKGFPPQVVKHFFG 420

QY 421 ISIRVDAAFQYKGFPPFSGSKOFEYNIKTNITRMTNTWFOCKEKNSSGFDINKE 480
 DB 421 ISIRVDAAFQYKGFPPFSGSKOFEYNIKTNITRMTNTWFOCKEKNSSGFDINKE 480

QY 481 KAHSGGKILYHKSLSLFIQVHLLKNTSIY 512
 DB 481 KAYSGEVETLHQSLSLFIQVHLLKNTSIY 512

RESULT 5
 O93342 PRELIMINARY; PRT; 472 AA.

ID O93342
 AC O93342;
 DT 01-NOV-1998 (Tremblrel. 08, Created)
 DT 01-NOV-1998 (Tremblrel. 08, Last sequence update)
 DT 01-MAR-2004 (Tremblrel. 26, Last annotation update)
 DE Matrix metalloproteinase.
 OS Gallus gallus (Chicken).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
 OC Gallus.
 OC NCBI_TaxID=9031;
 RN [1]_TaxID=9031;
 RP SEQUENCE FROM N.A.
 RA Yang M., Kurkinen M.;
 RT "Cloning of a novel matrix metalloproteinase (MMP) from chicken embryo fibroblasts";
 RL J. Biol. Chem. 0:0-0 (1998).
 DR EMBL; AF062392; AAC33733.1; -;
 DR HSSP; P45452; 830C.
 DR MEROPS; M10.027; -;
 DR GO; GO:0005578; C:extracellular matrix; IEA.
 DR GO; GO:0004222; F:metalloendopeptidase activity; IEA.
 DR GO; GO:0006508; P:proteolysis and peptidolysis; IEA.

DR

Query Match 46.6%; Score 1286.5; DB 2; Length 478;
 Best local similarity 52.9%; Pred. No. 3.2e-96;
 Matches 254; Conservative 69; Mismatches 140; Indels 17; Gaps 8;

QY 1 MKRLLLCLFFITSSAPPLVRMTENE-ENQLAQAYLNQFYSLIEGHLVQSKNRLI 59
 Db 1 MQLPALLLFCGVCSAYPVDRAAEDENNMLTQQYLENYLNGDKVPFVRNRSGPV 60
 QY 60 DDKIREMQAFGLTVTKGLDSNTLEMTKTCRCQGVDPVQGYTLPG---WRKNLTIVRII 116
 Db 61 VEKIREMQKFLGLEVTGKVDSDTLAMRRRCRCQGVDPVQGVDF-TTFPGMPKWKTHLTIVRI 119
 QY 117 NYTPDMARAADVAIRAIOGLEWVSKVTPLEKTKISGLADIAMIAPTRVTRHGRCPYFDPGL 176
 Db 120 NYTPDLPDAVDAISAIEKALNVKWEVPLTFSRTDEGEADIKISFVNRDHGDP-NPFDGPG 178
 QY 177 GVLGHAFFPGPLGGDTHFEDENWYKDGAGNLFVAAHEFGHGLSHNSDQTLMPF 236
 Db 179 NVLGHAFFPGPGIYGDAHFDDDDQWTSDTSGTNLFLVAHELGHSLGLPHSADPSALMYP 238
 QY 237 NY-VSLDPKPYLQSDINGIQSIYGLPK-----VPK--PKETTPHACDPLTFD 286
 Db 239 VYNVLADLARFHLSSQDVGNGIQSLGPPEDSSNDPVPPTESVPPGPGTFAACDPTLSD 298
 QY 287 AITTPREVFMFKRHLMRIYDITDVEFELIASFWPSLPADLQAAY-ENPRDKILVFKD 345
 Db 299 AISTLGEFLFKDRHFWKSLKTLTSPGLFSLSSFWPSLPSGLDAAEYTSKDIVIFPKG 358
 QY 346 ENFWMTIRGAVLPDYPKSHITLGFGRVKKIDAACVTKTRKTYFVFGWCRFDEMTQT 405
 Db 359 NQFWMRGTEVQAGYKPGHITLGFPTTKVKKIDAAVDFKCKKTYFVFGDKYWRFDEKRS 418
 QY 406 MDKGFQRVVKFPGGISIRVDAAFQYKGFEEFSGSKQFENYKTKNITRIMRTNFWQC 465
 Db 419 MEFGPKQIAEDFPGVDSVDAAFAEFGFYFNGSSQLEFDPNAKKVTHVLKSNWLNC 478

RESULT 8
 ID MM03 RABBIT STANDARD; PRT; 478 AA.
 AC P28563;
 DT 01-DEC-1992 (Rel. 24, Created)
 DT 01-DEC-1992 (Rel. 24, Last sequence update)
 DT 05-JUL-2004 (Rel. 44, Last annotation update)
 DE Stromelysin-1 precursor (EC 3.4.24.17) (Matrix metalloproteinase-3)
 DE (MMP-3) (Transin-1) (SL-1).
 GN Name=MMP3;
 OS Oryctolagus cuniculus (Rabbit).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.
 OX NCBI TaxID=9986;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=86077214; PubMed=2825726;
 RA Fini M.E., Karmilowicz M.J., Ruby P.L., Beeman A.M., Borges K.A.,
 RA Brinckerhoff C.E.;
 RT "Cloning of a complementary DNA for rabbit proactivator. A
 RT metalloproteinase that activates synovial cell collagenase, shares
 RT homology with stromelysin and transin, and is coordinately regulated
 RT with collagenase.";
 RL Arthritis Rheum. 30:1254-1264 (1987).
 RN [2]
 RP SEQUENCE OF 1-167 FROM N.A.
 RX MEDLINE=87156645; PubMed=3030290;
 RA Whitham S.E., Murphy G., Angel P., Rahmsdorf H.J., Smith B., Lyons A.,
 RA Harris T.J.R., Reynolds J.J., Herrlich P., Docherty A.J.P.;
 RT "Comparison of human stromelysin and collagenase by cloning and
 RT sequence analysis.";
 RL Biochem. J. 240:913-916 (1986).
 CC -!- FUNCTION: Can degrade fibronectin, laminin, gelatins of type I,
 CC III, IV, and V; collagens III, IV, X, and IX, and cartilage
 CC proteoglycans. Activates procollagenase.

CC CC -!- CATALYTIC ACTIVITY: Preferential cleavage where P1', P2' and P3'
 CC CC are hydrophobic residues.
 CC CC -!- COFACTOR: Binds 2 zinc ions and 4 calcium ions per subunit (By
 CC CC similarity).
 CC CC -!- SIMILARITY: Belongs to peptidase family M10A.
 CC CC -!- SIMILARITY: Contains 1 hemoexin-like domain.
 CC CC -----
 CC CC This SWISS-PROT entry is copyright. It is produced through a collaboration
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 CC CC or send an email to license@isb-sib.ch).
 CC CC -----
 CC CC EMBL; M25664; AAA31467.1; -
 CC CC PIR; A37306; KCRBS1.
 CC CC HSSP; P08254; IG05.
 CC CC MEROPS; M10.005; -
 CC CC InterPro; IPR000585; Hemoexin.
 CC CC InterPro; IPR006026; Peptidase M.
 CC CC InterPro; IPR001818; Pept M10A M12B.
 CC CC InterPro; IPR006025; Pept M.Zn_Bs.
 CC CC InterPro; IPR009070; PGD-like.
 CC CC Pfam; PF00045; Hemoexin_4.
 CC CC Pfam; PF00413; Peptidase M10; 1.
 CC CC Pfam; PF03933; Peptidase M10_N; 1.
 CC CC PRINTS; PR00138; MATRINX.
 CC CC SMART; SM00120; HX; 4.
 CC CC SMART; SM00235; Zmc; 1.
 CC CC PROSITE; PS00546; CYSTEINE_SWITCH; 1.
 CC CC PROSITE; PS00024; HEMOEXIN; 1.
 CC CC PROSITE; PS00142; ZINC_PROTEASE; 1.
 CC CC Calcium-binding; Collagen degradation;
 CC CC Glycoprotein; Hydrolase; Metal-binding; Metalloprotease; Signal; Zinc;
 CC CC Zymogen.
 CC CC SIGNAL 1 17 Probable.
 CC CC PROPEP 18 100 Activation peptide.
 CC CC CHAIN 101 478 Stromelysin-1.
 CC CC DOMAIN 288 478 Hemoexin-like.
 CC CC SITE 93 93 Cysteine switch (Potential).
 CC CC METAL 125 125 Calcium 1 (By similarity).
 CC CC METAL 159 159 Calcium 2 (By similarity).
 CC CC METAL 169 169 Zinc 1 (By similarity).
 CC CC METAL 171 171 Zinc 1 (By similarity).
 CC CC METAL 176 176 Calcium 3 (By similarity).
 CC CC METAL 177 177 Calcium 3 (via carbonyl oxygen) (By
 CC CC similarity).
 CC CC METAL 179 179 Calcium 3 (via carbonyl oxygen) (By
 CC CC similarity).
 CC CC METAL 181 181 Calcium 3 (via carbonyl oxygen) (By
 CC CC similarity).
 CC CC METAL 184 184 Zinc 1 (By similarity).
 CC CC METAL 191 191 Calcium 2 (via carbonyl oxygen) (By
 CC CC similarity).
 CC CC METAL 193 193 Calcium 2 (via carbonyl oxygen) (By
 CC CC similarity).
 CC CC METAL 195 195 Calcium 2 (By similarity).
 CC CC METAL 197 197 Zinc 1 (By similarity).
 CC CC METAL 199 199 Calcium 3 (By similarity).
 CC CC METAL 200 200 Calcium 1 (By similarity).
 CC CC METAL 202 202 Calcium 1 and 3 (By similarity).
 CC CC METAL 219 219 Zinc 2 (catalytic) (By similarity).
 CC CC METAL 220 220 By similarity.
 CC CC METAL 223 223 Zinc 2 (catalytic) (By similarity).
 CC CC METAL 229 229 Zinc 2 (catalytic) (By similarity).
 CC CC METAL 298 298 Calcium 4 (via carbonyl oxygen) (By
 CC CC similarity).
 CC CC METAL 390 390 Calcium 4 (via carbonyl oxygen) (By
 CC CC similarity).
 CC CC METAL 439 439 Calcium 4 (via carbonyl oxygen) (By
 CC CC similarity).
 CC CC CARBOHYD 121 121 N-linked (GlcNAc...) (Potential).

RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
 RA Fahey J., Helton E., Kettman M., Madan A., Rodrigues S., Sanchez A.,
 RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
 RA Krzywinski M.I., Skalska U., Smallos D.E., Schnerch A., Schein J.E.,
 RA Jones S.J., Marra M.A.;
 RT "Generation and initial analysis of more than 15,000 full-length human
 and mouse cDNA sequences";
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
 [2]
 RN SEQUENCE FROM N.A.
 RC TISSUE=PCR rescued clones;
 RA Strausberg R.;
 RL Submitted (Apr-2004) to the EMBL/GenBank/DBJ databases.
 DR EMBL; BC069676; AAH69676.1; -
 SQ SEQUENCE 477 AA; 53978 MW; 7497490A861DEBA9 CRC64;
 Query Match 45.4%; Score 1254; DB 2; Length 477;
 Best Local Similarity 51.5%; Pred. No. 1.4e-93;
 Matches 247; Conservative 70; Mismatches 145; Indels 18; Gaps 9;
 QY 1 MKRLLLCLFFITFSSAFPLVRMTENE--NMOLAQAYLNQFYSLEIGHNLSVQSKRSLI 59
 DB 1 MKSLPILLLLCVAVCSAYPLDGAAGDTSNNLVQKYLENYIDLEKDVQFVRKDSGPV 60
 QY 60 DDKIREMAQAFGLTVTGKLDNSTLEIMKTPRCGVDPVQGYTLPG---WRKYNLTYYRII 116
 DB 61 VKKIREMQKFLGVTGKLDSDTLEVMKPRCGVPDVGHF-RTFPGIPKWRKTHLYRIV 119
 QY 117 NYTPDMARAADVDAIQEGLEWKSVPKTLKTKISKGIADIAMIARTRVHGRCPY-PDGP 175
 DB 120 NYTPDLPKDAVDSAVEKALKVWEVTPLTFSRYEGEADIMISPAVREHG--DFYPPDGP 177
 QY 176 LGVLGHAFPGPGGLGGDTHFEDENWTKDAGENLFLVAHFGHALGLSHNDQTALMF 235
 DB 178 GNVLAHAYAFPGPGINGDAHDDDDQWTKDTGTNLFVAHFGHALGLSHSANTALMY 237
 QY 236 PNVVSL-DPRKYPISQDDINGIQSIYG-----GLPKVPAP--PKEPTIPHACDPLTDF 286
 DB 238 PLVHSLTDLTFRLSQDDINGIQSLYGPDPSPETPLVPTPEVPPEPGTANCDPALSFD 297
 QY 287 AITTFREVMPFKORHLWRIYDITDVEFELIASFWPSLPADLOAAVE-NPRDKTLVFKD 345
 DB 298 AVSTLRGEILLFKDRHFRWKSRLKLEPELHLISSFWPSLPDGVDAAEVTSKDLVFIK 357
 QY 346 ENFWMIRGYAVLPDYPKSIHTLPGPRVKKIDAAVCDKTKRTKTYFFVGIWCRFDEMTQT 405
 DB 358 NQFWAIRGNEVRAGYPRGIHTLGGPPTVRKIDAAISDKKNTYFFVEDKYWRDEKNS 417
 QY 406 MDKGFPPQVVKHFFGIGSIRVDAAFQYKGFPPFSRGSKOFENYKNTKNTIRMTNTWFOC 465
 DB 418 MEGFPKQIAEDFPDGIDSKIDAVFEFGFFYFFTGSSQLEFPDPAKVTHTLKNSWLNLC 477
 RESULT 10
 AAH69716 PRELIMINARY; PRT; 477 AA.
 AC AAH69716;
 DT 20-MAY-2004 (TRENBLrel. 27, Created)
 DT 20-MAY-2004 (TRENBLrel. 27, Last sequence update)
 DE Matrix metalloproteinase 3, preproprotein.
 GN MMP3.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX [1]
 RN SEQUENCE FROM N.A.
 RC TISSUE=PCR rescued clones;
 RX MEDLINE=22388257; PubMed=12477932;
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,

FT DISULFID 291 478 By similarity
 FT CONFLICT 83 N -> D (in Ref. 2).
 FT CONFLICT 128 R -> K (in Ref. 2).
 SQ SEQUENCE 478 AA; 53942 MW; CA742E31A4549D40 CRC64;
 Query Match 46.0%; Score 1271.5; DB 1; Length 478;
 Best Local Similarity 51.9%; Pred. No. 5.4e-95;
 Matches 250; Conservative 75; Mismatches 136; Indels 21; Gaps 9;
 QY 1 MKRLLLCLFFITFSSAFPLVRMTENE--NMOLAQAYLNQFYSLEIGHNLSVQSKRSL 58
 DB 1 MKTLPILLLLCVAVCSAYPLDGAASRDADTTNMDLLQQLYLENYNLEKDVQFVRKDSPP 60
 QY 59 IDKIREMAQAFGLTVTGKLDNSTLEIMKTPRCGVDPVQGYTLPG---WRKYNLTYYRI 115
 DB 61 VVKKIQEMQKFLGVTGKLDNSTLEIVKPRCGVPDVGHFS-TFPGTPKWTHTLTYRI 119
 QY 116 INYTPDMARAADVDAIQEGLEWKSVPKTLKTKISKGIADIAMIARTRVHGR-CPRYFDG 174
 DB 120 VNTYTPDLPRDAVDAAEKALKVWEVTPLTFSRYEGEADIMISFGVREHGDRIIP--FDG 177
 QY 175 PLGVGHAFPGPGGLGGDTHFEDENWTKDAGENLFLVAHFGHALGLSHNDQTALM 234
 DB 178 PGNVLAHAYAFPGPGINGDAHDDDDQWTKDTGTNLFVAHFGHALGLSHSANTALM 237
 QY 235 PNVVSL-DPRKYPISQDDINGIQSIYG-----GLPKVPAPKPEPTIPHACDPLT 284
 DB 238 YPVYNAFTDLARFSLQDDVDGIIQSLYGPAPASPDNSGVPMPEVPPGSGT-FVMCDPLS 296
 QY 285 FDAITTFREVMPFKORHLWRIYDITDVEFELIASFWPSLPADLOAAVE-NPRDKTLV 343
 DB 297 FDLSTLRGEILLFKDRYFRWKSRLKLEPELHLISSFWPSLPADVAAYEIVISRTVFI 356
 QY 344 KDNFWMIRGYAVLPDYPKSIHTLPGPRVKKIDAAVCDKTKRTKTYFFVGIWCRFDEMT 403
 DB 357 KGTQFWAIRGNEVRAGYPRSIHTLGGPPTVRKIDAAISDKKNTYFFVEDKYWRFDEKR 416
 QY 404 QTMKGFPPQVVKHFFGIGSIRVDAAFQYKGFPPFSRGSKOFENYKNTKNTIRMTNTW 463
 DB 417 QSLFPGFPRHTAEDFPDGIDSKIDAVFEAFGFFYFSGSQSEFDPNKKVTHVLKNSWF 476
 QY 464 QC 465
 DB 477 QC 478
 RESULT 9
 AAH69676 PRELIMINARY; PRT; 477 AA.
 AC AAH69676;
 DT 20-MAY-2004 (TRENBLrel. 27, Created)
 DT 20-MAY-2004 (TRENBLrel. 27, Last sequence update)
 DE Matrix metalloproteinase 3, preproprotein.
 GN MMP3.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX [1]
 RN SEQUENCE FROM N.A.
 RC TISSUE=PCR rescued clones;
 RX MEDLINE=22388257; PubMed=12477932;
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
 RA Klausner R.D., Collins F.S., Wagner K.H., Shenmen C.M., Schuler G.D.,
 RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh P.,
 RA Diachenko L., Marusan K., Farmer A.A., Rubin G.M., Hong L.,
 RA Stapleton M., Soares M.B., Donald M.F., Casavant T.L., Scheetz T.E.,
 RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
 RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullany S.J.,
 RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

GN Name=MMP3; Synonyms=STMY1;
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A., AND SEQUENCE OF 18-24.
 RX MEDLINE=88198243; PubMed=3360803;
 RA Saus J., Quinones S., Otani Y., Nagase H., Harris E.D. Jr.,
 RA Kurkinen M.;
 RA "The complete primary structure of human matrix metalloproteinase-3.
 RT Identity with stromelysin.";
 RJ J. Biol. Chem. 263:6742-6745 (1988).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Fibroblast;
 RX MEDLINE=87156645; PubMed=3032090;
 RA Whitham S.E., Murphy G., Angel P., Ramsdorf H.J., Smith B., Lyons A.
 RA Harris I.J.R., Reynolds J.J., Herrlich P., Docherty A.J.P.;
 RT "Comparison of human stromelysin and collagenase by cloning and
 RT sequence analysis.";
 RL Biochem. J. 240:913-916 (1986).
 RN [3]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=88016164; PubMed=3477804;
 RA Wilhelm S.M., Collier I.B., Kronberger A., Eisen A.Z., Marmer B.L.,
 RA Grant G.A., Bauer E.A., Goldberg G.I.;
 RA "Human skin fibroblast stromelysin: structure, glycosylation,
 RT substrate specificity, and differential expression in normal and
 RT tumorigenic cells.";
 RL Proc. Natl. Acad. Sci. U.S.A. 84:6725-6729 (1987).
 RN [4]
 RP SEQUENCE FROM N.A.
 RA Lin D., Duncan M., Allen E., Araujo R., Aparicio A., Chai A.,
 RA Chung E., Davis K., Pederspiel N., Hyman R., Kalman S., Komp C.,
 RA Kurdi O., Lashkari D., Lew H., Namath A., Oefner P., Roberts D.,
 RA Heller R., Davis R.W.;
 RN Submitted (DEC-1996) to the EMBL/GenBank/DBJ databases.
 RN [5]
 RP SEQUENCE FROM N.A., AND VARIANT GLU-45.
 RA Bieder M.J., Carrington D.P., Chung M.-W., Lee K.L., Yi Q.,
 RA Nickerson D.A.;
 RT "SeattLESNPs. NHLBI HL6682 program for genomic applications, UW-
 RT FHCRC, Seattle, WA (URL: <http://pga.gs.washington.edu>).";
 RN Submitted (AUG-2001) to the EMBL/GenBank/DBJ databases.
 RN [6]
 RP ZYMOGEN ACTIVATION.
 RX MEDLINE=90344802; PubMed=2383557;
 RA Nagase H., Englund J.J., Suzuki K., Salvesen G.;
 RT "stepwise activation mechanisms of the precursor of matrix
 RT metalloproteinase 3 (stromelysin) by proteinases and (4-
 RT aminophenyl)mercuric acetate";
 RL Biochemistry 29:5783-5789 (1990).
 RN [7]
 RP STRUCTURE BY NMR OF CATALYTIC DOMAIN.
 RX MEDLINE=95384761; PubMed=7656014;
 RA Gooley P.R., O'Connell J.F., Marcy A.I., Cuca G.C., Salowe S.P.,
 RA Bush B.L., Hermes J.D., Esser C.K., Hagmann W.K., Springer J.P.,
 RA Johnson B.A.;
 RT "The NMR structure of the inhibited catalytic domain of human
 RT stromelysin-1.";
 RN Nat. Struct. Biol. 1:111-118 (1994).
 RN [8]
 RP STRUCTURE BY NMR OF 100-267.
 RX MEDLINE=99043696; PubMed=9827994;
 RA Stockman B.J., Waldon D.J., Gates J.A., Scahill T.A.,
 RA Kloosterman D.A., Mizsak S.A., Jacobsen E.J., Belonga K.L.,
 RA Mitchell M.A., Mao B., Petke J.D., Goodman L., Powers E.A.,
 RA Ledbetter S.R., Kayes P.S., Vogeli G., Marshall V.P., Petzold G.L.,
 RA Poornan R.A.;
 RT "Solution structures of stromelysin complexed to thiazazole
 RT inhibitors.";
 RL Protein Sci. 7:2281-2286 (1998).
 RL

Biochemistry 37:14048-14056(1998).

CC -!- FUNCTION: Can degrade fibronectin, laminin, gelatins of type I, III, IV and V; collagens III, IV, X, and IX, and cartilage proteoglycans. Activates procollagenase.

CC -!- CATALYTIC ACTIVITY: Preferential cleavage where P1', P2' and P3' are hydrophobic residues.

CC -!- COFACTOR: Binds 2 zinc ions and 4 calcium ions per subunit.

CC -!- SIMILARITY: Belongs to peptidase family M10A.

CC -!- SIMILARITY: Contains 1 hemopexin-like domain.

CC

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CC

EMBL; X05232; CAA28859.1; -

DR EMBL; J03209; AAA36321.1; -

DR EMBL; U78045; AAB36942.1; -

DR EMBL; AF405705; AAK95247.1; -

DR PIR; A28156; KCHU1

DR PDB; 1B3D; X-ray; A/B=100-272.

DR PDB; 1B8Y; X-ray; A=100-286.

DR PDB; 1B1W; X-ray; A/B=100-272.

DR PDB; 1BM6; NMR; @=100-272.

DR PDB; 1BQO; X-ray; A/B=100-272.

DR PDB; 1C3I; X-ray; A/B=100-272.

DR PDB; 1C8T; X-ray; A/B=103-269.

DR PDB; 1CAQ; X-ray; A=100-267.

DR PDB; 1CIC; X-ray; A=100-267.

DR PDB; 1CQR; X-ray; A/B=100-272.

DR PDB; 1D5J; X-ray; A/B=100-272.

DR PDB; 1D7X; X-ray; A/B=100-272.

DR PDB; 1D8F; X-ray; A/B=100-272.

DR PDB; 1D8M; X-ray; A/B=100-272.

DR PDB; 1G05; X-ray; A/B=100-272.

DR PDB; 1G49; X-ray; A/B=100-272.

DR PDB; 1G4K; X-ray; A/B/C=100-267.

DR PDB; 1HFS; X-ray; @=105-264.

DR PDB; 1HV7; X-ray; A/B=100-272.

DR PDB; 1M1W; Model; A=100-268.

DR PDB; 1O09; NMR; A=100-267.

DR PDB; 1Q1A; X-ray; A/B/C/D=106-267.

DR PDB; 1Q1C; X-ray; A/B/C/D=106-266.

DR PDB; 1SLM; X-ray; @=18-272.

DR

Query Match 45.2%; Score 1250; DB 1; Length 477;

Best Local Similarity 51.2%; Pred. No. 3e-93;

Matches 246; Conservative 71; Mismatches 145; Indels 18; Gaps 9;

QY 1 MKRLLLCLFFITSSAPFLVRMTNEE-NNQLAQYLNQYSLIEIGNHLVQSKNSLI 59

DB 1 MKSLPILLLCVAVCSAYPLDGAARGEDTSNNLVQKYLENYDLKKVQKQVRRKDSGFV 60

QY 60 DDKIREMQAFLGTVTKLDSNTLIMKTPRGVPDVGQYGVTVPG---WRKYNLYRII 116

DB 61 VKKIREMQRFLEVTGKLDSDTLLEVMKPRGVPDVGHF-RTFPGIPKWKTHLYRIV 119

QY 117 NYTPDMARAADVAIOEGLEVMVSKVTPLKFTKISKIGIADIIMAFRTVRVHGRCPRY-FDGP 175

DB 120 NYTPDLPRDAVDVAVEKALKVWEEVTLTFLSRLEGEADIMISFAVRHSG--DFYPPDPG 177

QY 176 LQVLGHAPPGGLGDDTHEDENWTKDAGFNFLVAAEHFGHALGLSHNDQALMF 235

DB 178 GNVLAHAYAPGEGINGDAHFDDEQWTKDTTGNLFLVAAEHIGLSGLFHSANTALMY 237

QY 236 PNVSL-DPRKYPGLSQDDINGIQSYG-----GLPKVPK-----PKEPTIPHACDPLDTPD 286

DB 238 FLYHSLTDLTRFLSQDDINGIQSYGPPDPSPETPLVPTPEVPPEPGTPANCDDPALSFD 297

QY 287 AITTFRRVWFKGRLHRIYYDITDVFELIASFWPSLPADLQAAYE-NPRDKILVFKD 345

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Db 298 AVSTLRGELIFKDRHFWKSLRKLPELHLISFWSLPSGVDAAEVTSKDLVIFPKG 357
Qy 346 ENFMWIRGYAVLPDYPKSIHTLPGFGRVKKIDAAVCDKTRTKTYFFVGVGWCWREDEMTQT 405
Db 358 NQFWAIRNEVRAGYPRGIHTLGPFTVRKIDAAISDKENKNTYFFVEDKCYWREDEKRS 417
Qy 406 MDKGFQBVVHFGPISIRVDAAYQYKGFPSRSGKQFENYKTKNITRIMTRNTWFOC 465
Db 418 MEPGFPQIAEDFGIDSKIDAVFEEFGFFYFTGSSQLFEDPNAKKVTHTLKNSMLNC 477

RESULT 12
Q98857 PRELIMINARY; PRT; 483 AA.
AC Q98857;
DT 01-FEB-1997 (TREMELrel. 02, Created)
DT 01-FEB-1997 (TREMELrel. 02, Last sequence update)
DT 01-OCT-2003 (TREMELrel. 25, Last annotation update)
DE Stromelysin-1/2-a.
OS Cynops pyrrhogaster (Japanese common newt).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Caudata; Salamandroidea; Salamandridae; Cynops.
OX NCBI_TaxID=8330;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Limb;
RX MEDLINE=96270627; PubMed=8629202;
RA Miyazaki K., Uchiyama K., Imokawa Y., Yoshizato K.;
RT "Cloning and characterization of cDNAs for matrix metalloproteinases
of regenerating newt limbs.";
RL Proc. Natl. Acad. Sci. U.S.A. 93:6819-6824 (1996).
DR EMBL; D82053; BA011524.1; -
DR HSSP; P33435; 1CKV.
DR GO; GO:000578; C:extracellular matrix; IEA.
DR GO; GO:004222; F:metalloendopeptidase activity; IEA.
DR GO; GO:0006508; F:proteolysis and peptidolysis; IEA.
DR InterPro; IPR000585; Hemopexin.
DR InterPro; IPR006026; Peptidase M.
DR InterPro; IPR001818; Pept M10A M12B.
DR InterPro; IPR006025; Pept M Zn BS.
DR Pfam; PF00045; Hemopexin; 4.
DR Pfam; PF00413; Peptidase M10; 1.
DR Pfam; PF03933; Peptidase M10_N; 1.
DR PRINTS; PR00138; MATRXIN.
DR SMART; SM00120; HX; 4.
DR SMART; SM00235; ZnMc; 1.
DR PROSITE; PS00024; HEMOPEXIN; 1.
DR PROSITE; PS00142; ZINC_PROTEASE; UNKNOWN 1.
SQ SEQUENCE 483 AA; 54171 MW; 4ABDF98A36E90EAF CRC64;

Query Match 45.1%; Score 1247; DB 2; Length 483;
Best Local Similarity 51.0%; Pred. No. 5.4e-93;
Matches 247; Conservative 72; Mismatches 137; Indels 28; Gaps 9;

Qy 4 LLLCLFFITSSAPPLVRYMTENE-ENMQLAQALNQPSYLEIECNHLVQSKNRLIDDK 62
Db 6 LLLLC---VHTYAPFAVPATEDRGNEQLAEYLKXFNLYNEDGTPITRKKH-SPFSEK 61
Qy 63 IREMQAFGLVTGKLDNTLEIMKTPRCGPDVGQYGV--TLPCWRKYNLTIRIINTP 120
Db 62 LQEMQAFGLVTVGKLDNTLEIMHKPRCGVADVAEYSHFGFRPTWRTSLTYRILGYTP 121
Qy 121 DMARAADVAIOEGLVMSKVTPLEKFTKISKIADIIMIAFTRVHRCPRY-FDGPLGLV 179
Db 122 DMAEADVTAIRRAFKWSVDVTPLETSRIYECTADIQISFGAGVHG--DFYFPDGPHTL 179
Qy 180 GHAPPPGCLGDTDFDEENWTKDAGENFLVAHAEFGHGLSHSNDQTALMFPNYV 239
Db 180 AHAFAPGNSIGDAHDFDEETWTAGSAGYNFLVAHAEFGHGLSHGSDRSALMPTYS 239
Qy 240 SLDRPKYPLSQDDINGIOSIYGLPK-VPAPKP-----EPTIPHACDPD 282

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Db 240 YIDPARFLPQDDVDGIQALYGASENPVPTTPQATTTTSTTTSSPINSDIPT 299
Qy 283 LTFDAITTFREVMFPKGRHLWRIYYDITDVEFLIASFWLSLADLOAAAYENPR-DKIL 341
Db 300 LVFDAITTLRGEIILFFKDSFWRRVPTIKYVNTPISTSWESLPSGIAAYENPETDQIF 359
Qy 342 VFKDENFMWIRGYAVLPDYPKSIHTLPGFGRVKKIDAAVCDKTRTKTYFFVGVGWCWREDE 401
Db 360 LFGSKKWALQGFILLNYPKNIDKLGFRVRKHNAAYVLTQTKTYFFPAGEQYWSYDE 419
Qy 402 MTQTMKGFPQVVRVHFGPISIRVDAAYQYKGFPSRSGKQFENYKTKNITRIMTRNT 461
Db 420 ARKTMKESPRIEDDFPGIGKVVHAFEDNGLLYFTSGHKQFENMKSKKVTRLKNTS 479
Qy 462 WFOC 465
Db 480 WLCG 483

RESULT 13
MM03 HORSE
ID MM03 HORSE STANDARD; PRT; 477 AA.
AC Q28397;
DT 30-MAY-2000 (Rel. 39, Created)
DT 30-MAY-2000 (Rel. 39, Last sequence update)
DT 01-OCT-2004 (Rel. 45, Last annotation update)
DE Stromelysin-1 precursor (EC 3.4.24.17) (Matrix metalloproteinase-3)
DE (MMP-3).
GN Name=MMP3;
OS Equus caballus (Horse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Perissodactyla; Equidae; Equus.
OX NCBI_TaxID=9796;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Cartilage;
RX MEDLINE=99074117; PubMed=9858406;
RA Richardson D.W., Dodge G.R.;
RT "Molecular characteristics of equine Stromelysin and the tissue
inhibitor of metalloproteinase 1.";
RL Am. J. Vet. Res. 59:1557-1562 (1998).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Cartilage;
RX MEDLINE=98104320; PubMed=9442239;
RA Balkman C.E., Nixon A.J.;
RT "Molecular cloning and cartilage gene expression of equine Stromelysin
1 (matrix metalloproteinase 3).";
RL Am. J. Vet. Res. 59:30-36 (1998).
RN [3]
RP 3D-STRUCTURE MODELING.
RA Mallena S.C., Sharma J.A.R.P.;
RT "Theoretical model of horse Stromelysin.";
RT Submitted (MAR-2002) to the PDB data bank.
CC -!- FUNCTION: Can degrade fibronectin, laminin, gelatins of type I,
III, IV, and V; Collagens III, IV, X, and IX, and cartilage
proteoglycans. Activates procollagenase.
CC -!- CATALYTIC ACTIVITY: Preferential cleavage where P1', P2' and P3'
are hydrophobic residues.
CC -!- COFACTOR: Binds 2 zinc ions and 4 calcium ions per subunit (By
similarity).
CC -!- SIMILARITY: Belongs to peptidase family M10A.
CC -!- SIMILARITY: Contains 1 hemopexin-like domain.
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or send an email to license@isb-sib.ch).
CC -----
CC EMBL; U62529; AAB05774.1; -

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DR PDB: 1L9I; Model; A=100-267.
DR MEROPS; M10.005; -.
DR InterPro; IPR000585; Hemopexin.
DR InterPro; IPR006026; Peptidase M.
DR InterPro; IPR001818; Pept M10A M12B.
DR InterPro; IPR006025; Pept M Zn BS.
DR InterPro; IPR009070; PGSD_like.
DR Pfam; PF00045; Hemopexin_4.
DR Pfam; PF00413; Peptidase_M10; 1.
DR Pfam; PF03933; Peptidase_M10_N; 1.
DR PRINTS; PR00138; MATRILIXIN.
DR SMART; SM00120; HX; 4.
DR SMART; SM00235; ZmMc; 1.
DR PROSITE; PS00546; CYSTEINE_SWITCH; FALSE_NEG.
DR PROSITE; PS00024; HEMOPEXIN; 1.
DR PROSITE; PS00142; ZINC_PROTEASE; 1.
DR 3D-structure; Calcium-binding; Collagen degradation;
KW Extracellular matrix; Glycoprotein; Hydrolase; Metal-binding;
KW Metalloprotease; Signal; Zinc; Zymogen.
FT SIGNAL 1 17 Potential.
FT PROPEP 18 99 Activation peptide.
FT CHAIN 100 477 Hemopexin-1.
FT DOMAIN 287 477 Hemopexin-like.
FT SITE 92 92 Cysteine switch (Potential).
FT METAL 124 124 Calcium 1 (By similarity).
FT METAL 158 158 Calcium 2 (By similarity).
FT METAL 168 168 Zinc 1 (By similarity).
FT METAL 170 170 Zinc 1 (By similarity).
FT METAL 175 175 Calcium 3 (By similarity).
FT METAL 176 176 Calcium 3 (via carbonyl oxygen) (By similarity).
FT METAL 178 178 Calcium 3 (via carbonyl oxygen) (By similarity).
FT METAL 180 180 Calcium 3 (via carbonyl oxygen) (By similarity).
FT METAL 183 183 Zinc 1 (By similarity).
FT METAL 190 190 Calcium 2 (via carbonyl oxygen) (By similarity).
FT METAL 192 192 Calcium 2 (via carbonyl oxygen) (By similarity).
FT METAL 194 194 Calcium 2 (By similarity).
FT METAL 196 196 Zinc 1 (By similarity).
FT METAL 198 198 Calcium 3 (By similarity).
FT METAL 199 199 Calcium 1 (By similarity).
FT METAL 201 201 Calcium 1 and 3 (By similarity).
FT METAL 218 218 Zinc 2 (catalytic) (By similarity).
FT ACT_SITE 219 219 By similarity.
FT METAL 222 222 Zinc 2 (catalytic) (By similarity).
FT METAL 228 228 Zinc 2 (catalytic) (By similarity).
FT METAL 297 297 Calcium 4 (via carbonyl oxygen) (By similarity).
FT METAL 389 389 Calcium 4 (via carbonyl oxygen) (By similarity).
FT METAL 438 438 Calcium 4 (via carbonyl oxygen) (By similarity).
FT CARBOHYD 120 120 N-linked (GlcNAc... ) (Potential).
FT DISULFID 290 477 By similarity.
FT CONFLICT 346 346 V -> E (in Ref. 2).
FT TURN 104 105
FT STRAND 113 118
FT TURN 123 124
FT HELIX 127 144
FT STRAND 148 151
FT STRAND 159 164
FT STRAND 182 184
FT TURN 180 193
FT STRAND 195 198
FT TURN 199 200
FT STRAND 203 204
FT STRAND 210 211
FT HELIX 212 224
FT TURN 225 225
FT TURN 232 233

FT TURN 235 236
FT HELIX 253 263
SQ SEQUENCE 477 AA; 54190 MW; 361CE1427E09A272 CRC64;

Query Match 45.0%; Score 1244; DB 1; Length 477;
Best Local Similarity 50.8%; Pred. No. 9.4e-93;
Matches 244; Conservative 73; Mismatches 145; Indels 18; Gaps 8;

QY 1 MKRLLLCLFFITFSAPFLVMTENEE-NMQLAQAYLNQFYSLIEGHNHLVSKNRSLI 59
Db 1 MKNLPITILLILCVAAACSAYPLDRSARDEDSNMDDLQYLEKYDYGKEMQYVRRKDSGPI 60
QY 60 DDKIREMOQAFGLTVTKGLDSNTLEMTKPRCGVPDVGQVGYTLPG---WRKNLTVRII 116
Db 61 VKKIEMQKFLGKLVTKGLDSNTVEVMHKSRCVDPVGHF-TTFPGMPKWSKTHLTVRI 119
QY 117 NYTPDMARAADVEIAIOEGLEVMSKVTPKFTKISKIADIIMIAFRTRVHGR-CPRYFDGP 175
Db 120 NYTQDLPRDAVSDVEKALKIWEVITPLTFSRIYEGEADIMITFAVREHGDFP--FDGP 177
QY 176 LGVIGHAFPPGCLGGDTHFDEDEWTKGAGNLFVAAHEFGHALGSHSNDQTALMF 235
Db 178 GKVLAHAYPPGPGMGNDHAFDDDEHWTGKDSGINFLLVAAHELGSLGLYHSTNTALMY 237
QY 236 PNVVSL-DRPKYPLSODDINGQSIYGLPKVPKPKPTIPH-----ACPDLTED 286
Db 238 PLYNTLKGPARVLSQDDVTGQSLYGGPPASPDSVPEPPEPPAPGTLAMCDPALSPD 297
QY 287 AITFERREVMFFKGRHLRIYYDITDVEFELIASFWPSLPADLQAAAYE-NPRDKILVFKD 345
Db 298 AISTLGRGELFFKORYFWRKTRTLVPEFHPISSEFWPSLPSGIDAAVEVTSRDSVFIKFG 357
QY 346 ENFMWIRGYAVLPDYPKSIHTLGFGRVKIDAAVCDKTRKTYFFVGVWCFWDFEMTQT 405
Db 358 NKFWAIRGNEBQAGYPRGIHTLGFPTVRKIDAAIEFKOKTYFFVEDKYWRFKRQS 417
QY 406 MKGFGPQRVVKVPPGISIRVDAAFQYKGFPPFSRSGSQFEYNIKTKNITRMTNWFQC 465
Db 418 MEFGYKQIAEDFPFGIDSKLDAAFESFGFFYFSGSSQFEEDNNAKVTHVLSKSNWFNC 477

RESULT 14
M10_MOUSE STANDARD; PRT; 476 AA.
AC Q55123;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Stromelysin-2 precursor (EC 3.4.24.22) (Matrix metalloproteinase-10)
DE (MMP-10) (Transin-2) (SL-2).
GN Name=Mmp10;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]_TaxID=10090;
RP SEQUENCE FROM N.A.
RC STRAIN=BALB/c;
RX MEDLINE=98087420; PubMed=9427548;
RA Madlener M., Werner S.;
RT "cDNA cloning and expression of the gene encoding murine Stromelysin-2
(RMMP-10).";
RL Gene 202:75-81(1997).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Cecum;
RX MEDLINE=22354683; PubMed=12466851; DOI=10.1038/nature01266;
RA Okazaki Y., Furuno M., Kasukawa T., Adachi J., Bono H., Kondo S.,
RA Nikaido I., Osato N., Saito R., Suzuki H., Yamanaka I., Kiyosawa H.,
RA Yagi K., Tomaru Y., Hasegawa Y., Nogami A., Schonbach C., Gojobori T.,
RA Baldarelli R., Hill D.P., Bult C., Hume D.A., Quackenbush J.,
RA Schriml L.M., Kanapin A., Matsuda H., Batalov S., Beisel K.W.,
RA Blake J.A., Bradt D., Brusic V., Chothia C., Corbani L.E., Cousins S.,

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Dalla E., Dragani T.A., Fletcher C.F., Forrest A., Frazer K.S.,
 GAasterland T., Gariboldi M., Gissi C., Godzic A., Gough J.,
 RA Grimmond S., Gutinich S., Hirokawa N., Jackson I.J., Jarvis E.D.,
 RA Kanai A., Kawaji H., Kawasawa Y., Kedzierski R.M., King B.L.,
 RA Konagaya A., Kurochkin I.V., Lee Y., Lenhard B., Lyons P.A.,
 RA Maglott D.R., Maltais L., Marchionni L., McKenzie L., Miki H.,
 RA Nagashima T., Numa K., Okido T., Pavan W.J., Portea G., Pesole G.,
 RA Petrovsky N., Pillai R., Pontius J.U., Qi D., Ramachandran S.,
 RA Ravasi T., Reed J.C., Reed D.J., Reid J., Ring B.Z., Ringwald M.,
 RA Sanderlin A., Schneider C., Sample C.A., Setou M., Shimada K.,
 RA Sultana R., Takenaka Y., Taylor M.S., Teasdale R.D., Tomita M.,
 RA Varaldo R., Wagner L., Walestedt C., Wang Y., Watanabe Y., Wells C.,
 RA Wilming L.G., Wynshaw-Boris A., Yanagisawa M., Yang I., Yang L.,
 RA Yuan Z., Zavolan M., Zhu Y., Zimmer A., Carninci P., Hayatsu N.,
 RA Hirozane-Kishikawa T., Konno H., Nakamura M., Sakazume N., Sato K.,
 RA Shiraki T., Waki K., Kawai J., Aizawa K., Arakawa T., Fukuda S.,
 RA Hara A., Haashizume W., Imotani K., Ishii Y., Itoh M., Kagawa I.,
 RA Miyazaki A., Sakai K., Sasaki D., Shibata K., Shinagawa A.,
 RA Yasunishi A., Yoshino M., Waterston R., Lander E.S., Rogers J.,
 RA Birney E., Hayashizaki Y.,
 RT "Analysis of the mouse transcriptome based on functional annotation of
 RT 60,770 full-length cDNAs";
 RL Nature 420:563-573 (2002).
 CC -I- FUNCTION: Can degrade fibronectin, gelatins of type I, III, IV,
 CC and V; weakly collagens III, IV, and V. Activates procollagenase.
 CC -I- CATALYTIC ACTIVITY: Similar to stromelysin 1, but action on
 CC collagen types III, IV and V is weak.
 CC -I- COFACTOR: Binds 2 zinc ions per subunit, calcium (By similarity).
 CC -I- TISSUE SPECIFICITY: Expressed in small intestine. Weak levels in
 CC heart and lung.
 CC -I- INDUCTION: By wounding.
 CC -I- SIMILARITY: Belongs to peptidase family M10A.
 CC -I- SIMILARITY: Contains 1 hemoexin-like domain.
 CC
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
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 CC
 CC -----
 CC ENBL; Y13185; CAA73641.1; -;
 DR EMBL; AK020292; BAB32058.1; -;
 DR FTR; JC6505; JG6505.
 DR HSP; P08254; LG05.
 DR MEROPS; M10.006; -;
 DR MGD; MGI:97007; Mmp10.
 DR InterPro; IPR000585; Hemoexin.
 DR InterPro; IPR006026; Peptidase M.
 DR InterPro; IPR001843; Pept M10A_M10C.
 DR InterPro; IPR001818; Pept M10A_M12B.
 DR InterPro; IPR006025; Pept_M_zn_BS.
 DR InterPro; IPR009070; PGDB_like.
 DR Pfam; PF02051; Fragilysin; 1.
 DR Pfam; PF00045; Hemoexin; 4.
 DR Pfam; PF00413; Peptidase M10; 1.
 DR Pfam; PF03933; Peptidase_M10_N; 1.
 DR PRINTS; PR00138; MATRXIN.
 DR SMART; SM00120; HX; 4.
 DR SMART; SM00235; ZnMc; 1.
 DR PROSITE; PS00546; CYSTEINE SWITCH; 1.
 DR PROSITE; PS00024; HEMOPEXIN; 1.
 DR PROSITE; PS00142; ZINC_PROTEASE; 1.
 KW Calcium; Collagen degradation; Extracellular matrix; Hydrolase;
 KW Metalloprotease; Signal; Zinc; Zymogen.
 FT SIGNAL 1 17 Probable.
 FT PROPEP 18 99 Activation peptide (By similarity).
 FT CHAIN 100 476 Stromelysin-2.
 FT FT DOMAIN 286 476 Hemoexin-like.
 FT SITE 92 92 Cysteine switch (By similarity).
 FT METAL 218 218 Zinc (catalytic) (By similarity).
 FT ACT SITE 219 219 By similarity.

FT	METAL	222	222	Zinc (catalytic) (By similarity).
FT	METAL	228	228	Zinc (catalytic) (By similarity).
FT	DISULFID	289	476	By similarity
SQ	SEQUENCE	476 AA;	53911 MW; 2EBIC41468FOAC6 CRC64;	

Query Match 45.0%; Score 1243.5; DB 1; Length 476;
Best Local Similarity 50.8%; Pred. No. 1e-92;
Matches 244; Conservative 77; Mismatches 140; Indels 19; Gaps 9;

Qy	1	MKRLLLICLPFI	TFSSAPFL	VRMTENE	NMQLAAQ	YLNOFYS	LEIGNH	LVQSKRS	LI 59
Db	1	MEPLAILALL	SPLTCSAY	PLHGA	VTQGH	PSMDLA	QAQYLE	KYINP	KNEKQIF
Qy	60	DDKIREMQA	FFGLTV	TCKLDS	NTLEIM	KTPRC	GVDP	GVQY	GYTLPG
Db	61	VKKIQEMQ	KFLGLE	MTCKLDS	NTMELM	HKPRC	GVDP	VGGS	TFPGSP
Qy	117	NYTPDMARA	AVDAIR	QBLE	SVKVP	PLKFT	KISG	IADMI	AFRTVR
Db	120	NYTPDLPRQ	VSQVSA	EKALK	WVEV	PLTFS	RIS	EGEAD	IMISF
Qy	176	LGVLGHAF	PPGGLGG	THDE	ENWTKO	GAGFN	FLV	AAHE	RGHALG
Db	178	GQSLAHAY	PPGPGY	GVDFH	DDKWT	LAPSG	TNLF	LVAA	HELGSL
Qy	236	PNY-VSLD	PRKYP	PLSQD	DI	QSI	YGG	-----	LPKVP
Db	238	PVTRFST	SPANF	HL	SQD	IEG	ISLY	GAGSS	DATV
Qy	287	AITTFREV	MFKGR	HLW	RIY	YDIT	VEFEL	IAS	FWPSLP
Db	297	SVSTLR	GEVLF	FKD	YPR	WRSHN	PEPE	FLIS	AFWPT
Qy	346	ENFWMR	IGYAV	LDY	PKSI	IHTL	GPGR	VKKID	AAVCD
Db	357	SQFWAV	RGN	EVQAG	YPKGI	HTLGP	PTPV	VKKID	AAVFE
Qy	406	MDKGF	OPRV	VKHP	PGS	IRV	DAAF	QYKGR	FFFSR
Db	417	MDKGF	PFQI	TDDP	FG	HP	QVDA	VHE	FGFF

RESULT 15
NM10 HUMAN ID _NM10 HUMAN STANDARD; PRG; 476 AA.
AC P09238;
DT 01-MAR-1989 (Rel. 10, Created)
DT 01-MAR-1989 (Rel. 10, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Stromelysin-2 precursor (EC 3.4.24.22) (Matrix metalloproteinase-10)
DE (WMP-10) (Transin-2) (SL-2).
GN Name=MMP10; Synonyms=STMY2.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=88339885; PubMed=2844164;
RA Muller D., Quantin B., Gesnel M.-C., Millon-Colliard R., Abecassis J.,
RA Breatnach R.;
RT "The collagenase gene family in humans consists of at least four
RT members.";
RL Biochem. J. 253:187-192(1988).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Ovary;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strauberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shennen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A., Rubin G.M., Hong I.,
RN [3]

Matches	244;	Conservative	77;	Mismatches	136;	Indels	18;	Gaps
QY	4	LLLLCLFFITFSAPPLVLRWTENEE-NMQIAQAYLVNQFYSLIEIGNHLVQSKNRSLLDDK	62					
Db	7	LVLVLL---PVCSSPLSGAAKBEDSNKDLAQQLLEKYNNLEKDVQP-RRKDSNLLVKK	62					
QY	63	IREMQAFGLTGVTKLDSNTLEIMTKPRCGVPDVGQYGY--TLPGWRKYNLTIRIINTP	120					
Db	63	IQGMQKPLGLEVTGKLDTDLTLEVWRKPRCGVPDVGHFSSFPGMKPKWRKTHUTYRLVNTYP	122					
QY	121	DMARAAVDEAIOBQGLEVSWSKVTPLKFTKISKGIADIMIAFRTRVHGRCPRYFDGGLGVLG	180					
Db	123	DLPRDAVSAIEALKVWEEVTPLTFSRLYEADIMISPAVKEHGD-YSFDGPGCHSLA	181					
QY	181	HAPPGPGLGDDTHFDEDEWTKDGCAGFNFLVAAHBEFGHGLGSHSNDQTLALPPNYVS	240					
Db	182	HAYPPGEGLYGDIHFDDDEKWTEDASGNTFLVAAHELGHSLGSHFSANTEALMPLVLYNS	241					
QY	241	L-DPRKPLSQDDINGIQSIYGGLPKVPKAPKPT-----IPHACDPLDTFOAITTF	291					
Db	242	FTELAQRLSQDDVNGIQLSYGPPPTASTEELPVTKSVPSGSEMPAKCDPALSPDAISTL	301					
QY	292	RREVMFPKGHLWRIYYDITDVEBELIASFWPSLPADLQAAYE-NPRDKILVFKDENFWM	350					
Db	302	RGEYLPFKDRIYFWRRSWNPEPEPHLISAEWPSLPSYLDAAAYEVSRSRTVFIFKGNERWA	361					
QY	351	IRGVAVLPDYPKSIHTLIGFPGRCVKKIDAAVCDDTKTRTKTYFVGVICWCFDEMTQMDKGF	410					
Db	362	IRGNEVQAGPRGLHTLIGFPPTIRKIDAAVSDKEKKTYTFAADKYWRFDENSQSWEQGF	421					
QY	411	QORVVKHFPGISIRVDAAFOYKGFFFFSRGSQKQFEYNIKTKNITRIMTNTWTFQC	465					
Db	422	PRITADFPGEVPEKPVDAVLOAFGEYFYFFSGSOFEDPNARWVTHILKSNLSLHC	476					

Search completed: November 15, 2004, 21:01:16
Job time : 112 secs

GenCore version 5.1.6
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OM nucleic - protein search, using frame_plus_n2p model

Run on: November 15, 2004, 20:20:25 ; Search time 218.5 Seconds
(without alignments)
5269.233 Million cell updates/sec

Title: US-10-729-807-28

Perfect score: 2930

Sequence: 1 gcttcagctgaagaagaga.....aattcgttcaaatagaa 1627

Scoring table:

BLOSUM62
Xgapop 10.0 , Xgapext 0.5
Ygapop 10.0 , Ygapext 0.5
Delop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 1568699 seqs, 353819137 residues

Total number of hits satisfying chosen parameters: 3137398

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Command line parameters:

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-Q=/cgn2_1/USPTO_spool/US10729807/runat_15112004_131152_14743/app_query.fasta_1.1799
-DB=Published Applications AA_QMFT-fastan -SUFFIX=rapb -MINMATCH=0.1
-LOOPCL=0 -LOOPEXT=0 -UNITS=bits -START=1 -END=-1 -MATRIX=blosum62
-TRANS=human40.cdi -LIST=45 -DOCLALIGN=200 -THR SCORE=pct -THR MAX=100
-THR MIN=0 -ALIGN=15 -MODE=LOCAL -OUTFMT=ptc -NORM=ext -HEAPSIZE=500 -MINLEN=0
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-LONGLOG -DEV TIMEOUT=120 -WARN TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5
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Database :

Published Applications AA:
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2: /cgn2_6/ptodata/1/pubpaa/PCT_NEW_PUB.pep.*
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20: /cgn2_6/ptodata/1/pubpaa/US60_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result Query

No.	Score	Match	Length	DB	ID	Description
1	2763	94.3	513	10	US-09-862-631-4	Sequence 4, Appli
2	2763	94.3	513	16	US-10-729-807-10	Sequence 10, Appl
3	2752	93.9	513	10	US-09-759-130B-173	Sequence 173, App
4	2752	93.9	513	14	US-10-028-072-192	Sequence 192, App
5	2752	93.9	513	14	US-10-140-808-192	Sequence 192, App
6	2752	93.9	513	14	US-10-121-049-192	Sequence 192, App
7	2752	93.9	513	14	US-10-123-904-192	Sequence 192, App
8	2752	93.9	513	14	US-10-140-470-192	Sequence 192, App
9	2752	93.9	513	14	US-10-175-746-192	Sequence 192, App
10	2752	93.9	513	14	US-10-176-918-192	Sequence 192, App
11	2752	93.9	513	14	US-10-176-921-192	Sequence 192, App
12	2752	93.9	513	14	US-10-137-865-192	Sequence 192, App
13	2752	93.9	513	14	US-10-140-474-192	Sequence 192, App
14	2752	93.9	513	14	US-10-142-431-192	Sequence 192, App
15	2752	93.9	513	14	US-10-143-114-192	Sequence 192, App
16	2752	93.9	513	14	US-10-140-003-192	Sequence 192, App
17	2752	93.9	513	14	US-10-142-419-192	Sequence 192, App
18	2752	93.9	513	14	US-10-123-262-192	Sequence 192, App
19	2752	93.9	513	14	US-10-142-423-192	Sequence 192, App
20	2752	93.9	513	14	US-10-121-050-192	Sequence 192, App
21	2752	93.9	513	14	US-10-141-755-192	Sequence 192, App
22	2752	93.9	513	14	US-10-143-032-192	Sequence 192, App
23	2752	93.9	513	14	US-10-123-108-192	Sequence 192, App
24	2752	93.9	513	14	US-10-123-236-192	Sequence 192, App
25	2752	93.9	513	14	US-10-123-261-192	Sequence 192, App
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33	2752	93.9	513	14	US-10-140-925-192	Sequence 192, App
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35	2752	93.9	513	14	US-10-124-824-192	Sequence 192, App
36	2752	93.9	513	14	US-10-127-825A-192	Sequence 192, App
37	2752	93.9	513	14	US-10-127-829A-192	Sequence 192, App
38	2752	93.9	513	14	US-10-127-835A-192	Sequence 192, App
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40	2752	93.9	513	14	US-10-127-901A-192	Sequence 192, App
41	2752	93.9	513	14	US-10-128-693A-192	Sequence 192, App
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44	2752	93.9	513	14	US-10-131-823A-192	Sequence 192, App
45	2752	93.9	513	14	US-10-131-824A-192	Sequence 192, App

ALIGNMENTS

RESULT 1
US-09-862-631-4
; Sequence 4, Application US/09862631
; Publication No. US20030032164A1
; GENERAL INFORMATION:
; APPLICANT: Holmgren, Erik
; APPLICANT: Kihlen, Mats
; APPLICANT: Wood, Tim
; APPLICANT: Ekblom, Jonas
; TITLE OF INVENTION: Novel Matrix Metalloproteinases
; FILE REFERENCE: 00014regus
; CURRENT APPLICATION NUMBER: US/09/862,631
; PRIORITY FILING DATE: 2000-05-22
; PRIOR FILING DATE: 2000-05-22
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 4
; LENGTH: 513
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-862-631-4

301	ArgHisLeuTrpArgIleTyrTyrAspIleThrAspValGluPheGluLeuIleAlaSer	320
984	TTCTGGGCATCTCTGCAGCTGATCTGCAAGCTGCATACGAGAACCCAGAGATAGATT	1043
321	PheTrpProSerLeuProAlaAspLeuGlnAlaAlaTyrGluAsnProArgAspLysIle	340
1044	CTGGTTTTAAAGATGAAACTTCTGGATGATCAGAGGATATGCTGTCITTCGCCAGATTAT	1103
341	LeuValPheLysAspGluAsnPheTrpMetIleArgGlyTyrAlaValLeuProAspTyr	360
1104	CCCAATCCATCCATACATTAAGTGTTCACAGGAGCTGTGAAGAAATAAGATGCAGCCGCT	1163
361	ProLysSerIleHisThrLeuGlyPheProGlyArgValLysIleAspAlaAlaVal	380
1164	TGTCATTAAGACCACAAGAAAACCTACTCTCTTCCTGGGCATTTGGTGCTCGAGGTTTGAT	1223
381	CysAspLysThrThrArgLysThrTyrPhePheValGlyIleTyrCysTrpArgPheAsp	400
1224	GAAATGACCCCAACCATCGACAAGATTCCTCCGAGAGAGTGGTAAACACTTTTCCTGGA	1283
401	GluMetThrGlnThrMetAspLysGlyPheProGlnArgValLysHisPheProGly	420
1284	ATCAGTATCCGTGTGATGCTGCTTCCAGTACAAAGATTCTTCTTTTCAGCCGTGGA	1343
421	IleSerIleArgValAspAlaAlaPheGlnTyrLysGlyPhePhePheSerArgGly	440
1344	TCAAAGCAATTTGAATACAAACATTAAAGACAAAGAATATTACCCGAATCATGAGAACTAAT	1403
441	SerLysGlnPheGluTyrAsnIleLysThrLysAsnIleThrArgIleMetArgThrAsn	460
1404	ACTTGGTTTCAATGCAAAGAACCAAGAACTCTCATTTGGTTTGGTATATCAACAAGAA	1463
461	ThrTrpPheGlnCysLysGluProLysAsnSerPheGlyPheAspIleAsnLysGlu	480
1464	AAAGCACATTCAGGAGGCATAAAGATATTGTATCATAAAGAGTTTAAAGCTGTGTTATTTT	1523
481	LysAlaHisSerGlyGlyIleLysIleLeuTyrHisLysSerLeuSerLeuPheIlePhe	500
1524	GGTATTGTTCAATTGCTGAAAACACTTCTATTTATCAA	1562
501	GlyIleValHisLeuLeuLysAsnThrSerIleTyrGln	513

US-10-729-807-28 (1-1627) X US-09-759-130B-173 (1-513)

RESULT 4
US-10-028-072-192
; Sequence 132, Application US/10028072
; Publication No. US2003000431A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Bresini, Maureen
; APPLICANT: Berge, Laura
; APPLICANT: Desnoyers, Luc
; APPLICANT: Filvaroff, Ellen

APPLICANT: Gao,Wei-Qiang
APPLICANT: Gerritsen,Mary E.
APPLICANT: Goddard,Audrey
APPLICANT: Godowski,Paul J.
APPLICANT: Gurney,Austin L.
APPLICANT: Sherwood,Steven
APPLICANT: Smith,Victoria
APPLICANT: Stewart,Timothy A.
APPLICANT: Tumas,Daniel
APPLICANT: Watanabe,Colin K
APPLICANT: Wood,William
APPLICANT: Zhang
TITLE OF INVENTION:
FILE REFERENCE:
CURRENT APPLICATION NUMBER: US/10/028,072
CURRENT FILING DATE: 2001-12-19
PRIOR APPLICATION NUMBER: 60/049911
PRIOR FILING DATE: 1997-06-18
PRIOR APPLICATION NUMBER: 60/056974
PRIOR FILING DATE: 1997-08-26
PRIOR APPLICATION NUMBER: 60/059113
PRIOR FILING DATE: 1997-09-17
PRIOR APPLICATION NUMBER: 60/059115
PRIOR FILING DATE: 1997-09-17
PRIOR APPLICATION NUMBER: 60/059117
PRIOR FILING DATE: 1997-09-17
PRIOR APPLICATION NUMBER: 60/059122
PRIOR FILING DATE: 1997-09-17
PRIOR APPLICATION NUMBER: 60/059184
PRIOR FILING DATE: 1997-09-17
PRIOR APPLICATION NUMBER: 60/059263
PRIOR FILING DATE: 1997-09-18
PRIOR APPLICATION NUMBER: 60/059352
PRIOR FILING DATE: 1997-09-19
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PRIOR APPLICATION NUMBER: 60/062287
PRIOR FILING DATE: 1997-10-17
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PRIOR APPLICATION NUMBER: 60/062816
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PRIOR APPLICATION NUMBER: 60/063045
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PRIOR FILING DATE: 1998-01-23
PRIOR APPLICATION NUMBER: 60/073612
PRIOR FILING DATE: 1998-02-04
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PRIOR FILING DATE: 1998-02-09
PRIOR APPLICATION NUMBER: 60/074092
PRIOR FILING DATE: 1998-02-09
PRIOR APPLICATION NUMBER: 60/077791
PRIOR FILING DATE: 1998-03-12
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PRIOR FILING DATE: 1998-03-20
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PRIOR APPLICATION NUMBER: 60/079663
PRIOR FILING DATE: 1998-02-27
PRIOR APPLICATION NUMBER: 60/079728
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PRIOR FILING DATE: 1998-03-31
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PRIOR FILING DATE: 1998-04-09
PRIOR APPLICATION NUMBER: 60/081229
PRIOR FILING DATE: 1998-04-09
PRIOR APPLICATION NUMBER: 60/081695
PRIOR FILING DATE: 1998-04-14
PRIOR APPLICATION NUMBER: 60/081817
PRIOR FILING DATE: 1998-04-15
PRIOR APPLICATION NUMBER: 60/081818
PRIOR FILING DATE: 1998-04-15
PRIOR APPLICATION NUMBER: 60/082999
PRIOR FILING DATE: 1998-04-24
PRIOR APPLICATION NUMBER: 60/083322
PRIOR FILING DATE: 1998-04-28
PRIOR APPLICATION NUMBER: 60/083545
PRIOR FILING DATE: 1998-04-29
PRIOR APPLICATION NUMBER: 60/084600
PRIOR FILING DATE: 1998-05-07
PRIOR APPLICATION NUMBER: 60/084627
PRIOR FILING DATE: 1998-05-07
PRIOR APPLICATION NUMBER: 60/084637
PRIOR FILING DATE: 1998-05-07
PRIOR APPLICATION NUMBER: 60/085149
PRIOR FILING DATE: 1998-05-12
PRIOR APPLICATION NUMBER: 60/085323
PRIOR FILING DATE: 1998-05-13
PRIOR APPLICATION NUMBER: 60/085338
PRIOR FILING DATE: 1998-05-13
PRIOR APPLICATION NUMBER: 60/085339
PRIOR FILING DATE: 1998-05-13

QY	264	AACACCCCTTGAGATCATGAAGACACCCAGGTGGGTGCTGATGTGGCCAGTATGGC	323
Db	81	AsnThrLeuGluIleMetLysThrProArgCysGlyValProAspValGlyGlnTyrGly	100
QY	324	TACACCCCTCCCTGGTGGAGAAAATACAACCTCACCTACAGATAATAAATACTATACCG	383
Db	101	TyrThrLeuProGlyTyrArgLysTyrAsnLeuThrTyrArgIleIleAsnTyrThrPro	120
QY	384	GATATGGCAGAGCTGTGTGATGAGGCTATCCAGAAGGTTTAGAAGTGTGGAGCAAA	443
Db	121	AspMetAlaArgAlaAlaValAspGluAlaIleGlnGluGlyLeuGluValTyrSerLys	140
QY	444	GTCACTCCCACTAAAATTCACCAAGATTTCAAAGGGGATTCACAGACATCATGATTCCTTT	503
Db	141	ValThrProLeuLysPheThrLysIleSerLysGlyIleAlaAspIleMetIleAlaPhe	160
QY	504	AGGACTCGAGTCCATGGTGGTGTCTCGCTATTTTGTATGCTCCCTCGGAGTGTCTGCG	563
Db	161	ArgThrArgValHisGlyArgCysProArgTyrPheAspGlyProLeuGlyValLeuGly	180
QY	564	CATGCTCTTCTCTGCTCGGTCTGGGTGGTGACACTCATTTTGTGCTGCTCATGAAATTTGGT	623
Db	181	HisAlaPheProProGlyProGlyLeuGlyGlyAspThrHisPheAspGluAspGluAsn	200
QY	624	TGGACCAAGGATGGAGCAGGATTCAACTTGTCTTGTGGCTGCTCATGAAATTTGGT	683
Db	201	TyrThrLysAspGlyAlaGlyPheAsnLeuPheLeuValAlaAlaHisGluPheGlyHis	220
QY	684	GCACTGGGCTCTCTCACTCCCAATGATCAACAGCCTTGATGTTCCCAATATGCTCC	743
Db	221	AlaLeuGlyLeuSerHisSerAsnAspGlnThrAlaLeuMetPheProAsnTyrValSer	240
QY	744	CTGGATCCCAAGAAATACCCACTTTCTCAGGATGATATCAATGGAATCCAGTCCATCTAT	803
Db	241	LeuAspProArgLysTyrProLeuSerGlnAspIleAsnGlyIleGlnSerIleTyr	260
QY	804	GGAGGTCTGCTAAGTACTGCTAAGCCAAAGAACCCACTATATACCCCATGCTGTGAC	863
Db	261	GlyGlyLeuProLysValProAlaLysProLysGluProThrIleProHisAlaCysAsp	280
QY	864	CCTGACTTGACTTTTGACGCTATCACACTTTCCGAGAGAGTAAATGTTCTTTAAAGGC	923
Db	281	ProAspLeuThrPheAspAlaIleThrThrPheArgGluValMetPhePheLysGly	300
QY	924	AGGCACCTATGGAGGATCTATTATGATATACCGATGTTGAGTTTGAATTAATGCTTCA	983
Db	301	ArgHisLeuThrPheArgLysTyrThrPheValGluPheGluLeuLeuAlaSer	320
QY	984	TTCTGGCCATCTCTGCCAGCTGATCTGCAAGCTGCATACGAGAACCCGAGAGATAGATT	1043
Db	321	PheThrProSerLeuProAlaAspLeuGlnAlaAlaTyrGluAsnProArgAspLysIle	340
QY	1044	CTGGTTTTTAAAGATGAAACTTCTGGATGATCAGAGGATGCTGCTGCTGCCAGATTAT	1103
Db	341	LeuValPheLysAspGluAsnPheThrPheMetIleArgGlyTyrAlaValLeuProAspTyr	360
QY	1104	CCCAATCCCATCATACATATTAGGTTTTTCCAGAGCTGTGAAGAAAATAGATGCGCCGTC	1163
Db	361	ProLysSerIleHisThrLeuGlyPheProGlyArgValLysLysIleAspAlaVal	380
QY	1164	TGTGATAAGACCAAGAAAACCTACTCTTTTGTGGGCATTTGGTGTGGAGTTTGTAT	1223
Db	381	CysAspLysThrThrArgLysThrTyrPhePheValGlyIleTyrCysThrArgPheAsp	400
QY	1224	GAATGACCCCAACCATGGACAAAGGATTTCCCGCAGAGAGTGGTGAACACATTTCTCGGA	1283
Db	401	GluMetThrGlnThrMetAspLysGlyPheProGlnArgValValLysHisPheProGly	420
QY	1284	ATCAGTATCCGTGTTGATGCTGCTTTCCAGTACAAAGGATTTCTTTTTCAGCCGTTGA	1343
Db	421	IleSerIleArgValAspAlaAlaPheGlnTyrLysGlyPhePhePheSerArgGly	440
QY	1344	TCAAAGCAATTGGAATCAACATTAAGACAAAGATATTATCCCGAATCATGAGAACTAAT	1403

PRIOR APPLICATION NUMBER: 60/085579		QY	264	AACACCTTGAGATCATGAAGACACCCAGGTGGGTGCTGATGTGGCCAGTATGGC	323
PRIOR FILING DATE: 1998-05-15					
PRIOR APPLICATION NUMBER: 60/085697		Db	81	AsnThrLeuGluIleMetLysThrProArgCysGlyValProAspValGlyGlnTyrGly	100
PRIOR FILING DATE: 1998-05-15					
PRIOR APPLICATION NUMBER: 60/085704		QY	324	TACACCTTCCTGGTGGAGAAAATACAACCTCACCTACAGATAATAAATACTATACCG	383
PRIOR FILING DATE: 1998-05-15					
PRIOR APPLICATION NUMBER: 60/086414		Db	101	TyrThrLeuProGlyTyrArgLysTyrAsnLeuThrTyrArgIleIleAsnTyrThrPro	120
PRIOR FILING DATE: 1998-05-22					
PRIOR APPLICATION NUMBER: 60/086430		QY	384	GATATGGCAGAGCTGTGTGATGAGGCTATCCAGAAGGTTTAGAAGTGTGGAGCAAA	443
PRIOR FILING DATE: 1998-05-22					
PRIOR APPLICATION NUMBER: 60/087106		Db	121	AspMetAlaArgAlaAlaValAspGluAlaIleGlnGluGlyLeuGluValTyrSerLys	140
PRIOR FILING DATE: 1998-05-28					
PRIOR APPLICATION NUMBER: 60/088026		QY	444	GTCACTCCCACTAAAATTCACCAAGATTTCAAAGGGGATTCACAGACATCATGATTCCTTT	503
PRIOR FILING DATE: 1998-06-04					
PRIOR APPLICATION NUMBER: 60/088730		Db	141	ValThrProLeuLysPheThrLysIleSerLysGlyIleAlaAspIleMetIleAlaPhe	160
PRIOR FILING DATE: 1998-06-10					
PRIOR APPLICATION NUMBER: 60/088741		QY	504	AGGACTCGAGTCCATGGTGGTGTCTCGCTATTTTGTATGCTCCCTCGGAGTGTCTGCG	563
PRIOR FILING DATE: 1998-06-10					
PRIOR APPLICATION NUMBER: 60/088810		Db	161	ArgThrArgValHisGlyArgCysProArgTyrPheAspGlyProLeuGlyValLeuGly	180
PRIOR FILING DATE: 1998-06-10					
PRIOR APPLICATION NUMBER: 60/089599		QY	564	CATGCTCTTCTCTGCTCGGTCTGGGTGGTGACACTCATTTTGTGCTGCTCATGAAATTTGGT	623
PRIOR FILING DATE: 1998-06-17					
PRIOR APPLICATION NUMBER: 60/089907		Db	181	HisAlaPheProProGlyProGlyLeuGlyGlyAspThrHisPheAspGluAspGluAsn	200
PRIOR FILING DATE: 1998-06-18					
PRIOR APPLICATION NUMBER: 60/089947		QY	624	TGGACCAAGGATGGAGCAGGATTCAACTTGTCTTGTGGCTGCTCATGAAATTTGGT	683
PRIOR FILING DATE: 1998-06-19					
PRIOR APPLICATION NUMBER: 60/090349		Db	201	TyrThrLysAspGlyAlaGlyPheAsnLeuPheLeuValAlaAlaHisGluPheGlyHis	220
PRIOR FILING DATE: 1998-06-23					
PRIOR APPLICATION NUMBER: 60/090429		QY	684	GCCTGGGCTCTCTCACTCCCAATGATCAACAGCCTTGATGTTCCCAATATGCTCC	743
PRIOR FILING DATE: 1998-06-24					
PRIOR APPLICATION NUMBER: 60/090445		Db	221	AlaLeuGlyLeuSerHisSerAsnAspGlnThrAlaLeuMetPheProAsnTyrValSer	240
PRIOR FILING DATE: 1998-06-24					
PRIOR APPLICATION NUMBER: 60/090538		QY	744	CTGGATCCCAAGAAATACCCACTTTCTCAGGATGATATCAATGGAATCCAGTCCATCTAT	803
PRIOR FILING DATE: 1998-06-24					
PRIOR APPLICATION NUMBER: 60/090863		Db	241	LeuAspProArgLysTyrProLeuSerGlnAspIleAsnGlyIleGlnSerIleTyr	260
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PRIOR APPLICATION NUMBER: 60/091360		QY	804	GGAGGTCTGCTAAGTACTGCTAAGCCAAAGAACCCACTATATACCCCATGCTGTGAC	863
PRIOR FILING DATE: 1998-07-01					
PRIOR APPLICATION NUMBER: 60/091519		Db	261	GlyGlyLeuProLysValProAlaLysProLysGluProThrIleProHisAlaCysAsp	280
PRIOR FILING DATE: 1998-07-02					
PRIOR APPLICATION NUMBER: 60/091982		QY	864	CTGACTTGACTTTTGACGCTATCACACTTTCCGAGAGAGTAAATGTTCTTTAAAGGC	923
PRIOR FILING DATE: 1998-07-07					
PRIOR APPLICATION NUMBER: 60/091982		Db	281	ProAspLeuThrPheAspAlaIleThrThrPheArgGluValMetPhePheLysGly	300
PRIOR FILING DATE: 1998-07-07					
PRIOR APPLICATION NUMBER: 60/091982		QY	924	AGGCACCTATGGAGGATCTATTATGATATACCGATGTTGAGTTTGAATTAATGCTTCA	983
PRIOR FILING DATE: 1998-07-07					
PRIOR APPLICATION NUMBER: 60/091982		Db	301	ArgHisLeuThrPheArgLysTyrThrPheValGluPheGluLeuLeuAlaSer	320
PRIOR FILING DATE: 1998-07-07					
PRIOR APPLICATION NUMBER: 60/091982		QY	984	TTCTGGCCATCTCTGCCAGCTGATCTGCAAGCTGCATACGAGAACCCGAGAGATAGATT	1043
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PRIOR APPLICATION NUMBER: 60/091982		Db	321	PheThrProSerLeuProAlaAspLeuGlnAlaAlaTyrGluAsnProArgAspLysIle	340
PRIOR FILING DATE: 1998-07-07					
PRIOR APPLICATION NUMBER: 60/091982		QY	1044	CTGGTTTTTAAAGATGAAACTTCTGGATGATCAGAGGATGCTGCTGCTGCCAGATTAT	1103
PRIOR FILING DATE: 1998-07-07					
PRIOR APPLICATION NUMBER: 60/091982		Db	341	LeuValPheLysAspGluAsnPheThrPheMetIleArgGlyTyrAlaValLeuProAspTyr	360
PRIOR FILING DATE: 1998-07-07					
PRIOR APPLICATION NUMBER: 60/091982		QY	1104	CCCAATCCCATCATACATATTAGGTTTTTCCAGAGCTGTGAAGAAAATAGATGCGCCGTC	1163
PRIOR FILING DATE: 1998-07-07					
PRIOR APPLICATION NUMBER: 60/091982		Db	361	ProLysSerIleHisThrLeuGlyPheProGlyArgValLysLysIleAspAlaVal	380
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PRIOR APPLICATION NUMBER: 60/091982		QY	1164	TGTGATAAGACCAAGAAAACCTACTCTTTTGTGGGCATTTGGTGTGGAGTTTGTAT	1223
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PRIOR APPLICATION NUMBER: 60/091982		Db	381	CysAspLysThrThrArgLysThrTyrPhePheValGlyIleTyrCysThrArgPheAsp	400
PRIOR FILING DATE: 1998-07-07					
PRIOR APPLICATION NUMBER: 60/091982		QY	1224	GAATGACCCCAACCATGGACAAAGGATTTCCCGCAGAGAGTGGTGAACACATTTCTCGGA	1283
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PRIOR APPLICATION NUMBER: 60/091982		Db	401	GluMetThrGlnThrMetAspLysGlyPheProGlnArgValValLysHisPheProGly	420
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PRIOR APPLICATION NUMBER: 60/091982		QY	1284	ATCAGTATCCGTGTTGATGCTGCTTTCCAGTACAAAGGATTTCTTTTTCAGCCGTTGA	1343
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PRIOR APPLICATION NUMBER: 60/091982		Db	421	IleSerIleArgValAspAlaAlaPheGlnTyrLysGlyPhePhePheSerArgGly	440
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PRIOR APPLICATION NUMBER: 60/091982		QY	1344	TCAAAGCAATTGGAATCAACATTAAGACAAAGATATTATCCCGAATCATGAGAACTAAT	1403
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PRIOR APPLICATION NUMBER: 60/085579		QY	264	AACACCTTGAGATCATGAAGACACCCAGGTGGGTGCTGATGTGGCCAGTATGGC	323
PRIOR FILING DATE: 1998-05-15					
PRIOR APPLICATION NUMBER: 60/085697		Db	81	AsnThrLeuGluIleMetLysThrProArgCysGlyValProAspValGlyGlnTyrGly	100
PRIOR FILING DATE: 1998-05-15					
PRIOR APPLICATION NUMBER: 60/085704		QY	324	TACACCTTCCTGGTGGAGAAAATACAACCTCACCTACAGATAATAAATACTATACCG	383
PRIOR FILING DATE: 1998-05-15					
PRIOR APPLICATION NUMBER: 60/086414		Db	101	TyrThrLeuProGlyTyrArgLysTyrAsnLeuThrTyrArgIleIleAsnTyrThrPro	120
PRIOR FILING DATE: 1998-05-22					
PRIOR APPLICATION NUMBER: 60/086430		QY	384	GATATGGCAGAGCTGTGTGATGAGGCTATCCAGAAGGTTTAGAAGTGTGGAGCAAA	443
PRIOR FILING DATE: 1998-05-22					
PRIOR APPLICATION NUMBER: 60/087106		Db	121	AspMetAlaArgAlaAlaValAspGluAlaIleGlnGluGlyLeuGluValTyrSerLys	140
PRIOR FILING DATE: 1998-05-28					
PRIOR APPLICATION NUMBER: 60/088026		QY	444	GTCACTCCCACTAAAATTCACCAAGATTTCAAAGGGGATTCACAGACATCATGATTCCTTT	503
PRIOR FILING DATE: 1998-06-04					
PRIOR APPLICATION NUMBER: 60/088730		Db	141	ValThrProLeuLysPheThrLysIleSerLysGlyIleAlaAspIleMetIleAlaPhe	160
PRIOR FILING DATE: 1998-06-10					
PRIOR APPLICATION NUMBER: 60/088741		QY	504	AGGACTCGAGTCCATGGTGGTGTCTCGCTATTTTGTATGCTCCCTCGGAGTGTCTGCG	563
PRIOR FILING DATE: 1998-06-10					
PRIOR APPLICATION NUMBER: 60/088810		Db	161	ArgThrArgValHisGlyArgCysProArgTyrPheAspGlyProLeuGlyValLeuGly	180
PRIOR FILING DATE: 1998-06-10					
PRIOR APPLICATION NUMBER: 60/089599		QY	564	CATGCTCTTCTCTGCTCGGTCTGGGTGGTGACACTCATTTTGTGCTGCTCATGAAATTTGGT	623
PRIOR FILING DATE: 1998-06-17					
PRIOR APPLICATION NUMBER: 60/089907		Db	181	HisAlaPheProProGlyProGlyLeuGlyGlyAspThrHisPheAspGluAspGluAsn	200
PRIOR FILING DATE: 1998-06-18					
PRIOR APPLICATION NUMBER: 60/089947		QY	624	TGGACCAAGGATGGAGCAGGATTCAACTTGTCTTGTGGCTGCTCATGAAATTTGGT	683
PRIOR FILING DATE: 1998-06-19					
PRIOR APPLICATION NUMBER: 60/090349		Db	201	TyrThrLysAspGlyAlaGlyPheAsnLeuPheLeuValAlaAlaHisGluPheGlyHis	220
PRIOR FILING DATE: 1998-06-23					
PRIOR APPLICATION NUMBER: 60/090429		QY	684	GCCTGGGCTCTCTCACTCCCAATGATCAACAGCCTTGATGTTCCCAATATGCTCC	743
PRIOR FILING DATE: 1998-06-24					
PRIOR APPLICATION NUMBER: 60/090445		Db	221	AlaLeuGlyLeuSerHisSerAsnAspGlnThrAlaLeuMetPheProAsnTyrValSer	240
PRIOR FILING DATE: 1998-06-24					
PRIOR APPLICATION NUMBER: 60/090538		QY	744	CTGGATCCCAAGAAATACCCACTTTCTCAGGATGATATCAATGGAATCCAGTCCATCTAT	803
PRIOR FILING DATE: 1998-06-24					
PRIOR APPLICATION NUMBER: 60/090863		Db	241	LeuAspProArgLysTyrProLeuSerGlnAspIleAsnGlyIleGlnSerIleTyr	260
PRIOR FILING DATE: 1998-06-26					
PRIOR APPLICATION NUMBER: 60/091360		QY	804	GGAGGTCTGCTAAGTACTGCTAAGCCAAAGAACCCACTATATACCCCATGCTGTGAC	863
PRIOR FILING DATE: 1998-07-01					
PRIOR APPLICATION NUMBER: 60/091519		Db	261	GlyGlyLeuProLysValProAlaLysProLysGluProThrIleProHisAlaCysAsp	280
PRIOR FILING DATE: 1998-07-02					
PRIOR APPLICATION NUMBER: 60/091982		QY	864	CTGACTTGACTTTTGACGCTATCACACTTTCCGAGAGAGTAAATGTTCTTTAAAGGC	923
PRIOR FILING DATE: 1998-07-07					
PRIOR APPLICATION NUMBER: 60/091982		Db	281	ProAspLeuThrPheAspAlaIleThrThrPheArgGluValMetPhePheLysGly	300
PRIOR FILING DATE: 1998-07-07					
PRIOR APPLICATION NUMBER: 60/091982		QY	924	AGGCACCTATGGAGGATCTATTATGATATACCGATGTTGAGTTTGAATTAATGCTTCA	983
PRIOR FILING DATE: 1998-07-07					
PRIOR APPLICATION NUMBER: 60/091982		Db	301	ArgHisLeuThrPheArgLysTyrThrPheValGluPheGluLeuLeuAlaSer	320
PRIOR FILING DATE: 1998-07-07					
PRIOR APPLICATION NUMBER: 60/091982		QY	984	TTCTGGCCATCTCTGCCAGCTGATCTGCAAGCTGCATACGAGAACCCGAGAGATAGATT	1043
PRIOR FILING DATE: 1998-07-07					
PRIOR APPLICATION NUMBER: 60/091982		Db	321	PheThrProSerLeuProAlaAspLeuGlnAlaAlaTyrGluAsnProArgAspLysIle	340
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PRIOR APPLICATION NUMBER: 60/091982		QY	1044	CTGGTTTTTAAAGATGAAACTTCTGGATGATCAGAGGATGCTGCTGCTGCCAGATTAT	1103
PRIOR FILING DATE: 1998-07-07					
PRIOR APPLICATION NUMBER: 60/091982		Db	341	LeuValPheLysAspGluAsnPheThrPheMetIleArgGlyTyrAlaValLeuProAspTyr	360
PRIOR FILING DATE: 1998-07-07					
PRIOR APPLICATION NUMBER: 60/091982		QY	1104	CCCAATCCCATCATACATATTAGGTTTTTCCAGAGCTGTGAAGAAAATAGATGCGCCGTC	1163
PRIOR FILING DATE: 1998-07-07					
PRIOR APPLICATION NUMBER: 60/091982		Db	361	ProLysSerIleHisThrLeuGlyPheProGlyArgValLysLysIleAspAlaVal	380
PRIOR FILING DATE: 1998-07-07					
PRIOR APPLICATION NUMBER: 60/091982		QY	1164	TGTGATAAGACCAAGAAAACCTACTCTTTTGTGGGCATTTGGTGTGGAGTTTGTAT	1223
PRIOR FILING DATE: 1998-07-07					
PRIOR APPLICATION NUMBER: 60/091982		Db	381	CysAspLysThrThrArgLysThrTyrPhePheValGlyIleTyrCysThrArgPheAsp	400
PRIOR FILING DATE: 1998-07-07					
PRIOR APPLICATION NUMBER: 60/091982		QY	1224	GAATGACCCCAACCATGGACAAAGGATTTCCCGCAGAGAGTGGTGAACACATTTCTCGGA	1283
PRIOR FILING DATE: 1998-07-07					
PRIOR APPLICATION NUMBER: 60/091982		Db	401	GluMetThrGlnThrMetAspLysGlyPheProGlnArgValValLysHisPheProGly	420
PRIOR FILING DATE: 1998-07-07					
PRIOR APPLICATION NUMBER: 60/091982		QY	1284	ATCAGTATCCGTGTTGATGCTGCTTTCCAGTACAAAGGATTTCTTTTTCAGCCGTTGA	1343
PRIOR FILING DATE: 1998-07-07					
PRIOR APPLICATION NUMBER: 60/091982		Db	421	IleSerIleArgValAspAlaAlaPheGlnTyrLysGlyPhePhePheSerArgGly	440
PRIOR FILING DATE: 1998-07-07					
PRIOR APPLICATION NUMBER: 60/091982		QY	1344	TCAAAGCAATTGGAATCAACATTAAGACAAAGATATTATCCCGAATCATGAGAACTAAT	1403
PRIOR FILING DATE: 1998-07-07					

US-10-729-807-28 (1-1627) x US-10-028-072-192 (1-513)

QY	24	ATGAAGCCCTTCTGCTTCTGTTGTTTCTTTTATAACATTTCTTCTGCAATTCCTTA	83
Db	1	MetLysArgLeuLeuLeuPheLeuPhePheIleThrPheSerSerAlaPheProLeu	20
QY	84	GTCCGGATGACGGAATGACAAATATGCAACTGGCTCAGGCATATCTCAACAGTTC	143
Db	21	ValArgMetThrGluAsnGluGluAsnMetGlnLeuAlaGlnAlaTyrLeuAsnGlnPhe	40
QY	144	TACTCTCTTGAATAGAGGAATCATCTTGTTCAAAGCAAGATAGGAGTCTCATAGAT	203
Db	41	TyrSerLeuGluIleGluGlyAsnHisLeuValGlnSerLysAsnArgSerLeuIleAsp	60
QY	204	GACAAATTCGGAAATGCAAGCATTTTGTGATGACAGTCACTGGAAGAACTGCACTCA	263
Db	61	AspLysIleArgGluMetGlnAlaPhePheGlyLeuThrValThrGlyLysLeuAspSer	80

Alignment Scores:
Pred. No.: 1,98e-273 Length: 513
Score: 2752.00 Matches: 512
Percent Similarity: 99.81% Conservative: 0
Best Local Similarity: 99.81% Mismatches: 1
Query Match: 93.92% Indels: 0
DB: 14 Gaps: 0

Db 441 SerLysGlnPheGluTyrrAsnlellyThrLysAsnlellyThrArgileMetArgThrAsn 460
 QY 1404 ACTTGGTTTCAATGCAAGAACCAAGAACTCCTCATTTGGTTTGTATATCAACAAGGAA 1463
 Db 461 ThrTrpPheGlnCysLysGluProLysAsnSerSerPheGlyPheAspileAsnLysGlu 480
 QY 1464 AAAGCACATTCAGGAGGATAAAGATATGTATCATAGAGTTTAAGCTTGTATTTT 1523
 Db 481 LysAlaHisSerGlyGlyIleLysleuTyrrHisLysSerLeuSerLeuPhelePhe 500
 QY 1524 GGTATTGTTCATTCCTGCAAAACACTTCTATTATCAAA 1562
 Db 501 GlyIleValHisLeuLeuLysAsnThrSerIleTyrrGln 513

RESULT 5

US-10-140-808-192
 ; Sequence 192, Application US/10140808
 ; Publication No. US20030017563A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Baker, Kevin P.
 ; APPLICANT: Beresini, Maureen
 ; APPLICANT: DeForge, Laura
 ; APPLICANT: Desnoyers, Luc
 ; APPLICANT: Filvaroff, Ellen
 ; APPLICANT: Gao, Wei-Qiang
 ; APPLICANT: Gerritsen, Mary E.
 ; APPLICANT: Goddard, Audrey
 ; APPLICANT: Godowski, Paul J.
 ; APPLICANT: Gurney, Austin L.
 ; APPLICANT: Sherwood, Steven
 ; APPLICANT: Smith, Victoria
 ; APPLICANT: Stewart, Timothy A.
 ; APPLICANT: Tumas, Daniel
 ; APPLICANT: Watanabe, Colin K
 ; APPLICANT: Wood, William
 ; APPLICANT: Zhang, Zemin
 ; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
 ; FILE OF INVENTION: ACIDS ENCODING THE SAME
 ; FILE REFERENCE: P333031C182
 ; CURRENT APPLICATION NUMBER: US/10/140,808
 ; CURRENT FILING DATE: 2002-05-07
 ; Prior Application removed - See File Wrapper or Palm
 ; NUMBER OF SEQ ID NOS: 550
 ; SEQ ID NO 192
 ; LENGTH: 513
 ; TYPE: PRT
 ; ORGANISM: Homo Sapien
 US-10-140-808-192

Alignment Scores:
 Pred. No.: 1,98e-273 Length: 513
 Score: 2752.00 Matches: 512
 Percent Similarity: 99.81% Conservative: 0
 Best Local Similarity: 99.81% Mismatches: 1
 Query Match: 93.92% Indels: 0
 DB: 14 Gaps: 0

US-10-729-807-28 (1-1627) x US-10-140-808-192 (1-513)

QY 24 ATGAAGCGCTTCTGCTTCTGTGTTGTTCTTTATACATTTTCTTCTGCATTTCCTTA 83
 Db 1 MetLysArgLeuLeuLeuPheLeuPheIleThrPheSerAlaPheProLeu 20
 QY 84 GTCCGGATGACGGAATGAAGAAATATCAACTGGCTCAGGCATATCTCAACCAAGTTC 143
 Db 21 ValArgMetThrGluAsnGluGluAsnMetGlnLeuAlaGlnAlaTyrrLeuAsnGlnPhe 40
 QY 144 TACTCTCTGAATAGAGGGAATCATCTTGTTCAGAGCAAGAAATAGGAGTCTCATAGAT 203
 Db 41 TyrSerLeuGluIleGluGlyAsnHisLeuValGlnSerLysAsnArgSerLeuIleAsp 60
 QY 204 GACAAATTCGGGAATGCAAGCATTTTGGATTGACATGACTGGAAACTGGACTCA 263

Db 61 AspLysIleArgGluMetGlnAlaPhePheGlyLeuThrValThrGlyLysLeuAspSer 80
 QY 264 AACACCCCTTGAGATCATGAACACCCAGGTGTGGGTGCTGATGTGGCCAGCATATGCC 323
 Db 81 AsnThrLeuGluIleMetLysThrProArgCysGlyValProAspValGlyGlnTyrrGly 100
 QY 324 TACACCCCTCCCTGGGTGGAGAAATACAACTCAGATACAGAAATATAAACTATATCTCCG 383
 Db 101 TyrThrLeuProGlyTyrrArgLysTyrrAsnLeuThrTyrrArgIleleAsnTyrrThrPro 120
 QY 384 CATATGGCAGCAGCTGCTGTGGATGAGGCTATCCAAAGAGTTTAAAGTGTGGAGCAAA 443
 Db 121 AspMetAlaArgAlaAlaValAspGluAlaIleGlnGluGlyLeuGluValTyrrSerLys 140
 QY 444 GTCACTCCCACTAAATTCACCAAGATTTCAAAGGGATTGAGACATCATGATTCCTCTT 503
 Db 141 ValThrProLeuLysPheThrLysIleSerLysGlyIleAlaAspileMetIleAlaPhe 160
 QY 504 AGGACTCGAGTCCATGTGCTGCTCTCTATTTTGTATGGTCCCTTGGGAGTGTCTGCC 563
 Db 161 ArgThrArgValHisGlyArgCysProArgTyrrPheAspGlyProLeuGlyValLeuGly 180
 QY 564 CATGCTTTCTCTCTGCTGGTCCGGTCTGGGTGTGACACTCATTTTGTAGATGAGATGAAAC 623
 Db 181 HisAlaPheProProGlyProGlyLeuGlyGlyAspThrHisPheAspGluAspGluAsn 200
 QY 624 TGGACCAAGATGAGCAGGATTCAACTGTCTTCTGTGGCTGCTCATGAATTTGGTCAT 683
 Db 201 TrpThrLysAspGlyAlaGlyPheAsnLeuPheLeuValAlaHisGlnPheGlyHis 220
 QY 684 GCACCTGGGCTCTCTCACTCCAAATCATCAACAGAGCTTGTATGTTCCCAAAATATGTCTC 743
 Db 221 AlaLeuGlyLeuSerHisSerAsnAspGlnThrAlaLeuMetPheProAsnTyrrValSer 240
 QY 744 CTGGATCCCGAGAAATACCCACTTTCTCAGGATGATATCAATGGAATCCAGTCCATCTAT 803
 Db 241 LeuAspProArgLysTyrrProLeuSerGlnAspAspileAsnGlyIleGlnSerIleTyrr 260
 QY 804 GGAGTCTGCTTAAGTACTCTGTAAGCAAGGACCCACTATACCCCATCCCTGTGAC 863
 Db 261 GlyGlyLeuProLysValProAlaLysProLysGluProThrIleProHisAlaCysAsp 280
 QY 864 CTGACTTGACTTTTGAAGTATCAACTTCCGAGAGAGTAAATGTTCTTTTAAAGGC 923
 Db 281 ProAspLeuThrPheAspAlaIleThrThrPheArgArgGluValMetPhePheLysGly 300
 QY 924 AGGCACCTATGAGGATCTATTATGATATCAAGGATGTTGAGTTTGAATTAATTTGTTCA 983
 Db 301 ArgHisLeuTipArgIleTyrrAspIleThrAspValGluPheGluLeuIleAlaSer 320
 QY 984 TTCTGGCATCTCTCCAGCTGATCTGCAAGCTGCATACAGAACCCAGAGATAGATT 1043
 Db 321 PheTrpProSerLeuProAlaAspLeuGlnAlaTyrrGluAsnProArgAspLysIle 340
 QY 1044 CTGGTTTTTAAAGATGAAACTTCTGGATGATCAGAGGATATGCTGTCTTGCAGATTAT 1103
 Db 341 LeuValPheLysAspGluAsnPheTrpMetIleArgGlyTyrrAlaValLeuProAspTyrr 360
 QY 1104 CCCAAATCCATCATACATTAGTGTTCAGGACGCTGTGAAGAAATAGATGAGCCGCTC 1163
 Db 361 ProLysSerIleHisThrLeuGlyPheProGlyArgValLysLysIleAspAlaAlaVal 380
 QY 1164 TGTGATAACACCAAGAAACCTACTTCTTGTGGCATTTGGTCTGGAGTTTGTAT 1223
 Db 381 CysAspLysThrThrArgLysThrTyrrPhePheValGlyIleTyrrCysTrpArgPheAsp 400
 QY 1224 GAAATCACCAACCACTGACAAAGATTCGCGCAGAGAGTGGTAAACACATTTCTCTGA 1283
 Db 401 GluMetThrGlnThrMetAspLysGlyPheProGlnArgValValLysHisPheProGly 420
 QY 1284 ATCAGTATCCGTGTGTGATGCTGCTTCCAGTACAAAGGATTCCTTTTTCAGCCGTGA 1343

Db 421 IleSerIleArgValAlaAlaPheGlnTyrIleGlyPhePhePheSerArgGly 440
QY 1344 TCRAAGCAATTTGATACAAATTAAGCAAGATATATACCGAATCATGAGAACTAAT 1403
Db 441 SerIleGlnPheGluTyrAsnIleIleYsThrLysAsnIleThrArgIleMetArgThrAsn 460
QY 1404 ACTTGGTTTCAATGCAAGAACCAAGAACTCTCATTTGTTTGTATATCAACAAGGAA 1463
Db 461 ThrTrpPheGlnCysLysGluProLysAsnSerPheGlyPheAspIleAsnLysGlu 480
QY 1464 AAACACATTCAGAGGCAATTAAGATATGTATCATAGAGTTTAAGCTGTTTATTTT 1523
Db 481 LysAlaHisSerGlyGlyIleLysIleLeuTyrHisLysSerLeuSerLeuPheIlePhe 500
QY 1524 GGTATTGTTCAATTCCTGCAAAACACATCTTATTTATCAA 1562
Db 501 GlyIleValHisLeuLeuLysAsnThrSerIleTyrGln 513

RESULT 6

US-10-121-049-192
; Sequence 192, Application US/10121049
; Publication No. US20030022239A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Beresini, Maureen
; APPLICANT: DeForge, Laura
; APPLICANT: Desnoyers, Luc
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Sherwood, Steven
; APPLICANT: Smith, Victoria
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Watanabe, Colin K
; APPLICANT: Wood, William
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; TITLE OF INVENTION: ACIDS ENCODING THE SAME
; FILE REFERENCE: P3330R1C17
; CURRENT APPLICATION NUMBER: US/10/121,049
; CURRENT FILING DATE: 2002-04-12
; Prior Application removed - See File Wrapper or Palm
; NUMBER OF SEQ ID NOS: 550
; SEQ ID NO 192
; LENGTH: 513
; TYPE: PRT
; ORGANISM: Homo Sapien
US-10-121-049-192

Alignment Scores:
Pred. No.: 1.98e-273 Length: 513
Score: 2752.00 Matches: 512
Percent Similarity: 99.81% Conservative: 0
Best Local Similarity: 99.81% Mismatches: 1
Query Match: 93.92% Indels: 0
DB: 14 Gaps: 0

US-10-729-807-28 (1-1627) x US-10-121-049-192 (1-513)

QY 24 ATGAAGCGCTTCTGCTTCTGTGTTCTTTTATACATTTCTTCTGCTATTCCTTTA 83
Db 1 MetLysArgLeuLeuLeuPheLeuPhePheIleThrPheSerAlaPheProLeu 20
QY 84 GTCGGATGACGAAATGAGAAATATGCAACTGGCTCAGGCATATCTCAACCACTTC 143
Db 21 ValArgMetThrGluAsnGluGluAsnMetGlnLeuAlaGlnAlaTyrLeuAsnGlnPhe 40
QY 144 TACTCTTCAATAGAGGATCATCTTGTTCAAAGCAAGATAGGAGTCTCATAGAT 203

Db 41 TyrSerLeuGluIleGluGlyAsnHisLeuValGlnSerLysAsnArgSerLeuIleAsp 60
QY 204 GACAAATTCGGAAATCAAGCAATTTTTCGATTTGACAGTCACTGGAATACTGACTCA 263
Db 61 AspLysIleArgGluMetGlnAlaPhePheGlyLeuThrValThrGlyLysLeuAspSer 80
QY 264 AACACCTTTGATGATCATGACACACCCAGGTGTGGGTGCTGATGCGGCAGTATGCG 323
Db 81 AsnThrLeuGluIleMetLysThrProArgCysGlyValProAspValGlyGlnTyrGly 100
QY 324 TACACCTTCCTCGGTGAGAAATAACAACCTCACTACAGATAATAAATACTACTCCG 383
Db 101 TyrThrLeuProGlyTyrArgLysTyrAsnLeuThrTyrArgLysIleAsnTyrThrPro 120
QY 384 GATATGACAGAGCTGCTGTGGATGAGGCTATCAAGAAGGTTTGAAGTGTGGAGCAA 443
Db 121 AspMetAlaArgAlaAlaValAspGluAlaIleGlnGluGlyLeuGluValTrpSerLys 140
QY 444 GTCACTCCACTTAAATTCACCAAGATTTCAAGGGGATTCAGACATCATGATTCCTTT 503
Db 141 ValThrProLeuLysPheThrLysIleSerLysGlyIleAlaAspIleMetIleAlaPhe 160
QY 504 AGGACTCGAGTCCATGCTCGGTGCTCGCTATTTTGTATGCTCCCTGGAGTGTGCTGC 563
Db 161 ArgThrArgValHisGlyArgCysProArgTyrPheAspGlyProLeuGlyValLeuGly 180
QY 564 CATGCTTTCTCTGCTCGGTGCTCGGTGCTGACACTCATTTTGTAGTGAAGATGAAAC 623
Db 181 HisAlaPheProGlyProGlyLeuGlyAspThrHisPheAspGluAspGluAsn 200
QY 624 TGGACCAAGATGAGCAGAGATCAACTGTTCTTCTGCTGCTGCTGCTGCTGCTGCTG 683
Db 201 TrpThrLysAspGlyAlaGlyPheAsnLeuPheLeuValAlaAlaHisGluPheGlyHis 220
QY 684 GCACGTGGGCTCTCTCACTCCAAATGATCAAAACAGCCTTGTATGTTCCCAAAATATGCTCC 743
Db 221 AlaLeuGlyLeuSerHisSerAsnAspGlnThrAlaLeuMetPheProAsnTyrValSer 240
QY 744 CTGATCCCAAGAAATACCCACTTTCTCAGATGATATCAATGGAATCCAGTCCATCTAT 803
Db 241 LeuAspProArgLysTyrProLeuSerGlnAspAspIleAsnGlyIleGlnSerIleTyr 260
QY 804 GSAGTCTGCTAAGTACCTGCTAAGCCAAAGAACCCACTATACCCCATGCTGCTGAC 863
Db 261 GlyGlyLeuProLysValProAlaLysProLysGluProThrIleProHisAlaCysAsp 280
QY 864 CCGACTTGACTTTTGACGCTATCACAACTTTCCGACAGAGAAGTAATGTTCTTTAAAGGC 923
Db 281 ProAspLeuThrPheAspAlaIleThrThrPheArgArgGluValMetPhePheLysGly 300
QY 924 AGGCACCTATGAGGATCTATATGATATCACGGATGTTGAGTTGAAATTAATGCTTCA 983
Db 301 ArgHisLeuTrpArgIleTyrTyrAspIleThrAspValGluPheGluLeuIleAlaSer 320
QY 984 TTCTGGCCATCTCTGCGAGTCTGCAAGCTGCTACAGAGTCCATACAGAACCCAGAGATAAGATT 1043
Db 321 PheTrpProSerLeuProAlaAspLeuGlnAlaAlaTyrGluAsnProArgAspLysIle 340
QY 1044 CTGGTTTTTAAGATGAAACTTCTCGATGATCAGAGGATATCTGCTGTCAGAGATTAT 1103
Db 341 LeuValPheLysAspGluAsnPheTrpMetIleArgGlyTyrAlaValLeuProAspTyr 360
QY 1104 CCCAAATCCATACATACATAGGTTTCCAGGAGCTGTGAGAAATAGATGAGCGGCTC 1163
Db 361 ProLysSerIleHisThrLeuGlyPheProGlyArgValLysLysIleAspAlaAlaVal 380
QY 1164 TGTGATAAGACCAACAAAGAAACCTACTCTTTTGTGGGATTTTGTGCTCGAGTTTGTAT 1223
Db 381 CysAspLysThrThrArgLysThrTyrPhePheValGlyIleTrpCysTrpArgPheAsp 400
QY 1224 GAAATGACCCCAACCATGACAAAGGATTTCCCGCAGAGAGTGTGTAAACACTTTCCTGGA 1283
Db 401 GluMetThrGlnThrMetAspLysGlyPheProGlnArgValValLysHisPheProGly 420

QY	1224	GAATGACCCAAACCATCGACAAGAAGATTCCCGAGAGAGTGTAAACAACACTTTCCTGGA	1283
Db	401	GluMetThrGlnThrMetAspLysGlyPheProGlnArgValValLysHisPheProGly	420
QY	1284	ATCAGTATCCGTTGTGTGCTGCTTCCAGTACAAAGATTCTCTCTTTTTCAGCCGNGGA	1343
Db	421	IleSerIleArgValAspAlaAlaPheGlnTyrLysGlyPhePhePhePheSerArgGly	440
QY	1344	TCGAAGCAAAATTGNAATCAACATTAAGACAAGAATAATTACCGAATCATGAGAACTAAT	1403
Db	441	SerLysGlnPheGlnTyrAsnIleLysThrLysAsnIleThrArgIleMetArgThrAsn	460
QY	1404	ACTGTGTTTCAATGCAAAAGAACCAAGAACTCCTCATTTGGTTTGTATATCAACAAGCAA	1463
Db	461	ThrTyrPheGlnCysLysGluProCysAsnSerSerPheGlyPheAspIleAsnLysGlu	480
QY	1464	AAAGCACAATTCAGAGGCATAAAGATATTCGATCATGAAGAGTTTAAGCTGTATTATTTT	1523
Db	481	LysAlaHisSerGlyGlyIleLysIleLeuYrHisLysSerLeuSerLeuPheIlePhe	500
QY	1524	GGTATTGTTTCATTTGCTGAAAAACAACCTCTATTATCAAA	1562
Db	501	GlyIleValHisLeuLeuLysAsnThrSerIleIleTyrGln	513

QY	84	GTCCGGATGACGGAAAAATGAAGAAAATATGCAACTGGCTCAGGCCATATCTCAACAGTTTC	143
Db	21	ValArgMetThrGluAsnGluGluAsnMetGlnLeuAlaGlnAlaTyrLeuAsnGlnPhe	40
QY	144	TACTCTCTTTGAAATAGAGAGGAAATCATCTTCTTCAAGCAAGAATAGAGTCTCATAGAT	203
Db	41	TyrSerLeuGluIleGluGlyAsnHisLeuValGlnSerIysAsnArgSerLeuIleAsp	60
QY	204	GACAAATTCGGGAAATCAACAGCATTTTTTGGATTGACAGTCACTGGGAAAACTGACATCA	263
Db	61	AspIysIleArgGluMetGlnAlaPhePheGlyLeuThrValThrGlyLysLeuAspSer	80
QY	264	AACACCTTTGAGATCATGAACACACCCAGGTGTGGGTGCTGTGATGTGGCCAGTATGGC	323
Db	81	AsnThrLeuGluIleMetLysThrProArgCysGlyValProAspValGlyGlnTyrGly	100
QY	324	TACACCTCCCTGGGTGGAGAAAAATACAACTCCACCTACAGAAATAATAAACTATACTCCG	383
Db	101	TyrThrLeuProGlyTyrArgLysTyrAsnLeuThrTyrArgIleIleAsnTyrThrPro	120
QY	384	GATATGGCACAGCTGCTGTGGATGAGGCTATCCAAGAGGTTTAGAAGTGTGGAGCAAA	443
Db	121	AspMetAlaArgAlaAlaValAspGluAlaIleGlnGlyLeuGluValTyrSerIys	140
QY	444	GTCACTCCACTAAAAATTCACCAAGATTTCAAAGGGGATTGCAGACATCATGATTCGCCTTT	503
Db	141	ValThrProLeuLysPheThrLysIleSerIysGlyIleAlaAspIleMetIleAlaPhe	160
QY	504	AGGACTCGAGTCGATGGTGGTGCCTGCTGCTATTTTGCATGCTCCCTTGGGAGTCTTGGC	563
Db	161	ArgThrArgValHisGlyArgCysProArgTyrPheAspGlyProLeuGlyValLeuGly	180
QY	564	CATGCCCTTCTCTCTGCTCGGGCTCGGTGGTCACACTCATTTTGTAGTGGAGATGAAAC	623
Db	181	HisAlaPheProProGlyProGlyLeuGlyArgThrHisPheAspGluAspGluAsn	200
QY	624	TGGACCAGGATGGAGCAGGATTCAACTTGTTTCTTGTGGCTGCTCATGAATTTGGTCAT	683
Db	201	TrpThrLysAspGlyAlaGlyPheAsnLeuPheLeuValaAlaHisGluPheGlyHis	220
QY	684	GCATGGGGCTCTCTCACTCCAATGATCAAAAGCCTTGATGTGTCCCAAAATATGTCTCC	743
Db	221	AlaLeuGlyLeuSerHisSerAsnAspGlnThrAlaLeuMetPheProAsnTyrValSer	240
QY	744	CTGGATCCCAAGAAATACCCACTTTCAGAGTAVATCAATGAATCCAGTCCATCATCTAT	803
Db	241	LeuAspProArgLysTyrProLeuSerGlnAspAspIleAsnGlyIleGlnSerIleTyr	260
QY	804	GGAGGTCGCTTAAGTACTCTGTAAGCCAAAGAAACCCACTATACCCCATGCTGTGAC	863
Db	261	GlyGlyLeuProLysValProAlaLysProLysGluProThrIleProHisAlaCysAsp	280
QY	864	CCTGACTTGACTTTTGACGCTATCACAACTTTCGCGAGAGAAGTAAATGTTCTTAAAGGC	923
Db	281	ProAspLeuThrPheAspAlaIleThrPheArgArgGluValMetPhePheLysGly	300
QY	924	AGGCACCTATGGAGGATCTATTATGATATCACGGATGTTGAGTTGAATTAATTTGCTTCA	983
Db	301	ArgHisLeuTrpArgIleTyrTyrAspIleThrAspValGluPheGluLeuIleAlaSer	320
QY	984	TTCTGGGCATCTCTGCCAGCTGATCTGCAGCTGCATACGAGNACCCGAGATAGATT	1043
Db	321	PheTrpProSerLeuProAlaAspLeuGlnAlaAlaTyrGluAsnProArgAspLysIle	340
QY	1044	CTGGTTTTAAAGATGAAACTTCTCGATGATCAGAGGATATGCTGCTCTTTCGCAGATTAT	1103
Db	341	LeuValPheLysAspGluAsnPheTrpMetIleArgGlyTyrAlaValLeuProAspTyr	360
QY	1104	CCCAATTCATCATACATTAGTGTTCAGGCGCTGTGAAGNAAATAGNATGAGCGCT	1163
Db	361	ProLysSerIleHisThrLeuGlyPheProGlyArgValLysLysIleAspAlaAlaVal	380
QY	1164	TGTGATAAGACCAACAAGAAAAACCTACTTCTTTTGTGGGCATTTTGGTGCTGGAGGTTTGT	1223

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Db      381  CysAspLysThrThrArgLysThrTyPhePheValGlyIleTyrCysTyrPargPheAsp 400
QY      1224  GAAATGACCCAAACCATGACAAAGAGTCCCGCAGAGAGTGGTAAACACTTTCTCTGGA 1283
Db      401  GluMetThrGlnThrMetAspLysGlyPheProGlnArgValValLysHisPheProGly 420
QY      1284  ATCAGTATCCGTTGATGCTGCTTCCAGTACAAAGAGTCTTCTTTTCAGCGTGA 1343
Db      421  IleSerIleArgValAspAlaPheGlnTyrLysGlyPhePheSerArgGly 440
QY      1344  TCAAAGCAATTTGAATACAACTTAAGACAAAGAAATATTACCGAATCATGAGAACTAAT 1403
Db      441  SerLysGlnPheGluTyrAsnIleLysThrLysAsnIleThrArgIleMetArgThrAsn 460
QY      1404  ACTGGTTTCAATGCAAGAACAAAGAACTCTCTCATTTGGTTTGGATATCAACAGGAA 1463
Db      461  ThrTyrPheGlnCysLysGluProLysAsnSerPheGlyPheAspIleAsnLysGlu 480
QY      1464  AAAGCACATTCCAGGCGCATTAAGATATTGTATCATTAAGAGTTTAAGCTGTTTATTTT 1523
Db      481  LysAlaHisSerGlyIleLysIleLysIleLysIleLysIleLysIleLysIleLysIle 500
QY      1524  GGTATTGTTCTATTGCTGAAAAACACTTCTATTATCAA 1562
Db      501  GlyIleValHisLeuLeuLysAsnThrSerIleTyrGln 513

RESULT 9
US-10-175-746-192
; Sequence 192, Application US/10175746
; Publication NO. US2003027270A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Beresini, Maureen
; APPLICANT: DeForge, Laura
; APPLICANT: Desnoyers, Luc
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Gurney, Austin I.
; APPLICANT: Sherwood, Steven
; APPLICANT: Smith, Victoria
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Watanabe, Colin K
; APPLICANT: Wood, William
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P3330RIC353
; CURRENT APPLICATION NUMBER: US/10/175,746
; CURRENT FILING DATE: 2002-06-19
; Prior Application removed - See File Wrapper or Palm
; NUMBER OF SEQ ID NOS: 550
; SEQ ID NO 192
; LENGTH: 513
; TYPE: PRT
; ORGANISM: Homo Sapien
US-10-175-746-192

Alignment Scores:
Pred. No.: 1,98e-273 Length: 513
Score: 2752.00 Matches: 512
Percent Similarity: 99.81% Conservative: 0
Best Local Similarity: 99.81% Mismatches: 1
Query Match: 93.92% Indels: 0
DB: 14 Gaps: 0

US-10-729-807-28 (1-1627) x US-10-175-746-192 (1-513)
QY      24  ATGAAGCGCCTTCGTCTCTGCTGTTGTTGTTCTTTTATAACATTTTCTTCGTGATTTCCCTTA 83
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Db      1  MetLysArgLeuLeuLeuLeuPheLeuPhePheIleThrPheSerSerAlaPheProLeu 20
QY      84  GTCCGGATGACCGAAAAATGAAGAAAATATGCAACTGGCTCAGGCATATCTCAACACGATTC 143
Db      21  ValArgMetThrGluAsnGluAsnMetGlnLeuAlaGlnAlaTyrLeuAsnGlnPhe 40
QY      144  TACTCTCTTGAATAGNAGGGGATCATCTTGTGTTTCAAGCAAGAAATAGGAGTCTCATAGAT 203
Db      41  TyrSerLeuGluIleGluGlyAsnHisLeuValGlnSerLysAsnArgSerLeuIleAsp 60
QY      204  GACAAAATTCGGGAAATGCAAGCATTTTGGATTGACAGTGCACACTGACGGAAAACTGGACTCA 263
Db      61  AspLysIleArgGluMetGlnAlaPhePheGlyLeuThrValThrGlyLysLeuAspSer 80
QY      264  AACACCTTGGAGTATCATGAAGACACCCAGGTGTGGGGTGCCTGATGTGGCCAGATATGCG 323
Db      81  AsnThrLeuGluIleMetLysThrProArgCysGlyValProAspValGlyGlnTyrGly 100
QY      324  TACACCTCCCTCGGTGGGAGAAATACACCTCACCCTACAGAAATTAAGAGTGGAGCAAA 383
Db      101  TyrThrLeuProGlyTyrPargLysTyrAsnLeuThrTyrArgIleIleAsnTyrThrPro 120
QY      384  GATATGGCACGAGCTGCTGTGATGAGGCTATCCAAAGAGGTTTGAAGTGTGGAGCAAA 443
Db      121  AspMetAlaArgAlaAlaValAspGluAlaIleGlnGluGlyLeuGluValTyrSerLys 140
QY      444  GTCACCTCCCTAAAATTCACCAAGATTTCAAGGGGATTCGACAGATCATGATGCTCTTT 503
Db      141  ValThrProLeuLysPheThrLysIleSerLysGlyIleAlaAspIleMetIleAlaPhe 160
QY      504  AGGACTCGAGTCCAGTCCGCTGCTCGCTATTTGATGTCCTCGGTGGAGTGTGGCTGGC 563
Db      161  ArgThrArgValHisGlyArgCysProArgTyrPheAspGlyProLeuGlyValLeuGly 180
QY      564  CATGCTTTCTCTCTCGGTCCGGTCTGGGTGTGTGACACTCATTTTGTGATGAGATGAAAAC 623
Db      181  HisAlaPheProGlyProGlyLeuGlyGlyAspThrHisPheAspGluAspGluAsn 200
QY      624  TGGACCAAGATGGAGCAGGATTCAACTGTTTCTTGTGGCTGCTCATGAATTTGTCAT 683
Db      201  TrpThrLysAspGlyAlaGlyPheAsnLeuPheLeuValAlaAlaHisGluPheGlyHis 220
QY      684  GCACCTGGGGCTCTCTCCTCAATGATCAACAGAGCTTGATGTCCTCCCAATATGTCCTCC 743
Db      221  AlaLeuGlyLeuSerHisSerAsnAspGlnThrAlaLeuMetPheProAsnTyrValSer 240
QY      744  CTGGATCCCGAAAAATACCCACTTTCTCAGGATGATATCAATGGAATCCAGATCCCATCTAT 803
Db      241  LeuAspProArgLysTyrProLeuSerGlnAspAspIleAsnGlyIleGlnSerIleTyr 260
QY      804  GGAGTCTCCCTAAGTACTCTCTAAGCAAGAACCCACTATATCCCATGCTGCTGTGAC 863
Db      261  GlyGlyLeuProLysValProAlaLysProLysGluProThrIleProHisAlaCysAsp 280
QY      864  CTGACTTTCAGCTTTTGAGCTATCAACTTTCCGACAGAGAAGTAAATGTTCTTTAAAGGC 923
Db      281  ProAspLeuThrPheAspAlaIleThrThrPheArgGluValMetPheLysGly 300
QY      924  AGGCACCTATGAGGATCTATTATGATATCAGGATTTGAGTTTGAATTAATTTGCTTCA 983
Db      301  ArgHisLeuTyrArgIleTyrThrAspIleThrAspValGluPheGluLeuIleAlaSer 320
QY      984  TTCTGGCCATCTCTCGCAGCTGATCTGCAGCTGCATACGAGAACCCAGAGATAGATT 1043
Db      321  PheTyrProSerLeuProAlaAspLeuGlnAlaAlaTyrGluAsnProArgAspLysIle 340
QY      1044  CTGGTTTTAAAGATGAAAACCTTCTGGATGATCAGAGGATATGCTGCTTGGCCAGATTAT 1103
Db      341  LeuValPheLysAspGluAsnPheThrMetIleArgGlyTyrAlaValLeuProAspTyr 360
QY      1104  CCCAAATCCATCCATACATTAGTGTTCAGGACCTGTGAGAAATAATAGATGACGCGTC 1163
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Db 361 ProlyserIleHisThrLeuGlyPheProGlyArgValLysLysIleAspAlaVal 380
QY 1164 TGTGATAGACCAAGAAACCTACTCTTTGTGGCAATTTGGTCTGGAGGTTTGTAT 1223
Db 381 CysAspIysThrThrArgLysThrTyrPhePheValGlyIleTrpCysTrpArgPheAsp 400
QY 1224 GAATGACCCAAACCAAGGATCCCGCAGAGAGTGGTAACAACACTTTCCTGGA 1293
Db 401 GluMetThrGlnThrMetAspLysGlyPheProGlnArgValValLysHisPheProGly 420
QY 1284 ATCAGTATCCGTGTGTGTCTTCCAGTACAAAGGATCTCTTTTTCAGCCGTGGA 1343
Db 421 IleSerIleArgValAspAlaPheGlnTyrLysGlyPhePhePheSerArgGly 440
QY 1344 TCAAGCAATTTGAATACAACTTAAGCAAGAATATTACCCGAATCATGAGAACTAAT 1403
Db 441 SerLysGlnPheGluTyrAsnIleLysThrLysAsnIleThrArgIleMetArgThrAsn 460
QY 1404 ACTTGGTTTCAATGCAAGAACCAAGAACTCCCTCATTTTGGTTTGTATATCAACAAGGAA 1463
Db 461 ThrTrpPheGlnCysLysGluProLysAsnSerSerPheGlyPheAspIleAsnLysGlu 480
QY 1464 AAAGCAATTCAGGAGGATTAAGATATTGTATCATAGAGTTTAAAGCTTGTATTTT 1523
Db 481 LysAlaHisSerGlyGlyIleLysIleLeuTyrHisLysSerLeuSerLeuPheIlePhe 500
QY 1524 GGTATTCTTCAATTTGCTGAAAAACACTTCTATTATCA 1562
Db 501 GlyIleValHisLeuLeuLysAsnThrSerIleTyrGln 513

RESULT 10

US-10-176-918-192
; Sequence 192, Application US/10176918
; Publication No. US20030027275A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Beresini, Maureen
; APPLICANT: DeForge, Laura
; APPLICANT: Desnoyers, Luc
; APPLICANT: Flivaroff, Ellen
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Sherwood, Steven
; APPLICANT: Smith, Victoria
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Watanabe, Colin K
; APPLICANT: Wood, William
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE INVENTION: ACIDS ENCODING THE SAME
; FILE REFERENCE: P3330R1C382
; CURRENT APPLICATION NUMBER: US/10/176,918
; CURRENT FILING DATE: 2002-06-20
; Prior Application removed - See File Wrapper or Palm
; NUMBER OF SEQ ID NOS: 550
; SEQ ID NO 192
; LENGTH: 513
; TYPE: PRT
; ORGANISM: Homo Sapien
US-10-176-918-192

Alignment Scores:
Pred. No.: 1.98e-273 Length: 513
Score: 2752.00 Matches: 512
Percent Similarity: 99.81% Conservative: 0
Best Local Similarity: 99.81% Mismatches: 1
Query Match: 93.92% Indels: 0
DB: 14 Gaps: 0

US-10-729-807-28 (1-1627) x US-10-176-918-192 (1-513)
QY 24 ATGAGGCGCTTCTGCTTCTGTTCTTTTATAACATTTCTTCTGCAATTTCCCTTA 83
Db 1 MetLysArgLeuLeuLeuPhePheIleThrPheSerSerAlaPheProLeu 20
QY 84 GTCGGATGACGAAATGAAAGAAATATCACTGCTCAGGCTCAGGCATATCTCAACAGTTC 143
Db 21 ValArgMetThrGluAsnGluGluAsnMetGlnLeuAlaGlnAlaTyrLeuAsnGlnPhe 40
QY 144 TACTCTCTTGAATAGAGGAATCATCTTGTTCAAAGCAAGATAGAGTCTCATAGAT 203
Db 41 TyrSerLeuGluIleGluGlyAsnHisLeuValGlnSerLysAsnArgSerLeuIleAsp 60
QY 204 GACAAATTCGGAATATGCAAGCATTTTGGATTGACAGTACTGAGAACTGGACTCA 263
Db 61 AspLysIleArgGluMetGlnAlaPhePheGlyLeuThrValThrGlyLysLeuAspSer 80
QY 264 AACACCTTCAGATCATGAAGACACCCAGGTGTGGGTGCTGATGTGGCCAGTATGGC 323
Db 81 AsnThrLeuGluIleMetLysThrProArgCysGlyValProaspValGlyGlnTyrGly 100
QY 324 TACACCTTCCTCGGTGGAGAAATACACCTCACCTACAGAATAATAAACTATACCTCG 383
Db 101 TyrThrLeuProGlyTyrArgLysTyrAsnLeuThrTyrArgIleIleAsnTyrThrPro 120
QY 384 GATATGCGCAGCTGCTGTGGATGAGGCTATCCAGAAGTTTAGAAGTGTGGAGCAA 443
Db 121 AspMetAlaArgAlaAlaValAspGluAlaIleGlnGluGlyLeuGluValTrpSerLys 140
QY 444 GTCACCTCACTAAATTCACCAAGATTTCAAAGGGATTGCAGACATCATGATTCCTTT 503
Db 141 ValThrProLeuLysPheThrLysIleSerLysGlyIleAlaIleMetIleAlaPhe 160
QY 504 AGCACTGAGTCCATGCTCGGTGCTCTCTGCTATTTTGTATGCTGCTTGGAGTCTGGC 563
Db 161 ArgThrArgValHisGlyArgCysProArgTyrPheAspGlyProLeuGlyValLeuGly 180
QY 564 CATGCTTTCTCTGCTCGGTCTGGGTGCTGGTGCACACTCATTTTGTAGGATGAAC 623
Db 181 HisAlaPheProProGlyProGlyLeuGlyGlyAspThrHisPheAspGluAspGluAsn 200
QY 624 TGCACCAAGGATGGAGCAGGATTCACCTTCTTCTGCTGCTCATGAATTTGGTCAT 683
Db 201 TrpThrLysAspGlyAlaGlyPheAsnLeuPheLeuValAlaAlaHisGluPheGlyHis 220
QY 684 GCACTGGGCTCTCTCACTCAATGATCAAAAGCCCTGTGATGTTCCAAATATGCTCC 743
Db 221 AlaLeuGlyLeuSerHisSerAsnAspGlnThrAlaLeuMetPheProAsnTyrValSer 240
QY 744 CTGGATCCCAAGAAATACCCACTTCTCAGGATCATCAATGAATCCAGTCCATCTAT 803
Db 241 LeuAspProArgLysTyrProLeuSerGlnAspIleAsnGlyIleGlnSerIleTyr 260
QY 804 GGAAGTCTGCTAAGGTACCTGCTTAAGCCAAAGAACCCACTATACCCCATGCTGTGAC 863
Db 261 GlyGlyLeuProLysValProAlaLysProLysGluProThrIleProHisAlaCysAsp 280
QY 864 CTTGACTTGACTTTTGTAGCTATCAAACTTCCGAGAGAGTAATGTTCTTTAAAGGC 923
Db 281 ProAspLeuThrPheAspAlaIleThrThrPheArgArgGluValMetPhePheLysGly 300
QY 924 AGGCACCTATGGAGGATCTATTATGATATCACGGATGTTGAGTTGATTAATGCTTCA 983
Db 301 ArgHisLeuTrpArgIleTyrTyrAspIleThrAspValGluPheGluLeuIleAlaSer 320
QY 984 TTCTGGCCATCTCTGCCAGCTGATCTGCAAGCTGCATACAGAACCCAGAGATAAGATT 1043
Db 321 PheTrpProSerLeuProAlaAspLeuGlnAlaAlaTyrGluAsnProArgAspLysIle 340
QY 1044 CTGTTTTTAAAGATGAAACTTCTGATGATCAGAGATATGCTGTGCTGCCAGATAT 1103
Db 341 LeuValPheLysAspGluAsnPheTrpMetIleArgGlyTyrAlaValLeuProAspTyr 360

QY 1104 CCCAAATCCATCATAGTTTCCAGGACGTTGAGAAATATAGTCAGCCGTC 1163
 Db |||||||
 361 ProLysSerIleHisThrLeuGlyPheProGlyArgValLysLysIleAspAlaVal 380
 QY 1164 TGTGATAAGACACCAAGAAAAACCTACTTCTTTGTGGCATTTGGTCTGGAGGTTTGAT 1223
 Db |||||||
 381 CysAspLysThrThrArgLysThrTyrPhePheValGlyIleTyrCysTyrPheArgPheAsp 400
 QY 1224 GAAATGACCAACATGACAAAGATTCCCGCAGAGAGTGTTGATAAAACATTTTCTCGGA 1283
 Db |||||||
 401 GluMetThrGlnThrMetAspLysGlyPheProGlnArgValValLysHisPheProGly 420
 QY 1284 ATCAGTATCCGTTGTGATCGTCTTCCAGTACAAAGGATCTCTTTTTCAGCCGTGGA 1343
 Db |||||||
 421 IleSerIleArgValAspAlaIlePheGlnTyrLysGlyPhePhePheSerArgGly 440
 QY 1344 TCAAGCAATTTGAATACAACTTAAGACAAAGAAATATTACCCGAAATCATGAGAACTAAT 1403
 Db |||||||
 441 SerLysGlnPheGluTyrAsnIleLysThrLysAsnIleThrArgIleMetArgThrAsn 460
 QY 1404 ACTTGTTTCAATGAAAGACAAAGAACTCTCTCATTTTGGTTTGTATCATCAACAAAGAA 1463
 Db |||||||
 461 ThrTrpPheGlnCysLysGluProLysAsnSerSerPheGlyPheAspIleAsnLysGlu 480
 QY 1464 AAAGACATTCAGGAGGCATTAAGATATTGTATCATCAAGAGTTTAAGCTGTGTTATTTT 1523
 Db |||||||
 481 LysAlaHisSerGlyIleLysIleLeuTyrHisLysSerLeuSerLeuPheIlePhe 500
 QY 1524 GGTATTGTTCAATTTGCTGAAAAACACTTCTATTATCAA 1562
 Db |||||||
 501 GlyIleValHisLeuLeuLysAsnThrSerIleTyrGln 513

RESULT 11

US-10-176-921-192
 ; Sequence 192, Application US/10176921
 ; Publication No. US20030027276A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Baker, Kevin P.
 ; APPLICANT: Beresini, Maureen
 ; APPLICANT: DeForge, Laura
 ; APPLICANT: Desnoyers, Luc
 ; APPLICANT: Filvaroff, Ellen
 ; APPLICANT: Gao, Wei-Qiang
 ; APPLICANT: Gerritsen, Mary E.
 ; APPLICANT: Goddard, Audrey
 ; APPLICANT: Godowski, Paul J.
 ; APPLICANT: Gurney, Austin L.
 ; APPLICANT: Sherwood, Steven
 ; APPLICANT: Smith, Victoria
 ; APPLICANT: Stewart, Timothy A.
 ; APPLICANT: Tumas, Daniel
 ; APPLICANT: Watanabe, Colin K
 ; APPLICANT: Wood, William
 ; APPLICANT: Zhang, Zemin
 ; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
 ; FILE REFERENCE: P3330R1C288
 ; CURRENT APPLICATION NUMBER: US/10/176,921
 ; CURRENT FILING DATE: 2002-06-20
 ; Prior Application removed - See File Wrapper or Palm
 ; NUMBER OF SEQ ID NOS: 550
 ; SEQ ID NO 192
 ; LENGTH: 513
 ; TYPE: PRT
 ; ORGANISM: Homo Sapien
 US-10-176-921-192

Alignment Scores:

Pred. No.: 1.98e-273 Length: 513
 Score: 2752.00 Matches: 512
 Percent Similarity: 99.81% Conservative: 0
 Best Local Similarity: 99.81% Mismatches: 1

Query Match: 93.92% Indels: 0
 DB: 14 Gaps: 0

US-10-729-807-28 (1-1627) x US-10-176-921-192 (1-513)

QY 24 ATGAAGCGCTTCTGCTCTGTTGTTTATTAACATTTTCTTCTGCATTTCCCTTA 83
 Db |||||||
 1 MetLysArgLeuLeuLeuLeuPheIleThrPheSerSerAlaPheProLeu 20
 QY 84 GTCGGATGACCGAAAAATGAGAAATATGCAACTGGCTCAGGCATATCTCAACCAAGTTC 143
 Db |||||||
 21 ValArgMetThrGluAsnGluAsnMetGlnLeuAlaGlnAlaTyrLeuAsnGlnPhe 40
 QY 144 TACTCTCTTGAATAGNAGGGAATCATCTTCTTCAAGCAAGAAATAGGAGTCTCATAGT 203
 Db |||||||
 41 TyrSerLeuGluIleGluGlyAsnHisLeuValGlnSerLysAsnArgSerLeuIleAsp 60
 QY 204 GACAAAATTCGGGAAATGCAAGCATTTTGTGATTGACAGTCACTCGGAAAACTGCACTCA 263
 Db |||||||
 61 AspLysIleArgGluMetGlnAlaPhePheGlyLeuThrValThrGlyLysLeuAspSer 80
 QY 264 AACACCTTTGAGATCATGAAGACACCCAGGTGTGGGTGCTGATGTGGCCAGATATGCG 323
 Db |||||||
 81 AsnThrLeuGluIleMetLysThrProArgCysGlyValProAspValGlyGlnTyrGly 100
 QY 324 TACACCTCCCTGGGTGGAGAAAAATACACCTCACCACAGATATATAACTATATCTCG 383
 Db |||||||
 101 TyrThrLeuProGlyTyrPargLysTyrAsnLeuThrTyrArgIleIleAsnTyrThrPro 120
 QY 384 GATATGGCACGAGCTGTGTGATGAGGTATCCCAAGAGGTTTAGAAGTGTGGAGCAA 443
 Db |||||||
 121 AspMetAlaArgAlaAlaValAspGluAlaIleGlnGluGlyLeuValTrpSerLys 140
 QY 444 GTCACCTCCACTAAAATTCACCAAGATTCACCAAGGATTCACCAAGGATTCACATCATGATGCCTTT 503
 Db |||||||
 141 ValThrProLeuLysPheThrLysIleSerLysGlyIleAlaAspIleMetIleAlaPhe 160
 QY 504 AGGACTCGAGTCCATGTCGGTGTCTGCTATTTTGTGTCCTCCCTGGAGTGTCTGCG 563
 Db |||||||
 161 ArgThrArgValHisGlyArgCysProArgTyrPheAspGlyProLeuGlyValLeuGly 180
 QY 564 CATGCTTTCTCTCTCCGGTCCGGTCTGGGTGTGACACACTCATTTTGTGATGAGATGAAAC 623
 Db |||||||
 181 HisAlaPheProGlyProGlyLeuGlyGlyAspThrHisPheAspGluAspGluAsn 200
 QY 624 TCGACCAAGGATGGAGCAGGATTCAACTTGTTTCTTGTGGCTGCTCATGAAATTTGTCAT 683
 Db |||||||
 201 TrpThrLysAspGlyAlaGlyPheAsnLeuPheLeuValAlaAlaHisGluPheGlyHis 220
 QY 684 GCACCTGGGGCTCTCTCCTCCAAATGATCAACAGCGCTTGATGTTCCCAATATTGTCTCC 743
 Db |||||||
 221 AlaLeuGlyLeuSerHisSerAsnAspGlnThrAlaLeuMetPheProAsnTyrValSer 240
 QY 744 CTGGATCCCGAAAAATACCCACTTTCTCAGGATGATATCAATGGAATCCAGTCCCATCTAT 803
 Db |||||||
 241 LeuAspProArgLysTyrProLeuSerGlnAspAspIleAsnGlyIleGlnSerIleTyr 260
 QY 804 GGAGTCTCTCCCTAAGTACCTGCTAAGCCAAAGGAACCCACTATACCCCATGCTGTGAC 863
 Db |||||||
 261 GlyGlyLeuProLysValProAlaLysProLysGluProThrIleProHisAlaCysAsp 280
 QY 864 CCTGACTTGACHTTTGAGCTATCACACTTCCCGCAGAGAGTAAATGTTCTTTAAAGGC 923
 Db |||||||
 281 ProAspLeuThrPheAspAlaIleThrThrPheArgArgGluValMetPhePheLysGly 300
 QY 924 AGGCACCTATGGAGGATCTATTATCATATCAGGATGTTGAGTTTGAATTAATTCCTTCA 983
 Db |||||||
 301 ArgHisLeuTrpArgIleTyrTyrAspIleThrAspValGluPheGluLeuIleAspSer 320
 QY 984 TTCTGGCCATCTCTCCAGCTGATCTGCAAGCTGCATACGAGAACCCAGAGATAGATT 1043
 Db |||||||
 321 PheTrpProSerLeuProAlaAspLeuGlnAlaAlaTyrGluAsnProArgAspLysIle 340

Db 321 PheTrpProSerLeuProAlaAspLeuGlnAlaIaTyrgluAsnProArgAspIle 340
QY 1044 CTGGTTTTAAAGATGAAACTCTGGATGATCAGAGGATATGCTGCTTGGCAGATTAT 1103
Db 341 LeuValPheLysAspGluAsnProMetIleArgGlyTyraValLeuProAspTyr 360
QY 1104 CCCAATCCATCATCATAGTTTCCAGGACGTGTGAAGAAATAGATGACGCCGTC 1163
Db 361 ProLysSerIleHisThrLeuGlyPheProGlyArgValLysLysIleAspAlaVal 380
QY 1164 TGTGTAAGACACACAGAAACCTACTTCTTGTGGCATTTGGTGCTGGAGGTTTGAT 1223
Db 381 CysAspLysThrThrArgLysThrTyraPheValGlyIleTrpCysTrpArgPheAsp 400
QY 1224 GAAATGACCCAAACCATGACAAAGGATCCCGCAGAGAGTGTAACAACTTTCCTGGA 1283
Db 401 GluMetThrGlnThrMetAspLysGlyPheProGlnArgValLysHisPheProGly 420
QY 1284 ATCAGTATCCGTTGATGCTGCTTCCAGTACAAAGGATCTCTTTTTCAGCCGTGA 1343
Db 421 IleSerIleArgValAspAlaPheGlnTyraLysGlyPhePheSerArgGly 440
QY 1344 TCAAAGCAATTTGAATACAAACATTAAGACAAAGAAATATTACCGAATCATGAGAACTAAT 1403
Db 441 SerLysGlnPheGluTyraSnnleLysThrLysAsnIleThrArgIleMetArgThrAsn 460
QY 1404 ACTTGTTTCAATGCAAGAACCAAGAACTCTCTATTTGGTTTTGATATCAACAGGAA 1463
Db 461 ThrTrpPheGlnCysLysGluProLysAsnSerSerPheGlyPheAspIleAsnLysGlu 480
QY 1464 AAAGCACTTCAGGAGCATTAAGATATGCTATCAAGAGTTAAGCTTGTTATTTT 1523
Db 481 LysAlaHisSerGlyGlyIleLysIleLeuTyraHisLysSerLeuSerLeuPheIlePhe 500
QY 1524 GGTATTGTTTCAATTTGCTGAAACAACTCTCTATTATCAAA 1562
Db 501 GlyIleValHisLeuLeuLysAsnThrSerIleTyraGln 513

RESULT 13

US-10-140-474-192
; Sequence 192, Application US/10140474
; Publication No. US20030032156A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Beresini, Maureen
; APPLICANT: DeForge, Laura
; APPLICANT: Desnoyers, Luc
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Sherwood, Steven
; APPLICANT: Smith, Victoria
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tamas, Daniel
; APPLICANT: Watanabe, Colin K
; APPLICANT: Wood, William
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P3330R1C162
; CURRENT APPLICATION NUMBER: US/10/140,474
; CURRENT FILING DATE: 2002-05-06
; Prior Application removed - See Palm or File Wrapper
; NUMBER OF SEQ ID NOS: 550
; SEQ ID NO 192
; LENGTH: 513
; TYPE: PRT
; ORGANISM: Homo Sapien
US-10-140-474-192

Alignment Scores: 1.98e-273 Length: 513
Pred. No.: 2752.00 Matches: 512
Score: 99.81% Conservative: 0
Percent Similarity: 99.81% Mismatches: 1
Best Local Similarity: 99.81% Indels: 0
Query Match: 99.92% Gaps: 0
DB: 14

US-10-729-807-28 (1-1627) x US-10-140-474-192 (1-513)

QY 24 ATGAAGCGCTTCTGCTTCTGTTTGTCTTTATAAACAATTTTCTCTGCAATTCCTCTTA 83
Db 1 MetLysArgLeuLeuLeuPheLeuPhePheIleThrPheSerSerAlaPheProLeu 20
QY 84 GTCGGATGACCGGAAATGAAGAAATATGCAACTGGCTCAGGCATATCTCAACGATTC 143
Db 21 ValArgMetThrGluAsnGluAsnMetGlnLeuAlaGlnAlaTyraLeuAsnGlnPhe 40
QY 144 TACTCTCTTGAATAGAAGGAATCATCTTGTTCAAAGCAAGAAATAGGAGTCTCATAGAT 203
Db 41 TyrSerLeuGluIleGluGlnHisLeuValGlnSerLysAsnArgSerLeuIleAsp 60
QY 204 GACAAATTCGGGAAATGCAAGCATTTTGTGATTCACAGTCTGCTGGAATACTGGACTCA 263
Db 61 AspLysIleArgGluMetGlnAlaPhePheGlyLeuThrValThrGlyLysLeuAspSer 80
QY 264 AACACCTTGGATCATGAAAGACACCCAGGTGTGGGTGCTGATGTGGGCGAGTATGGC 323
Db 81 AsnThrLeuGluIleMetLysThrProArgCysGlyValProAspValGlyGlnTyraGly 100
QY 324 TACACCTCCCTGGGTGGAGAAATACAACTCACCCTACAGAAATATAAATATCTCCG 383
Db 101 TyrThrLeuProGlyTrpArgLysTyraAsnLeuThrTyraArgIleIleAsnTyraThrPro 120
QY 384 GATATGGCAGAGTCTGCTGATGAGGTATTCCTCAAGAAAGTTTAGAAGTGTGGAGCAAA 443
Db 121 AspMetAlaArgAlaAlaValAspGluAlaIleGlnGluGlyLeuGluValTrpSerLys 140
QY 444 GTCATCTCCACTAAATTCACCAAGATTCAAAGGGATTCAGAGGATTCAGATGATGCTTT 503
Db 141 ValThrProLeuLysPheThrLysIleSerLysGlyIleAlaAspIleMetIleAlaPhe 160
QY 504 AGCACTCGAGTCCATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 563
Db 161 ArgThrArgValHisGlyArgCysProArgTyraPheAspGlyProLeuGlyValLeuGly 180
QY 564 CATGCTTTTCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 623
Db 181 HisAlaPheProGlyProGlyLeuGlyGlyAspThrHisPheAspGluAspGluAsn 200
QY 624 TGACCAAGATGAGGACAGGATTCAACTTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 683
Db 201 TrpThrLysAspGlyAlaGlyPheAsnLeuPheValAlaAlaHisGluPheGlyHis 220
QY 684 GCACTGGGCTCTCCACTCCATGATCAACAGCCCTGATGTTCCCAATATGCTCTCC 743
Db 221 AlaLeuGlyLeuSerHisSerAsnAspGlnThrAlaLeuMetPheProAsnTyraValSer 240
QY 744 CTGGATCCCAAGAAATACCCACTTTTCTCAGGATGATATCAATGGAATCCAGTCCATCTAT 803
Db 241 LeuAspProArgLysTyraProLeuSerGlnAspAspIleAsnGlyIleGlnSerIleTyra 260
QY 804 GGAGTCTGCTTAAGTACTCTGTAAGCAAGAAACCCACTATATACCCCATGCTGCTGAC 863
Db 261 GlyGlyLeuProLysValProAlaLysProLysGluProThrIleProHisAlaCysAsp 280
QY 864 CTGACTTCACTTTTACCGCTATCAACTTCCGAGAGAGTATGTTCTTTAAAGC 923
Db 281 ProAspLeuThrPheAspAlaIleThrThrPheArgGluValMetPhePheLysGly 300
QY 924 AGGCACCTATGAGGATCTATTATGATATCAAGGATTTGAGTTTGAATTAATGCTTCA 983

Db 301 ArgHisLeuTprAArgileTyTyAspIleThrAspValGluPheGluLeuIleAlaSer 320
QY 984 TTCGGCCATCTCTGCCAGTGAICTGCAAGCTGCATACAGAGACCCAGAGATAAGATT 1043
Db 321 PheTrpProSerLeuProAlaAspIleuGlnAlaIatyrGluAsnProArgAspIle 340
QY 1044 CTGGTTTTAAAGATGAAACTTCTGGATGATCAGAGATATGCTGCTCCGATTTAT 1103
Db 341 LeuValPheLysAspGluAsnPhetrPmetIleargGlyTyAlaValLeuProAspIyr 360
QY 1104 CCCAAATCCATCCATACATATTAGTTTCCAGAGCTGTGAAGAAAATAGATGCAAGCCGTC 1163
Db 361 ProLysSerIleHisThrLeuGlyPheProGlyArgValLysLysIleAspAlaAlaVal 380
QY 1164 TGTGATAAGACACAGAAAACCTACTCTTTTGGGCATTTGGTGTGAGGTTTGAT 1223
Db 381 CysAspLysThrThrArgLysThrTyPhePheValGlyIleIleTrpCysTrpArgPheAsp 400
QY 1224 GAAATGACCCAAACCATGGACAAAGGATTCCCGCAGAGAGTGGTAAACACACTTTCCTGGA 1283
Db 401 GluMetThrGlnThrMetAspLysGlyPheProGlnArgValValLysHisPheProGly 420
QY 1284 ATCAGTATCCGTGTGTGATGCTGCTTCCAGTACAAAGGATCTCTTTTTCAGCCGTTGA 1343
Db 421 IleSerIleArgValAspAlaAlaPheGlnTyLysGlyPhePhePheSerArgGly 440
QY 1344 TCAAGCAATTTGAATACAACTTAAGCAAGATATATCCGATCATGAGAACTAAT 1403
Db 441 SerLysGlnPheGluTyAsnIleLysThrLysAsnIleThrArgIleMetArgThrAsn 460
QY 1404 ACTTGGTTTCAATCAAGAAACCAAGAACCTCTCATTTGGTTTGTATATCAACAAAGAA 1463
Db 461 ThrTrpPheGlnCysLysGluProLysAsnSerSerPheGlyPheAspIleAsnLysGlu 480
QY 1464 AAAGCATTCCAGGAGGATTAAGATATGTATCATAGAGTTTAAGCTTGTATTATTTT 1523
Db 481 LysAlaHisSerGlyGlyIleLysIleLeuTyHisLysSerLeuSerLeuPheIlePhe 500
QY 1524 GGTATTGTTCAATTCCTGCAAAACACTCTATTATCAAA 1562
Db 501 GlyIleValHisLeuLeuLysAsnThrSerIleTyGln 513

RESULT 14

US-10-142-431-192
; Sequence 192, Application US/10142431
; Publication No. US2003036179A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Beresini, Maureen
; APPLICANT: DeForge, Laura
; APPLICANT: Desnoyers, Luc
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Goddard, Paul J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Sherwood, Steven
; APPLICANT: Smith, Victoria
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Watanabe, Colin K
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P3330R1C251
; CURRENT APPLICATION NUMBER: US/10/142,431
; CURRENT FILING DATE: 2002-05-10
; Prior Application removed - See File Wrapper or Palm
; NUMBER OF SEQ ID NOS: 550
; SEQ ID NO 192
; LENGTH: 513

; TYPE: PRT
; ORGANISM: Homo Sapien
US-10-142-431-192
Alignment Scores:
Pred. No.: 1,98e-273 Length: 513
Score: 2752.00 Matches: 512
Percent Similarity: 99.81% Conservative: 0
Best Local Similarity: 99.81% Mismatches: 1
Query Match: 93.92% Indels: 0
DB: 14 Gaps: 0
US-10-729-807-28 (1-1627) x US-10-142-431-192 (1-513)

QY 24 ATGAAGCGCTTCTGCTTCTGTTGTTTCTTTATACATTTTCTTCTGCAATTTCCCTTA 83
Db 1 MetLysArgLeuLeuLeuPheLeuPhePheIleThrPheSerSerAlaPheProLeu 20
QY 84 GTCGCGATGACGGAATAATGAAGAAAATATGCAACTGGCTCAGGCATATCTCAACCCAGTTC 143
Db 21 ValArgMetThrGluAsnGluGluAsnMetGlnLeuAlaGlnAlaTyLeuAsnGlnPhe 40
QY 144 TACTCTCTGAAATAGAGGAATCATCTTGTTCAAAGCAAGATAGAGTCTCATAGAT 203
Db 41 TyrSerLeuGluIleGluGlyAsnHisLeuValGlnSerLysAsnArgSerLeuIleAsp 60
QY 204 GACAAATTCGGGAANTGCAAGCATTTTTCGATTGACAGTACTGGAACCTGACTCA 263
Db 61 AspLysIleArgGluMetGlnAlaPhePheGlyLeuThrValThrGlyLysLeuAspSer 80
QY 264 AACACCTTGTAGATCATGAACACACACAGGTTGGGTGCTGTATGTGGCCAGTATGGC 323
Db 81 AsnThrLeuGluIleMetLysThrProArgCysGlyValProAspValGlyGlnTyGly 100
QY 324 TACACCTTCCCTGGTGGAGAAAATACAACTCCTACAGATTAATAAATACTACTCCG 383
Db 101 TyrThrLeuProGlyTyArgLysTyAsnLeuThrTyArgIleIleAsnTyThrPro 120
QY 384 GATATGCGACGAGCTGCTGGATGAGGCTATCAAGAGGTTTAGAGTGTGGAGCAAA 443
Db 121 AspMetAlaArgAlaAlaValAspGluAlaIleGlnGluGlyLeuGluValTrpSerLys 140
QY 444 GTCACCTCCACTAAATTCACCAAGATTCAAAGGGGATTGACAGACATCATGATTCCTTT 503
Db 141 ValThrProLeuLysPheThrLysIleSerLysGlyIleAlaAspIleMetIleAlaPhe 160
QY 504 AGGACTCGAGTCCATGTGCTGCTCTCGTCTATTTTGTATGTCCTTGGAGTGTGGC 563
Db 161 ArgThrArgValHisGlyArgCysProArgTyPheAspGlyProLeuGlyValLeuGly 180
QY 564 CATGCCCTTCTCTGCTGCTGGGTCTGGGTGCTGACACTCATTTTGTAGATGAGATCAAAAC 623
Db 181 HisAlaPheProGlyProGlyProGlyLeuGlyAspThrHisPheAspGluAspGluAsn 200
QY 624 TGGACCAAGATGAGCAGGATTCAACTTGTCTTGTGGCTGCTCATGATTTGGTTCAT 683
Db 201 TrpThrLysAspGlyAlaGlyPheAsnLeuPheLeuValAlaAlaHisGluPheGlyHis 220
QY 684 GCATGGGGCTCTCTCACTCCAAATGATCAACAGCCTGTGATGTTCCCAAAATATGTCCTC 743
Db 221 AlaLeuGlyLeuSerHisSerAsnAspGlnThrAlaLeuMetPheProAsnTyValSer 240
QY 744 CTGGATCCAGAAAATACCCACTTTCACAGATCATATCAATGAATCCAGTCCATCAT 803
Db 241 LeuAspProArgLysTyProLeuSerGlnAspIleAsnGlyIleGlnSerIleTy 260
QY 804 GGAGTCTGCTTAAGTACCTGCTTAAGCCAAAGGAACCCATATACCCCATGCTGTGAC 863
Db 261 GlyGlyLeuProLysValProAlaLysProLysGluProThrIleProHisAlaCysAsp 280
QY 864 CTTGACTTGACTTTTGACGCTATCACAACCTTCCGAGAGAGTAATGTTCTTTAAAGCC 923
Db 281 ProAspLeuThrPheAspAlaIleThrThrPheArgArgGluValMetPhePheLysGly 300

QY 924 AGGCACCTATGGAGGATCTATTATGATATCACGGATGTTGAGTTGAATTAATTCCTTCA 983
 Db 301 ArgHisLeuTrpArgIleTyrTyrAspIleThrAspValGluPheGluLeuIleAlaSer 320
 QY 984 TTCTGGCCATCTCTGCCAGCTGTATCTCAAGCTGCATACAGAACCCAGAGATAAGATT 1043
 Db 321 PheTrpProSerLeuProAlaAspLeuGlnAlaIleTyrGluAsnProArgAspLysIle 340
 QY 1044 CTGGTTTTTAAAGATGAAACTCTTCGATGATCAGAGATATGCTGTCTGCCAGATTAT 1103
 Db 341 LeuValPheLysAspGluAsnPheTrpMetIleArgGlyTyrAlaValLeuProAspTyr 360
 QY 1104 CCAGAAATCCATCATACATAGGTTTTCCAGGAGCTGTGAAGAAATAGATGACGCGTC 1163
 Db 361 ProLysSerIleHisThrLeuGlyPheProGlyArgValLysLysIleAspAlaIleVal 380
 QY 1164 TGTGATAAGACCAAGAAAACCTACTCTCTTTGTGGGCATTTTGGTCTGCGAGTTTGAT 1223
 Db 381 CysAspLysThrThrArgLysThrTyrPhePheValGlyIleTyrCysTyrPArgPheAsp 400
 QY 1224 GAATGACCCAAACCATGGCAAGAGATTCCCGCAGAGAGTGTAACAACATTTCTCTGGA 1283
 Db 401 GluMetThrGlnThrMetAspLysGlyPheProGlnArgValValLysHisPheProGly 420
 QY 1284 ATCAGTATCGTGTGATGCTCTTCCAGTACAAAGGATTCTTCTTTTTCAGCCGTGGA 1343
 Db 421 IleSerIleArgValAspAlaAlaPheGlnTyrLysGlyPhePhePheSerArgGly 440
 QY 1344 TCAAAGCAATTGAATACAAACATTAAAGACAAAGATATTACCGAATCATGAGAACTAAT 1403
 Db 441 SerLysGlnPheGlnTyrAsnIleLysThrLysAsnIleThrArgIleMetArgThrAsn 460
 QY 1404 ACTTGTTTCAATGCAAGAACCAAGAACTCTCATTTTGGTTTGATATCAACAGGAA 1463
 Db 461 ThrTrpPheGlnCysLysGluProLysAsnSerSerPheGlyPheAspIleAsnLysGlu 480
 QY 1464 AAAGCACATTGAGGAGCATAAAGATATTGTATCATAAAGATTAAAGCTTGTTTATTTT 1523
 Db 481 LysAlaHisSerGlyLysIleLysIleLysLeuTyrHisLysSerLeuSerLeuPheIlePhe 500
 QY 1524 GGTATTGTCATTGCTGAAAAACACTTCTATTATCAA 1562
 Db 501 GlyIleValHisLeuLeuLysAsnThrSerIleTyrGln 513

RESULT 15

US-10-143-114-192
 ; Sequence 192, Application US/10143114
 ; Publication No. US20030036180A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Baker, Kevin P.
 ; APPLICANT: Beresini, Maureen
 ; APPLICANT: DeForge, Laura
 ; APPLICANT: Desnoyers, Luc
 ; APPLICANT: Filvaroff, Ellen
 ; APPLICANT: Gao, Wei-Qiang
 ; APPLICANT: Gerritsen, Mary E.
 ; APPLICANT: Goddard, Audrey
 ; APPLICANT: Godowski, Paul J.
 ; APPLICANT: Gurney, Austin L.
 ; APPLICANT: Sherwood, Steven
 ; APPLICANT: Smith, Victoria
 ; APPLICANT: Stewart, Timothy A.
 ; APPLICANT: Tumas, Daniel
 ; APPLICANT: Watanabe, Colin K
 ; APPLICANT: Wood, William
 ; APPLICANT: Zhang, Zemin
 ; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
 ; FILE REFERENCE: P3330KIC211
 ; CURRENT APPLICATION NUMBER: US/10/143,114
 ; CURRENT FILING DATE: 2002-05-09
 ; Prior Application removed - See Palm or File Wrapper

; NUMBER OF SEQ ID NOS: 550

; SEQ ID NO 192

; LENGTH: 513

; TYPE: PRT

; ORGANISM: Homo Sapien

US-10-143-114-192

Alignment Scores:

Pred. No.: 1.98e-273 Length: 513
 Score: 2752.00 Matches: 512
 Percent Similarity: 99.81% Conservative: 0
 Best Local Similarity: 99.81% Mismatches: 1
 Query Match: 93.92% Indels: 0
 DB: 14 Gaps: 0

US-10-729-807-28 (1-1627) x US-10-143-114-192 (1-513)

QY 24 ATGAAGCGCCTTCCTGCTTCCTGTTGTTCTTTTATAACATTTTCTTCGCAATTCCTTCA 83

Db 1 MetLysArgLeuLeuLeuLeuPheLeuPhePheIleThrPheSerSerAlaPheProLeu 20

QY 84 GTCGGATGACGGAATAATGAAGAAATATCAACTGGCTCAGGCATATCTCAACCACTTC 143

Db 21 ValArgMetThrGluAsnGluGluAsnMetGlnLeuAlaGlnIleTyrLeuAsnGlnPhe 40

QY 144 TACTCTCTTCAATAGAGGAATCATCTTGTTCACAGCAAGATAGAGTCTCATAGAT 203

Db 41 TyrSerLeuGluIleGluGlyAsnHisLeuValGlnSerLysAsnArgSerLeuLeuAsp 60

QY 204 GACAAAATTCGGAAATGCAAGCATTTTGTGGATTGACAGTGTGAGTGTGAAAACTGGACTCA 263

Db 61 AspLysIleArgGluMetGlnAlaPhePheGlyLeuThrValThrGlyLysLeuAspSer 80

QY 264 AACACCTTGAGATCATGAAAGACACCCAGGTGTGGGTGCTGATGTGGGCCAGATATGGC 323

Db 81 AsnThrLeuGluIleMetLysThrProArgCysGlyValProAspValGlyGlnTyrGly 100

QY 324 TACACCTCCCTCGGTGGAGAAATACACCTCACCTACAGATAATAAACTATCTACCG 383

Db 101 TyrThrLeuProGlyTrpArgLysTyrAsnLeuThrTyrArgIleIleAsnTyrThrPro 120

QY 384 GATATGGCACAGCTGCTGTGGATGAGGCTATCCAAGAAGTTTATAGAAGTGTGGAGCAA 443

Db 121 AspMetAlaArgAlaAlaValAspGluAlaIleGlnGluGlyLeuGluValTrpSerLys 140

QY 444 GTCACTCCACTAAAATTCACCAAGATTCAAAGGGGATTCAGACATCATTTGATAGAGTGA 503

Db 141 ValThrProLeuLysPheThrLysIleSerLysGlyIleAlaAspIleMetIleAlaPhe 160

QY 504 AGGACTCGAGTCATGTCGGTCTCCTCGCTATTTTGTATGGTCCCTTGGAGTGTTCGGC 563

Db 161 ArgThrArgValHisGlyArgCysProArgTyrPheAspGlyProLeuGlyValLeuGly 180

QY 564 CATGCTCTTCTCCTCGTCCGGTCTGGGTGTGGGTGTGGGTGTGGGTGTGGGTGTGGGT 623

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QY 624 TGGACCAAGATGAGCAGAGATTCAACTGTGTTCTTGTGGTCTGCTCATGAATTTGGTFCAT 683

Db 201 TrpThrLysAspGlyAlaGlyPheAsnLeuValAlaAlaHisGluPheGlyHis 220

QY 684 GCACTGGGCTCTCTCCTCCATGATCAACAGCCTTGTATGTTGTTCCCAATATGTTCTCC 743

Db 221 AlaLeuGlyLeuSerHisSerAsnAspGlnThrAlaLeuMetPheProAsnTyrValSer 240

QY 744 CTGGATCCCAAGAAATACCCACTTTCTCAGGATGATATCAATGGAATCCAGTCCATCTAT 803

Db 241 LeuAspProArgLysTyrProLeuSerGlnAspAspIleAsnGlyIleGlnSerIleTyr 260

QY 804 GGAGTCTGCTTAAGTACTGCTGAAGCCAAAGAAACCCACTATACCCCATGCTGCTGAC 863

Db 261 GlyGlyLeuProLysValProAlaLysProLysGluProThrIleProHisAlaCysAsp 280

QY 864 CCTGACTTGACTTTGGCGCTATCACAACTTTCCGACAGAGTAATGTTCTTTAAAGGC 923
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QY 281 ProAspLeuThrPheAspAlaIleThrPheArgArgGluValMetPhePheLysGly 300
Db |||||||
QY 924 AGGCACCTATGGAGGATCTATTATGATATCAGGATGTTGAGTTTGAATTAATTCCTTCA 983
Db |||||||
QY 301 ArgHisLeuTrpArgIleTyrTyrAspIleThrAspValGluPheGluLeuIleAlaSer 320
QY 984 TTCGGCCATCTCTCCAGCTGATCTGCAAGCTGATACGAGAACCCAGAGATAAGATT 1043
Db |||||||
QY 321 PheTrpProSerLeuProAlaAspLeuGlnAlaIleTyrGluAsnProArgAspLysIle 340
QY 1044 CTGGTTTAAAGATGAAGAACTTCTGGATGATCAGAGGATATGCTGCTTGCAGATTAT 1103
Db |||||||
QY 341 LeuValPheLysAspGluAsnPheTrpMetIleArgGlyTyrAlaValLeuProAspLys 360
QY 1104 CCCAAATCCATCCATPACATTAGGTTTCCAGGACGTGTGAAGAAATAGATCGACCGTC 1163
Db |||||||
QY 361 ProlsSerIleHisThrLeuGlyPheProGlyArgValLysLysIleAspAlaAlaVal 380
QY 1164 TGTGATAGACACACAGAAACCTACTTCTTTGGGCATTTGGTGTGGAGGTTTCAT 1223
Db |||||||
QY 381 CysAspLysThrThrArgLysThrTyrPhePheValGlyIleTrpCysTrpArgPheAsp 400
QY 1224 GAAATGACCCAAACCATGCACAAAGGATTCCCGCAGAGAGTGTAACACACTTTCCTGGA 1283
Db |||||||
QY 401 GluMetThrGlnThrMetAspLysGlyPheProGlnArgValLysHisPheProGly 420
QY 1284 ATCAGTATCCGTGTTGATGCTCTTTCCAGTACAAAGGATTCTCTTTTCAGCCGTGGA 1343
Db |||||||
QY 421 IleSerIleArgValAspAlaAlaPheGlnTyrLysGlyPhePhePheSerArgGly 440
QY 1344 TCAAAGCAATTTGAATACACATTAAAGCAAGAATATTACCGAATCATGAGAACTAAT 1403
Db |||||||
QY 441 SerLysGlnPheGluTyrAsnIleLysThrLysAsnIleThrArgIleMetArgThrAsn 460
QY 1404 ACTTGGTTTCAATGCAAGAACCAAGAACTCCTCATTTGGTTTGTATATCAACAGGAA 1463
Db |||||||
QY 461 ThrTrpPheGlnCysLysGluProlsAsnSerSerPheGlyPheAspIleAsnLysGlu 480
QY 1464 AAAGCACATTCAGGAGGCATAAGATATTGTATCATATAAGAGTTTAAGCTTGTTATTTT 1523
Db |||||||
QY 481 LysAlaHisSerGlyGlyIleLysIleLeuTyrHisLysSerLeuSerLeuPheIlePhe 500
QY 1524 GGTATTTGTTTCATTTGCTGAAAACACTTCTATTATCAA 1562
Db |||||||
QY 501 GlyIleValHisLeuLysAsnThrSerIleTyrGln 513

Search completed: November 15, 2004, 20:40:52
Job time : 243.5 secs

GenCore version 5.1.6
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OM protein - nucleic search, using frame_plus_p2n model

Run on: November 15, 2004, 21:10:33 ; Search time 775 Seconds
(without alignments)
3575.105 Million cell updates/sec

Title: US-10-729-807-10

Permute score: 2763

Sequence: 1 MKRLLLCFLFFITSSAPPL.....SLSLFPGIVLLKNTSIYQ 513

Scoring table:

BLOSUM62
Xgapop 10.0 , Xgapext 0.5
Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 3625171 seqs, 2700493622 residues

Total number of hits satisfying chosen parameters: 7250342

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Command line parameters:

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-DB=Published Applications NA -OFMT=fastap -SUFFIX=rnpb -MINMATCH=0.1
-LOOPEXT=0 -UNITS=bits -START=1 -END=-1 -MATRIX=blosum62
-TRANS=human40.cdi -LIST=45 -DOCLALIGN=200 -THR SCORE=pct -THR MAX=100
-THR MIN=0 -ALIGN=15 -MODB=LOCAL -OUTFMT=pc -NORM=ext -HEAPSIZ=500 -MINLEN=0
-MAXLEN=2000000000 -USER=US10729807 @CGN 1 1 480 @runat 15112004 131728 16871
-NCPU=6 -ICPU=3 -NO MAP -LARGEQUERY -NEG SCORES=0 -WAIT -DSPBLOCK=100
-LONGLOG -DEV TIMEOUT=120 -THREADS=30 -YGAPOP=10 -XGAPOP=10 -XGAPEXT=0.5
-Fgapop=6 -Fgapext=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database : Published Applications NA:

1: /cgn2_6/ptodata/1/pubpna/US07_PUBCOMB.seq:
2: /cgn2_6/ptodata/1/pubpna/PCT_NEW_PUB.seq:
3: /cgn2_6/ptodata/1/pubpna/US06_NEW_PUB.seq:
4: /cgn2_6/ptodata/1/pubpna/US06_PUBCOMB.seq:
5: /cgn2_6/ptodata/1/pubpna/US07_NEW_PUB.seq:
6: /cgn2_6/ptodata/1/pubpna/PCTUS_PUBCOMB.seq:
7: /cgn2_6/ptodata/1/pubpna/US08_NEW_PUB.seq:
8: /cgn2_6/ptodata/1/pubpna/US08_PUBCOMB.seq:
9: /cgn2_6/ptodata/1/pubpna/US09A_PUBCOMB.seq:
10: /cgn2_6/ptodata/1/pubpna/US09B_PUBCOMB.seq:
11: /cgn2_6/ptodata/1/pubpna/US09C_PUBCOMB.seq:
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20: /cgn2_6/ptodata/1/pubpna/US60_NEW_PUB.seq:
21: /cgn2_6/ptodata/1/pubpna/US60_PUBCOMB.seq:

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

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Result No.	Score	Query Match	Length	DB ID	Description
1	2763	100.0	1627	17	US-10-729-807-28
2	2763	100.0	1845	10	US-09-862-631-1
3	2752	99.6	1542	10	US-09-759-130B-172
4	2752	99.6	1542	17	US-10-741-790-172
5	2752	99.6	1647	14	US-10-028-072-191
6	2752	99.6	1647	14	US-10-140-808-191
7	2752	99.6	1647	14	US-10-121-049-191
8	2752	99.6	1647	14	US-10-123-304-191
9	2752	99.6	1647	14	US-10-140-470-191
10	2752	99.6	1647	14	US-10-175-746-191
11	2752	99.6	1647	14	US-10-176-918-191
12	2752	99.6	1647	14	US-10-176-321-191
13	2752	99.6	1647	14	US-10-137-865-191
14	2752	99.6	1647	14	US-10-140-474-191
15	2752	99.6	1647	14	US-10-142-431-191
16	2752	99.6	1647	14	US-10-143-114-191
17	2752	99.6	1647	14	US-10-140-002-191
18	2752	99.6	1647	14	US-10-142-419-191
19	2752	99.6	1647	14	US-10-123-262-191
20	2752	99.6	1647	14	US-10-142-423-191
21	2752	99.6	1647	14	US-10-121-050-191
22	2752	99.6	1647	14	US-10-141-755-191
23	2752	99.6	1647	14	US-10-143-032-191
24	2752	99.6	1647	14	US-10-123-108-191
25	2752	99.6	1647	14	US-10-123-236-191
26	2752	99.6	1647	14	US-10-123-261-191
27	2752	99.6	1647	14	US-10-140-921-191
28	2752	99.6	1647	14	US-10-140-928-191
29	2752	99.6	1647	14	US-10-121-045-191
30	2752	99.6	1647	14	US-10-123-292-191
31	2752	99.6	1647	14	US-10-123-903-191
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33	2752	99.6	1647	14	US-10-124-822-191
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41	2752	99.6	1647	14	US-10-127-901A-191
42	2752	99.6	1647	14	US-10-128-693A-191
43	2752	99.6	1647	14	US-10-131-813A-191
44	2752	99.6	1647	14	US-10-131-818A-191
45	2752	99.6	1647	14	US-10-131-823A-191

ALIGNMENTS

RESULT 1
US-10-729-807-28
; Sequence 28, Application US/10729807
; Publication No. US20040132158A1
; GENERAL INFORMATION:
; APPLICANT: BANDMAN, Olga; HILLMAN, Jennifer L.
; APPLICANT: TANG, Y. Tom; LAL, Preeti G.
; APPLICANT: YUE, Henry; AZIMZAI, Yalda
; APPLICANT: BAUGHN, Mariah R.; LU, Dyrung Alina M.
; TITLE OF INVENTION: HUMAN PEPTIDASES
; FILE REFERENCE: PF-0651-1 DIV
; CURRENT APPLICATION NUMBER: US/10/729,807
; CURRENT FILING DATE: 2003-12-05
; PRIOR APPLICATION NUMBER: US 09/889,238
; PRIOR FILING DATE: 2002-01-24
; PRIOR APPLICATION NUMBER: PCT/US00/00641
; PRIOR FILING DATE: 2000-01-11
; PRIOR APPLICATION NUMBER: US 60/172,247
; PRIOR FILING DATE: 1999-01-11
; PRIOR APPLICATION NUMBER: US 60/132,253
; PRIOR FILING DATE: 1999-05-03

; PRIOR APPLICATION NUMBER: US 60/136,653

; PRIOR FILING DATE: 1999-05-27

; NUMBER OF SEQ ID NOS: 39

; SOFTWARE: PERL Program

; SEQ ID NO 28

; LENGTH: 1627

; TYPE: DNA

; ORGANISM: Homo sapiens

; FEATURE:

; NAME/KEY: misc_feature

; OTHER INFORMATION: Incyte ID No: 3772696CB1

US-10-729-807-28

Alignment Scores:

Score: 0 Length: 1627
 Percent Similarity: 2763.00 Matches: 513
 Best Local Similarity: 100.00% Conservative: 0
 Query Match: 100.00% Mismatches: 0
 DB: 17 Indels: 0
 Gaps: 0

US-10-729-807-10 (1-513) x US-10-729-807-28 (1-1627)

QY 1 MetLysArgLeuLeuLeuLeuCysLeuPhePheLeuThrPheSerSerAlaPheProLeu 20
 DB 24 ATGAAGCGCTTCTGCTTCGTGTTGTTCTTTATACATTTCTTCTGCAATTCCTTTA 83
 QY 21 ValArgMetThrGluAsnGluGluAsnMetGlnLeuAlaValThrLeuAsnGlnPhe 40
 DB 84 GTCCGGATGACGAAATGAAGAAATATGCAATGGCTCAGGCAATATCTCAACCACTTC 143
 QY 41 TyrSerLeuGluLeuGluGluAsnHisLeuValGlnSerLysAsnArgSerLeuLeuAsp 60
 DB 144 TACTCTTGAATAGAGGAATCATCTTGTTCAGCAAGCAAGATGAGGTCTCATAGAT 203
 QY 61 AspLysLeuArgGluMetGlnAlaPhePheGlyLeuThrValThrGlyLysLeuAspSer 80
 DB 204 GACAAATTCGGGAATGCAAGCATTTTGTGATGACAGTGAGTGGAAATCGACTCA 263
 QY 81 AsnThrLeuGluLeuMetLysThrProArgCysGlyValProAspValGlyGlnTyrGly 100
 DB 264 AACACCTTCAGATCATGAAGACACCCAGGTGGGGTGGCTGATGGGCCAGATGTC 323
 QY 101 TyrThrLeuProGlyTyrArgLysTyrAsnLeuThrTyrArgLysLeuLeuLeuThrPro 120
 DB 324 TACACCTTCCTGGTGGAGAAATACACCTCACCTACAGATATATTAATATATCTCCG 383
 QY 121 AspMetAlaArgAlaAlaValAspGluAlaLeuGlnGluGlyLeuGluValTyrSerLys 140
 DB 384 GATATGGCAGAGCTGCTGGATGAGGTATCCAGAGGTTTAGAAGTGTGGAGCAA 443
 QY 141 ValThrProLeuLysPheThrLysLeuSerLysGlyLeuAlaAspLeuMetLeuAlaPhe 160
 DB 444 GTCACTCCCAATAAAATTCACCAAGATTCACAGGGGATTCAGACATCATGATGCTTT 503
 QY 161 ArgThrArgValHisGlyArgCysProArgTyrPheAspGlyProLeuGlyValLeuGly 180
 DB 504 AGGACTCGAGTCCATGGTGGTCTGCTGCTATTTGATGGTCCCTTGGAGTGTGGC 563
 QY 181 HisAlaPheProProGlyProGlyLeuGlyGlyAspThrHisPheAspGluAspGluAsn 200
 DB 564 CATGCCCTTCCTCCTGGTCCGGTCTGGGTGGTGGACACTCATTTGATGAGGATGAAAC 623
 QY 201 TrpThrLysAspGlyAlaGlyPheAsnLeuPheLeuValAlaAlaHisGluPheGlyHis 220
 DB 624 TGACCAAGATGGAGCAGATTCACCTGTTTCTTGTGGCTGCTCATGAATTTGTGTCAT 683
 QY 221 AlaLeuGlyLeuSerHisSerAsnAspGlnThrAlaLeuMetPheProAsnTyrValSer 240
 DB 684 GCACCTGGGCTCTCTCACTCCATGATCAACAGCCTTGATGTTCACAAATATGCTCC 743
 QY 241 LeuAspProArgLysTyrProLeuSerGlnAspAspLeuGlnSerLeuLeuThr 260

DB 744 CTGATCCCAAGAAATACCCACCTTTCTCAGATGATATCATGAAATCCAGTCCATCTAT 803
 QY 261 GlyGlyLeuProLysValProAlaLysProLysGluProThrLeuProHisAlaCysAsp 280
 DB 804 GGAGGTCTGCTAAGGTACCTGCTAAGCCAAAGCAACCACTATACCCATGCTGTGAC 863
 QY 281 ProAspLeuThrPheAspAlaLeuThrThrPheArgArgGluValMetPhePheLysGly 300
 DB 864 CCTGACTTGACTTTTGACGCTATCACAACTTTCCGACAGAAAGTAATGTTCTTTAAAGGC 923
 QY 301 ArgHisLeuTyrArgLysTyrAspLeuThrAspValGluPheGluLeuLeuAlaSer 320
 DB 924 AGCACCTATGAGGATCTATTATGATATACGAGTGTGAGTTGATTTAATGCTTCA 983
 QY 321 PheTyrProSerLeuProAlaAspLeuGlnAlaAlaTyrGluAsnProArgAspLysLeu 340
 DB 984 TTCTGGCCATCTCTGCGAGCTGATCTGCAAGCTGCATACGAGAACCCAGAGATAAGATT 1043
 QY 341 LeuValPheLysAspGluAsnPheTyrMetLeuArgGlyTyrAlaValLeuProAspTyr 360
 DB 1044 CTGGTTTTTAAGATGAAAACTTCTGATGATCAGAGGATATGCTGCTTGCAGATTAT 1103
 QY 361 ProLysSerLeuHisThrLeuGlyPheProGlyArgValLysLysLysLeuAspAlaAlaVal 380
 DB 1104 CCCAATCCATCCATACATTAGGTTTTCCAGGACGTTGTGAAGAAATAGATGCGCGTC 1163
 QY 381 CysAspLysThrThrArgLysThrTyrPhePheValGlyLeuTyrCysTyrTrpArgPheAsp 400
 DB 1164 TGTGATAAGACCAACAAAGAAACCTACTTCTTTGTGGCATTTTGTGCTGGAGTTTGTAT 1223
 QY 401 GluMetThrGlnThrMetAspLysGlyPheProGlnArgValLysHisPheProGly 420
 DB 1224 GAAATGACCCAAACCATGGACAAAGGATTTCCCGACAGAGTGTGTAACAACTTTCTTCTGGA 1283
 QY 421 IleSerIleArgValAspAlaAlaPheGlnTyrLysGlyPhePhePheSerArgGly 440
 DB 1284 ATCAGTATCGTGTGATGCTGCTTTCCAGTACAAAGGATTTCTTTTTCAGCCGTGGA 1343
 QY 441 SerLysGlnPheGluTyrAsnLeuLysThrLysAsnLeuThrArgLysMetArgThrAsn 460
 DB 1344 TCAAGCAATTTGATATACACATTAAGACAAAGATATTACCGGAATCATGAGAACTAAT 1403
 QY 461 ThrTrpPheGlnCysLysGluProLysAsnSerSerPheGlyPheAspLeuAsnLysGlu 480
 DB 1404 ACTTGTTTCAATGCAAGAACCAAAAGAACTCTCATTTTGGTTTGGATCAACAAAGAA 1463
 QY 481 LysAlaHisSerGlyGlyLysLysLeuTyrHisLysSerLeuSerLeuPheLeuPhe 500
 DB 1464 AAAGCACATTCAGAGGCAATAAGATATTGATATCAAGAGTTTAAAGCTTGTATTATTTT 1523
 QY 501 GlyLeuValHisLeuLeuLysAsnThrSerIleTyrGln 513
 DB 1524 GSTATTGTTTCAATTTGCTGAAACCACTTCTATTATTATCAA 1562

RESULT 2

US-09-862-631-1

; Sequence 1, Application US/09862631

; Publication No. US20030032164A1

; GENERAL INFORMATION:

; APPLICANT: Holmgren, Erik

; APPLICANT: Kihlen, Mats

; APPLICANT: Wood, Tim

; APPLICANT: Ekblom, Jonas

; TITLE OF INVENTION: No. US20030032164A1 Matrix Metalloproteinases

; FILE REFERENCE: 0001489US

; CURRENT APPLICATION NUMBER: US/09/862, 631

; PRIOR FILING DATE: 2001-05-22

; PRIOR APPLICATION NUMBER: 206119

; NUMBER OF SEQ ID NOS: 8

; SOFTWARE: PatentIn version 3.0

; SEQ ID NO 1

; LENGTH: 1845

TYPE: DNA
ORGANISM: Homo sapiens
US-09-862-631-1

Alignment Scores:

Pred. No.: 0
Score: 2763.00
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Query Match: 100.00%
DB: 10

Length: 1845
Matches: 513
Conservative: 0
Mismatches: 0
Indels: 0
Gaps: 0

US-10-729-807-10 (1-513) x US-09-862-631-1 (1-1845)

QY 1 MetLysArgLeuLeuLeuLeuCysLeuPhePheLeuThrPheSerSerAlaPheProLeu 20
DB 24 ATGAAGCGCTTCTGCTTCTGTTGTTCTTATATAACATTTCTTCTGATTTCCCTTA 83
QY 21 ValArgMetThrGluAenGluGluAsnMetGlnLeuAlaGlnAlaTyrLeuAsnGlnPhe 40
DB 84 GTCCGGATGACGGAATATGAAGAAATATGCACTGGCTCAGGCATATCTCAACCATTC 143
QY 41 TyrSerLeuGluLeuGluGluAsnHisLeuValGlnSerLysAsnArgSerLeuIleAsp 60
DB 144 TACTCTCTTGAATAGAGGAATCATCTTGTTCAGAGCAAGATAGGAGTCTCATAGAT 203
QY 61 AspLysIleArgGluMetGlnAlaPhePheGlyLeuThrValThrGlyLysLeuAspSer 80
DB 204 GACAAATTCGGGAATGCAAGCATTTTGGATTGACAGTGTGGGAAATCGGACTCA 263
QY 81 AsnThrLeuGluIleMetLysThrProArgCysGlyValProAspValGlyGlnTyrGly 100
DB 264 AACACCCCTTGAGATCATGAAGACACCCAGGTGTGGGGTGCCTGANGTGGCCAGTATGGC 323
QY 101 TyrThrLeuProGlyTyrArgLysTyrAsnLeuThrTyrArgIleIleAsnTyrThrPro 120
DB 324 TACACCCCTCCCTGGTGGAGAAATACAACTCACCCTACAGATATAAATACTACTCCG 383
QY 121 AspMetAlaArgAlaAlaValAspGluAlaIleGlnGluGlyLeuGluValTyrSerLys 140
DB 384 GATATGGCAGCTGCTGTGGATGAGGCTATCCAAAGAGTTTAGAAGTGTGGAGCAA 443
QY 141 ValThrProLeuLysPheThrLysIleSerLysGlyIleAlaAspIleMetIleAlaPhe 160
DB 444 GTCACTCCACTAAAATTCACCAAGATTTCAAAGGGGATTCAGACATCATGATGGCTTT 503
QY 161 ArgThrArgValHisGlyArgCysProArgTyrPheAspGlyProLeuGlyValLeuGly 180
DB 504 AGGACTGAGTCCATGGTGGTGTCTGCTATTTTGTATGGTCCCTTGGGAGTGTTCGC 563
QY 181 HisAlaPheProProGlyProGlyLeuGlyAspThrHisPheAspGluAspGluAsn 200
DB 564 CATGCTTTCCTCTGCTCCGGTCCGGGTGTGGGTGTGACACTCATTTTGTATGAGGATGAAAC 623
QY 201 TrpThrLysAspGlyValGlyPheAsnLeuPheLeuValAlaAlaHisGluPheGlyHis 220
DB 624 TGGACCAAGGATGGAGCAGGATTCACCTGTGTTCCTGTGGCTGTGCTCATGAATTTGGTCA 683
QY 221 AlaLeuGlyLeuSerHisSerAsnAspGlnThrAlaLeuMetPheProAsnTyrValSer 240
DB 684 GCACCTGGGGCTCTCATCTCCATGATCAACAGAGCTTGTATGTTCCCAAAATATGTCTCC 743
QY 241 LeuAspProArgLysTyrProLeuSerGlnAspIleAsnGlyIleGlnSerIleTyr 260
DB 744 CTGGATCCAGAAATACCCATTTCTCAGGATGATCAATGGAATCCAGTCCATCTAT 803
QY 261 GlyGlyLeuProLysValProAlaLysProLysGluProThrIleProHisAlaCysAsp 280
DB 804 GGAGGTCTGCCCTAAGTACTCTGAAGCAAGAAAGGAAACCCACTATACCCCATCCCTGTGAC 863
QY 281 ProAspLeuThrPheAspAlaIleThrThrPheArgArgGluValMetPhePheLysGly 300
DB 864 CCTGACTTGTACTTTTACCGCTATCACACTTTCCCGCAGAGAGTATGTTCTTTAAAGC 923

QY 301 AtcHisLeuTyrArgIleTyrTyrAspIleThrAspValGluPheGluLeuIleAlaSer 320
DB 924 AGGCACCTATGGAGGATCTATTATGATATCACGAGTTTGAGTTGAATTAATGCTTCA 983
QY 321 PheTyrProSerLeuProAlaAspLeuGlnAlaAlaTyrGluAsnProArgAspLysIle 340
DB 984 TTCTGGCCATCTCTGCCAGCTGATCTGCAAGCTGCATACCGAAGAACCCAGAGATAAGATT 1043
QY 341 LeuValPheLysAspGluAsnPheTyrMetIleArgGlyTyrAlaValLeuProAspTyr 360
DB 1044 CTGGTTTAAAGATGAAATCTTCGATGATCAGAGGATATGCTGCTTTCGAGATTAT 1103
QY 361 ProLysSerIleHisThrLeuGlyPheProGlyArgValLysLysIleAspAlaAlaVal 380
DB 1104 CCCAAATCCATCATCATATTAGTTTTCAGGAGCTGTGAAGAAATAGATGCGCCGTC 1163
QY 381 CysAspLysThrThrArgLysThrTyrPhePheValGlyIleTyrCysTyrTrpArgPheAsp 400
DB 1164 TGTGATAAGACCAACAGAAAAACCTACTTCTTTGTGGGCATTTTGTGCTGGAGTTTGTAT 1223
QY 401 GluMetThrGlnThrMetAspLysGlyPheProGlnArgValLysHisPheProGly 420
DB 1224 GAAATGCCCAACCATGGAACAAAGGATTCGCCGAGAGAGTGGTAAACACATTTTCCGGA 1283
QY 421 IleSerIleArgValAspAlaAlaPheGlnTyrLysGlyPhePhePhePheSerArgGly 440
DB 1284 ATCAGTATCCGTGTGTGATGCTGCTTTCAGTACAAAGGATTTCTTTTTCAGCCGTGA 1343
QY 441 SerLysGlnPheGluTyrAsnIleLysIleLysAsnIleThrArgIleMetArgThrAsn 460
DB 1344 TCAAGCAATTTTGAATACAACTTAAGACAAAGATATTATCCCGAATCATGAGAACTAAT 1403
QY 461 ThrTrpPheGlnCysLysGluProLysAsnSerSerPheGlyPheAspIleAsnLysGlu 480
DB 1404 ACTTGGTTTCAATGCAAGAACCAAGAACTCTCATTTGTTGTTGATATCAACAGGA 1463
QY 481 LysAlaHisSerGlyGlyIleLysIleLeuTyrHisLysSerLeuSerLeuPheIlePhe 500
DB 1464 AAACCACTTCAGAGGCGATTAAGATATTGATCATATAAGATTTTAAGCTGTTTATT 1523
QY 501 GlyIleValHisLeuLeuLeuLeuAsnThrSerIleTyrGln 513
DB 1524 GGTATGTTCTATTTGCTGAAAAACACTTCTATTATCAA 1562

RESULT 3

US-09-759-130B-172
Sequence 172, Application US/09759130B
Publication No. US20030022279A1
GENERAL INFORMATION:
APPLICANT: Millennium Pharmaceuticals, Inc.
APPLICANT: McCarthy, Sean A
APPLICANT: Fraser, Christopher C
APPLICANT: Sharp, John D
APPLICANT: Barnes, Thomas S
APPLICANT: Kirst, Susan J
APPLICANT: Mackay, Charles R
APPLICANT: Myers, Paul S
APPLICANT: Leiby, Kevin R
APPLICANT: Wrighton, Nicolas
APPLICANT: Goodearl, Andrew
APPLICANT: Holtzman, Douglas A
TITLE OF INVENTION: NOVEL GENES ENCODING PROTEINS HAVING
TITLE OF INVENTION: PROGNOSTIC, DIAGNOSTIC, PREVENTIVE, THERAPEUTIC, AND OTHER
FILE REFERENCE: MP100-5350NMIM
CURRENT APPLICATION NUMBER: US/09/759,130B
CURRENT FILING DATE: 2002-09-16
PRIORITY APPLICATION NUMBER: US 09/479,249
PRIORITY FILING DATE: 2000-01-07
PRIORITY APPLICATION NUMBER: US 09/559,497
PRIORITY FILING DATE: 2000-04-27
PRIORITY APPLICATION NUMBER: US 09/578,063

APPLICANT: Sharp, John D

Db 1381 ACTTGTTTCAATGCAAGAACCAAGAACTCTCATTTGGTTTGTATATCAACAAGAA 1440
QY 481 LyeAlahisSerGlyGlyIleLysIleLeuTyxHisLysSerLeuPheIlePhe 500
Db 1441 AAAGCATTTCAGGAGCATAAAGATATTGTAICATAGAGTTTAAGCTTGTTATTTT 1500
QY 501 GlyIleValHisLeuLeuLysAsnThrSerIleTyxGln 513
Db 1501 GGTATTGTTCAATTTGCTGAAACACACTCTTATTATCAA 1539

RESULT 5
US-10-028-072-191
Sequence 191, Application US/10028072
Publication No. US20030004311A1
GENERAL INFORMATION:
APPLICANT: Baker, Kevin P.
APPLICANT: Beresini, Maureen
APPLICANT: DeForge, Laura
APPLICANT: Desnoyers, Luc
APPLICANT: Filvaroff, Ellen
APPLICANT: Gao, Wei-Qiang
APPLICANT: Gerritsen, Mary E.
APPLICANT: Goddard, Audrey
APPLICANT: Godowski, Paul J.
APPLICANT: Gurney, Austin L.
APPLICANT: Sherwood, Steven
APPLICANT: Smith, Victoria
APPLICANT: Stewart, Timothy A.
APPLICANT: Tumas, Daniel
APPLICANT: Watanabe, Colin K
APPLICANT: Wood, William
APPLICANT: Zhang
FILE REFERENCE:
CURRENT APPLICATION NUMBER: US/10/028,072
PRIOR FILING DATE: 2001-12-19
PRIOR APPLICATION NUMBER: 60/049911
PRIOR FILING DATE: 1997-06-18
PRIOR APPLICATION NUMBER: 60/056974
PRIOR FILING DATE: 1997-08-26
PRIOR APPLICATION NUMBER: 60/059113
PRIOR FILING DATE: 1997-09-17
PRIOR APPLICATION NUMBER: 60/059115
PRIOR FILING DATE: 1997-09-17
PRIOR APPLICATION NUMBER: 60/059117
PRIOR FILING DATE: 1997-09-17
PRIOR APPLICATION NUMBER: 60/059122
PRIOR FILING DATE: 1997-09-17
PRIOR APPLICATION NUMBER: 60/059184
PRIOR FILING DATE: 1997-09-17
PRIOR APPLICATION NUMBER: 60/059263
PRIOR FILING DATE: 1997-09-18
PRIOR APPLICATION NUMBER: 60/059352
PRIOR FILING DATE: 1997-09-19
PRIOR APPLICATION NUMBER: 60/059588
PRIOR FILING DATE: 1997-09-19
PRIOR APPLICATION NUMBER: 60/059836
PRIOR FILING DATE: 1997-09-24
PRIOR APPLICATION NUMBER: 60/062250
PRIOR FILING DATE: 1997-10-17
PRIOR APPLICATION NUMBER: 60/062285
PRIOR FILING DATE: 1997-10-17
PRIOR APPLICATION NUMBER: 60/062287
PRIOR FILING DATE: 1997-10-17
PRIOR APPLICATION NUMBER: 60/062814
PRIOR FILING DATE: 1997-10-24
PRIOR APPLICATION NUMBER: 60/062816
PRIOR FILING DATE: 1997-10-24
PRIOR APPLICATION NUMBER: 60/063045
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PRIOR APPLICATION NUMBER: 60/063082
PRIOR FILING DATE: 1997-10-31
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PRIOR FILING DATE: 1997-10-17
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PRIOR FILING DATE: 1997-11-03
PRIOR APPLICATION NUMBER: 60/064809
PRIOR FILING DATE: 1997-11-07
PRIOR APPLICATION NUMBER: 60/065186
PRIOR FILING DATE: 1997-11-12
PRIOR APPLICATION NUMBER: 60/065846
PRIOR FILING DATE: 1997-11-17
PRIOR APPLICATION NUMBER: 60/066364
PRIOR FILING DATE: 1997-11-21
PRIOR APPLICATION NUMBER: 60/066453
PRIOR FILING DATE: 1997-11-24
PRIOR APPLICATION NUMBER: 60/066511
PRIOR FILING DATE: 1997-11-24
PRIOR APPLICATION NUMBER: 60/066770
PRIOR FILING DATE: 1997-11-24
PRIOR APPLICATION NUMBER: 60/069212
PRIOR FILING DATE: 1997-12-11
PRIOR APPLICATION NUMBER: 60/069278
PRIOR FILING DATE: 1997-12-11
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PRIOR FILING DATE: 1997-12-11
PRIOR APPLICATION NUMBER: 60/069694
PRIOR FILING DATE: 1997-12-16
PRIOR APPLICATION NUMBER: 60/072320
PRIOR FILING DATE: 1998-01-23
PRIOR APPLICATION NUMBER: 60/073612
PRIOR FILING DATE: 1998-02-04
PRIOR APPLICATION NUMBER: 60/074086
PRIOR FILING DATE: 1998-02-09
PRIOR APPLICATION NUMBER: 60/074092
PRIOR FILING DATE: 1998-02-09
PRIOR APPLICATION NUMBER: 60/077791
PRIOR FILING DATE: 1998-03-12
PRIOR APPLICATION NUMBER: 60/078910
PRIOR FILING DATE: 1998-03-20
PRIOR APPLICATION NUMBER: 60/079294
PRIOR FILING DATE: 1998-03-25
PRIOR APPLICATION NUMBER: 60/079663
PRIOR FILING DATE: 1998-02-27
PRIOR APPLICATION NUMBER: 60/079728
PRIOR FILING DATE: 1998-03-27
PRIOR APPLICATION NUMBER: 60/080165
PRIOR FILING DATE: 1998-03-31
PRIOR APPLICATION NUMBER: 60/081203
PRIOR FILING DATE: 1998-04-09
PRIOR APPLICATION NUMBER: 60/081229
PRIOR FILING DATE: 1998-04-09
PRIOR APPLICATION NUMBER: 60/081695
PRIOR FILING DATE: 1998-04-14
PRIOR APPLICATION NUMBER: 60/081817
PRIOR FILING DATE: 1998-04-15
PRIOR APPLICATION NUMBER: 60/081810
PRIOR FILING DATE: 1998-04-15

1044	Db	CTGGTTTTAAAGATGAAAACTTCTGGATCATCAGAGATATGCTGCTTGGCCAGATTAT	1103
361	Qy	ProLysSerIleHisThrLeuGlyPheProGlyArgValIlysIleAspAlaAVal	380
1104	Db	CCCAATCCATCCCATACATTAGGTTTCCAGAGCGTGAAGAAAAATAGATGCACCGTC	1163
381	Qy	CysAspLysThrThrArgLysThrTyrPhePheValGlyIleTyrCysTirArgPheAsp	400
1164	Db	TGTGATAAGACCACCAAGAAAAACCTACTTCTTGTGGGCATTTCGTCTGGAGTTTGAT	1223
401	Qy	GluMetThrGlnThrMetAspLysGlyPheProGlnArgValValIlysHisPheProGly	420
1224	Db	GAATATGACCCCAACCATGGGACAAAGAGATTCGCCGACAGAGTGGTAAACAACATTTCTCTGGA	1283
421	Qy	IleSerIleArgValAspAlaAAlapheGlnTyrLysGlyPhePhePheSerArgGly	440
1284	Db	ATCAGTATCCGTGTGTGATGCTGCTTCAGTATCAAGAGATTCTCTTTTTTCAGCCGTGGGA	1343
441	Qy	SerLysGlnPheGluTyrAsnIleLysThrLysAsnIleThrArgIleMetArgThrAsn	460
1344	Db	TCAAGCAATTTTGAATACACATTAAGACAAAAGAAATATTACCCGAATCATGAGAACTAAT	1403
461	Qy	ThrTrpPheGlnCysLysGluProIlyAsnSerSerPheGlyPheAspIleAsnLysGlu	480
1404	Db	ACTTGGTTTCAATCCAAAGAACCAAAAGAACTCCCTCATTTGGTTTGTATATCAACAAGAA	1463
481	Qy	LysAlaHisSerGlyGlyIleLysIleLeuTyrHisLysSerLeuSerLeuPheIlePhe	500
1464	Db	AAAGCACATTCAGAGGGCATAAAGATATTGTATCATAGAGTTTAAAGCTGTTTATTTTT	1523
501	Qy	GlyIleValHisLeuLeuLysAsnThrSerIleTyrGln	513
1524	Db	GGTATTGTTCAATTGGCTGAAAAACATCTTATTTATCAA	1562

RESULT 6

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US-10-140-808-191
; Sequence 191, Application US/10140808
; Publication No. US20030017563A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Beresini, Maureen
; APPLICANT: DeForge, Laura
; APPLICANT: Desnoyers, Luc
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Sherwood, Steven
; APPLICANT: Smith, Victoria
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Watanabe, Colin K
; APPLICANT: Wood, William
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; TITLE OF INVENTION: ACIDS ENCODING THE SAME
; FILE REFERENCE: P3330R1C182
; CURRENT APPLICATION NUMBER: US/10/140,808
; CURRENT FILING DATE: 2002-05-07
; Prior Application removed - See File Wrapper or Palm
; NUMBER OF SEQ ID NOS: 550
; SEQ ID NO 191
; LENGTH: 1647
; TYPE: DNA
; ORGANISM: Homo Sapien
US-10-140-808-191

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Alignment Scores:		
Pred. No.:	0	Length: 1647
Score:	2752.00	Matches: 512

Db 984 TTCTGCCATCTCTGCCAGCTGATCTGCAAGCTGCATACAGAACCCAGAGATAAGATT 1043
 QY 341 LeuValPheLysAspGluAsnPheTrpMetIleArgGlyTyrAlaValLeuProAspTyr 360
 Db 1044 CTGGTGTAAAGATGAAGAACTTCTGGATGATCAGAGGATATGCTGTCTGCCAGATTAT 1103
 QY 361 ProLysSerIleHisThrLeuGlyPheProGlyArgValLysLysIleAspAlaVal 380
 Db 1104 CCCAATCCATCCATACATTAGTTTCCAGAGCTGTGAGAGAAATAGATCAGCCGTC 1163
 QY 381 CysAspLysThrThrArgLysThrTyrPhePheValGlyIleTrpCysTrpArgPheAsp 400
 Db 1164 TGTGATAAGACCAAGAAACCTACTCTTTGTGGGCATTTGTGTGGAGTTTGTAT 1223
 QY 401 GluMetThrGlnThrMetAspLysGlyPheProGlnArgValValLysHisPheProGly 420
 Db 1224 GAAATGACCCCAACCATGACAAAGATTCCCGCAGAGAGTGGTAAACACATTTCTCTGGA 1283
 QY 421 IleSerIleArgValAspAlaPheGlnTyrLysGlyPhePhePheSerArgGly 440
 Db 1284 ATCAGTATCCGTGTGTGATGCTGTTCCAGTACAAAGGATTTCTTTTCAGCCGTGGA 1343
 QY 441 SerLysGlnPheGluTyrAsnIleLysThrLysAsnIleThrArgIleMetArgThrAsn 460
 Db 1344 TCAAGACCAATTTGAATACAAATTAAGACAAAGATATTACCCGAATCATGAGAACTAAT 1403
 QY 461 ThrTrpPheGlnCysLysGluProLysAsnSerSerPheGlyPheAspIleAsnLysGlu 480
 Db 1404 ACTTGGTTCAATGCAAGAACCAAGAACTCCTCATTTGGTTTGTATCATCAACAAAGGAA 1463
 QY 481 LysAlaHisSerGlyGlyIleLysIleLeuTyrHisLysSerLeuSerLeuPheIlePhe 500
 Db 1464 AAAGCACATTCAGGAGGCATAAAGATATTGATCATAGAGTTTAAGCTGTGTATTTT 1523
 QY 501 GlyIleValHisLeuLeuLysAsnThrSerIleTyrGln 513
 Db 1524 GGTATTGTTCAATTTGCTGAAACACCTTCTATTATCA 1562

RESULT 7

US-10-121-049-191
 ; Sequence 191, Application US/10121049
 ; Publication No. US2003002239A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Baker, Kevin P.
 ; APPLICANT: Beresini, Maureen
 ; APPLICANT: DeForge, Laura
 ; APPLICANT: Desnoyers, Luc
 ; APPLICANT: Filvaroff, Ellen
 ; APPLICANT: Gao, Wei-Qiang
 ; APPLICANT: Gerritsen, Mary E.
 ; APPLICANT: Goddard, Audrey
 ; APPLICANT: Godowski, Paul J.
 ; APPLICANT: Gurney, Austin L.
 ; APPLICANT: Sherwood, Steven
 ; APPLICANT: Smith, Victoria
 ; APPLICANT: Stewart, Timothy A.
 ; APPLICANT: Tamas, Daniel
 ; APPLICANT: Watanabe, Colin K
 ; APPLICANT: Wood, William
 ; APPLICANT: Zhang, Zemin
 ; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
 ; FILE OF INVENTION: ACIDS ENCODING THE SAME
 ; FILE REFERENCE: P3330R1C17
 ; CURRENT APPLICATION NUMBER: US/10/121,049
 ; CURRENT FILING DATE: 2002-04-12
 ; Prior Application removed - See File Wrapper or Palm
 ; NUMBER OF SEQ ID NOS: 550
 ; SEQ ID NO 191
 ; LENGTH: 1647
 ; TYPE: DNA
 ; ORGANISM: Homo Sapien
 US-10-121-049-191

Alignment Scores:
 Pred. No.: 0 Length: 1647
 Score: 2752.00 Matches: 512
 Percent Similarity: 99.81% Conservative: 0
 Best Local Similarity: 99.81% Mismatches: 1
 Query Match: 99.60% Indels: 0
 DB: 14 Gaps: 0
 US-10-729-807-10 (1-513) x US-10-121-049-191 (1-1647)
 QY 1 MetLysArgLeuLeuLeuLeuCysLeuPhePheIleThrPheSerSerAlaPheProLeu 20
 Db 24 ATGAAGCGCTTCTGCTTCTGTTTGTCTTTATAACATTTCTTCTGCAATTTCCCTTA 83
 QY 21 ValArgMetThrGluAsnGluAsnMetGlnLeuAlaGlnAlaTyrLeuAsnGlnPhe 40
 Db 84 GTCCGGATGACGGAAATATGAAGAAATATGCAACTGGCTCAGGCATATCTCAACAGTTC 143
 QY 41 TyrSerLeuGluIleGluGlyAsnHisLeuValGlnSerLysAsnArgSerLeuIleAsp 60
 Db 144 TACTCTCTTGAAATAGAGGGGAAATCATCTTGTTCAAGCAAGAAATAGGAGTCTCATAGAT 203
 QY 61 AspLysIleArgGluMetGlnAlaPhePheGlyLeuThrValThrGlyLysLeuAspSer 80
 Db 204 GACAAATTCGGAAATGCAAGCAATTTTTCGATTGACAGTCACTGGAACCTGGACTCA 263
 QY 81 AsnThrLeuGluIleMetLysThrProArgCysGlyValProAspValGlyGlnTyrGly 100
 Db 264 AACACCTTGTAGATCATGAAGACACCCAGGTGTGGGTGCTGTGTGGCCAGTATGSC 323
 QY 101 TyrThrLeuProGlyTyrArgLysTyrAsnLeuThrTyrArgIleIleAsnTyrThrPro 120
 Db 324 TACACCTTCCCTGGGTGGAGAAATACAACTCACCTACAGAAATTAATAACTACTCCG 383
 QY 121 AspMetAlaArgAlaValAspGluAlaIleGlnGluGlyLeuGluValTrpSerLys 140
 Db 384 GATATGGCAGCAGCTGCTGTGTGATGAGGCTATCCAAAGAGGTTTAGAAGTGTGGAGCAA 443
 QY 141 ValThrProLeuLysPheThrLysIleSerLysGlyIleAlaAspIleMetIleAlaPhe 160
 Db 444 GTCACTCCACTAAAATTCACCAAGGATTTCAAAGGGGATTGCAGACATCATGATTCCTTT 503
 QY 161 ArgThrArgValHisGlyArgCysProArgTyrPheAspGlyProLeuGlyValLeuGly 180
 Db 504 AGGACTCGAGTCCATGCGGTGCTCCTCGCTATTTGATGTGCTTGGGAGTGTCTGGC 563
 QY 181 HisAlaPheProGlyProGlyLeuGlyArgGlyAspThrHisPheAspGluAspGluAsn 200
 Db 564 CATGCTTTCTCTCTGCTGGTCCGGTCTGGGTGTGTGACACTCATTTTGTGATGAGGATGAAAAC 623
 QY 201 TrpThrLysAspGlyAlaGlyPheAsnLeuPheLeuValAlaAlaHisGluPheGlyHis 220
 Db 624 TGGACCAAGGATGGAGCAGGATTCAACTTGTCTGTGGCTGTCTCATGAATTTTGGTCTAT 683
 QY 221 AlaLeuGlyLeuSerHisSerAsnAspGlnThrAlaLeuMetPheProAsnTyrValSer 240
 Db 684 GCATCTGGGCTCTCTCACTCCAAATGATCAAAAGCCTTGAAGTTCCTCCAAATATGCTCC 743
 QY 241 LeuAspProArgLysTyrProLeuSerGlnAspIleAsnGlyIleGlnSerIleTyr 260
 Db 744 CTGGATCCCAAGAAATACCCACTTCTCAGGATGATATCAATGGAATCCAGTCCATCTAT 803
 QY 261 GlyGlyLeuProLysValProAlaLysProLysGluProThrIleProHisAlaCysAsp 280
 Db 804 GGAGGTCTGCTTAAGGTACCTGTCTAAGCCAAAGGAACCCACTATACCCCATGCTGTGAC 863
 QY 281 ProAspLeuThrPheAspAlaIleThrThrPheArgGluValMetPhePheLysGly 300
 Db 864 CTGACTTGACTTTTGTGCGCTATCACAACTTTCCGAGAGAAAGTAATGTTCTTTAAAGGC 923
 QY 301 ArgHisLeuTrpArgIleTyrTyrAspIleThrAspValGluPheGluLeuIleAlaSer 320
 Db 924 AGGCACCTATGGAGGATCTATATGATATCACGGATGTTGAGTTTGAATTAATTTGCTTCA 983

QY 321 PheTrpProSerLeuProAlaAspLeuGlnAlaAlaTyrGluAsnProArgAspLysIle 340
Db 984 TTCTGGCCATCTCTGCCAGCTGATCTGCAAGCTGCATACAGAAACCCAGAGATAAGATT 1043
QY 341 LeuValPheLysAspGluAsnPheTrpMetIleArgGlyTyrAlaValLeuProAspTyr 360
Db 1044 CTGGTTTTAAAGATGAAACCTTCTGGATGATCAGAGGATATGCTGCTTGGCAGATTAT 1103
QY 361 ProLysSerIleHisThrLeuGlyPheProGlyArgValLysLysLysIleAspAlaVal 380
Db 1104 CCCAATCCATCATACATTAGTTTCCAGGAGCTGTGAAGAAATAGATGAGCGGTC 1163
QY 381 CysAspLysThrThrArgLysThrTyrPhePheValGlyIleTrpCysTrpArgPheAsp 400
Db 1164 TGTGATAAGACCAACAAAGAAACCTACTTCTTTGTGGGCATTTGGTCTGGAGGTTTGTAT 1223
QY 401 GluMetThrGlnThrMetAspLysGlyPheProGlnArgValLysHisPheProGly 420
Db 1224 GAAATGACCCAAACCATGGACAAAGGATTCCTCCAGAGAGTGGTAAACACTTCTCTGGA 1283
QY 421 IleSerIleArgValAspAlaAlaPheGlnTyrLysGlyPhePhePheSerArgGly 440
Db 1284 ATCAGTATCGTGTGTGATGCTGCTTCCAGTACAAAGGATTTCTTTTTCAGCGTGA 1343
QY 441 SerLysGlnPheGlnTyrAsnIleLysThrLysAsnIleThrArgIleMetArgThrAsn 460
Db 1344 TCAAGCAATTTGAATACAAACATTAAGACAAAGATTAATCCCGAATCATGAGAACTAAT 1403
QY 461 ThrTrpPheGlnCysLysGluProLysAsnSerSerPheGlyPheAspIleAsnLysGlu 480
Db 1404 ACTTGGTTTCATGCAAGAACCAAGAACTCTCATTTGGTTTGTATCAACAGGAA 1463
QY 481 LysAlaHisSerGlyIleLysIleLysIleLysIleLysSerLysSerLeuSerLeuPheIlePhe 500
Db 1464 AAAGCATTTCAGGAGGCAATAAGATATTGTATCAATAAGATTAAAGCTTTTATTTT 1523
QY 501 GlyIleValHisLeuLeuLysAsnThrSerIleTyrGln 513
Db 1524 GGTATTGTTCATTGCTGAAACAACTTCTATTATCAA 1562

RESULT 8

US-10-123-904-191
; Sequence 191, Application US/10123904
; Publication No. US20030022328A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Beresini, Maureen
; APPLICANT: DeForge, Laura
; APPLICANT: Desnoyers, Luc
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerritsen, Mary B.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Sherwood, Steven
; APPLICANT: Smith, Victoria
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tamas, Daniel
; APPLICANT: Watanabe, Colin K
; APPLICANT: Wood, William
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; TITLE OF INVENTION: ACIDS ENCODING THE SAME
; FILE REFERENCE: P3330R1C54
; CURRENT APPLICATION NUMBER: US/10/123,904
; CURRENT FILING DATE: 2002-04-16
; Prior Application removed - See File Wrapper or Palm
; NUMBER OF SEQ ID NOS: 550
; SEQ ID NO 191
; LENGTH: 1647
; TYPE: DNA

; ORGANISM: Homo Sapien

US-10-123-904-191

Alignment Scores:
Pred. No.: 0 Length: 1647
Score: 2752.00 Matches: 512
Percent Similarity: 99.81% Conservative: 0
Best Local Similarity: 99.81% Mismatches: 1
Query Match: 99.60% Indels: 0
DB: 14 Gaps: 0

US-10-729-807-10 (1-513) x US-10-123-904-191 (1-1647)

QY 1 MetLysArgLeuLeuLeuLeuCysLeuPhePheIleThrPheSerSerAlaPheProLeu 20
Db 24 ATGAAGCGCTCTCTGCTCTCTGTTTGTCTTTATTAACATTTCTTCGTGATTTCCCTTA 83
QY 21 ValArgMetThrGluAsnGluGluAsnMetGlnLeuAlaGlnAlaTyrLeuAsnGlnPhe 40
Db 84 GTCCGGATGACGGAATAATGAAGAAATATGCAACTGGCTCAGCATATCTCAACCAAGTTC 143
QY 41 TyrSerLeuGluIleGluGlyAsnHisLeuValGlnSerLysAsnArgSerLeuIleAsp 60
Db 144 TACTCTCTTGAATAGAGGGAATCATCTTGTTCAAAGCAAGAAATAGGAGTCTCATAGAT 203
QY 61 AspLysIleArgGluMetGlnAlaPhePheGlyLeuThrValThrGlyLysLeuAspSer 80
Db 204 GACAAATTCGGGAATGCAAGCATTTTGGGATTGACAGTGAAGTGGAACTGGACTCA 263
QY 81 AsnThrLeuGluIleMetLysThrProArgCysGlyValProAspValGlyGlnTyrGly 100
Db 264 AACACCTTGAGATCATGAGACACCCAGGTGGGGTGCCTGATGTGGGCCAGTATGGC 323
QY 101 TyrThrLeuProGlyTrpArgLysTyrAsnLeuThrTyrArgIleIleAsnTyrThrPro 120
Db 324 TACACCTCTCCCTGGTGGAGAAATACACCTCACCTACAGAAATAATAACTATACCTCCG 383
QY 121 AspMetAlaArgAlaAlaValAspGluAlaIleGlnGluGlyLeuGluValTrpSerLys 140
Db 384 GATATGCGCAGCTGCTGTGGATGAGGCTATCCAGAGAGTTTAGNAGTGTGGAGCAA 443
QY 141 ValThrProLysPheThrLysIleSerLysGlyIleAlaAspIleMetIleAlaPhe 160
Db 444 GTCACCTCCACTAAATTCACCAAGATTTCAAGGGGATTCAGACATCATGATTCCTTT 503
QY 161 ArgThrArgValHisGlyArgCysProArgTyrPheAspGlyProLeuGlyValLeuGly 180
Db 504 AGGACTCGAGTCCATGCTGCTGCTGCTATTTTGTATGCTGCTCATGAATTTGGTGC 563
QY 181 HisAlaPheProGlyProGlyProGlyLeuGlyGlyAspThrHisPheAspGluAspGluAsn 200
Db 564 CATGCCCTTCTCTGCTCGGGTCTGGGTGGTGACATCATTTTGTAGTGGAGTGAAC 623
QY 201 TrpThrLysAspGlyAlaGlyPheAsnLeuValAlaAlaHisGluPheGlyHis 220
Db 624 TGGACCAAGGATGAGCAGGATTCAACTGTTCTTGTGGCTGCTCATGAATTTGGTGCAT 683
QY 221 AlaLeuGlyLeuSerHisSerAsnAspGlnThrAlaLeuMetPheProAsnTyrValSer 240
Db 684 GCACCTGGGGCTCTCTCACTCCAATGATCAACAGCCTTGATGTTCCTCAATTTATGTCCTC 743
QY 241 LeuAspProArgLysTyrProLeuSerGlnAspIleAsnGlyIleGlnSerIleTyr 260
Db 744 CTGGATCCCAAGAAATACCCACTTTCTCAGATGATATCAATGAATCCAGTCCATCAT 803
QY 261 GlyGlyLeuProLysValProAlaLysProLysGluProThrIleProHisAlaCysAsp 280
Db 804 GGAGTCTGCTAAGGTACCTGCTAAGCCAAAGAAACCACTATACCCCATGCTGCTGAC 863
QY 281 ProAspLeuThrPheAspAlaIleThrThrPheArgArgGluValMetPhePheLysGly 300
Db 864 CCTGACTTGACTTTTGTGCGCTATCACAACTTTCCGACAGAGAAATATGTTCTTTAAGGC 923

Qy	301	ArgHisLeuTrpArgGlyIleTyrTyrAspIleThrAspValGluPheGluLeuIleAlaSer	320
Db	924	AGGCACCTATGGAGGATCTATTATGATATACGATGTGTGAGTTTGAAATTAATTCGTTC	983
Qy	321	PheTrpProSerLeuProAlaAspLeuGlnAlaIaTyrGluAsnProArgAspLysIle	340
Db	984	TTCTGGCCATCTCTGCCAGCTGATCTGCAAGCTGCATACGAGAACCCGAGAGATAGATT	1043
Qy	341	LeuValPheLysAspGluAsnPheTrpMetIleArgGlyTyrAlaValLeuProAspTyr	360
Db	1044	CTGGTTTTTAAAGATGAAAACTTCTGGATGATCAGAGATATGCTGCTTCCAGATTAT	1103
Qy	361	ProLysSerIleHisThrLeuGlyPhePheProGlyArgValLysLysIleaspAlaIaVal	380
Db	1104	CCCAATCCATCCATACATTAGGTTTTCCAGAGCGTGTGAAGAAAAATAGATGCAGCCGTC	1163
Qy	381	CysAspLysThrThrArgLysThrTyrPhePheValGlyIleIleTyrCysTrpArgPheAsp	400
Db	1164	TGTGATAAGACCACAAGAAAAACCTACTCTTTCTGGGCATTTGGTGCTGGAGGTTTGAT	1223
Qy	401	GluMetThrGlnThrMetAspLysGlyPhePheProGlnArgValValLysHisPheProGly	420
Db	1224	GAAATGCCCAACCAATGGACAAGAGATTCCCGCAGAGAGTGGTAAACAACATTTCTCTCGA	1283
Qy	421	IleSerIleArgValAspAlaAlaPheGlnTyrLysGlyPhePhePhePheSerArgGly	440
Db	1284	ATCAGTATCCGTGTGTATGTGCTTTCAGTACAAAGATTCTCTTTTTCAGCCCGTGA	1343
Qy	441	SerLysGlnPheGluTyrAsnIleLysThrLysAsnIleThrArgIleMetArgThrAsn	460
Db	1344	TCAAAGCAATTTGTAATACACATTAAAGCAAAAGAAATATTACCCGAATCATGAGAACTAAT	1403
Qy	461	ThrTrpPheGlnCysLysGluProLysAsnSerSerPheGlyPheAspIleAsnLysGlu	480
Db	1404	ACTTGGTTTTCAATGCCAAGAACCAAGAAACTCCCTATTGGTTTGTATATCAACAAGGAA	1463
Qy	481	LysAlaHisSerGlyGlyIleLysIleLeuTyrHisLysSerLeuSerLeuPheIlePhe	500
Db	1464	AAAGCACATTCCAGAGGCATAAAGATATTGTATCATTAAGATTTAAGCTGTTTATTTTT	1523
Qy	501	GlyIleValHisLeuLeuLysAsnThrSerIleTyrGln	513
Db	1524	GGTATCTGCTATTTGGCTGAAAAACATCTCTATTATTATCA	1562

RESULT, T 9

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US2001-140-470-191
; Sequence 191, Application US/10140470
; Publication No. US20030022331A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Beresini, Maureen
; APPLICANT: DeForge, Laura
; APPLICANT: Desnoyers, Luc
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Sherwood, Steven
; APPLICANT: Smith, Victoria
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Watanabe, Colin K
; APPLICANT: Wood, William
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; TITLE OF INVENTION: ACIDS ENCODING THE SAME
; FILE REFERENCE: P3330R1C160
; CURRENT APPLICATION NUMBER: US/10/140,470
; CURRENT FILING DATE: 2002-05-06
; Prior Application removed - See Palm or File Wrapper
; NUMBER OF SEQ ID NOS: 550

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864 CCTGCTTGAATTTTTCAGCGTATCACAACTTTCGACAGAGTAATGTTCTTTAAAGGC 923
301 ATGHisLeuTrpArgIleTyrAspIleThrAspValGluPheGluLeuIleAlaSer 320
924 AGGCACCTATGGAGGATCTATTATGATATACCGATGTTGAGTTTGAATTAATGCTTCA 983
321 PheTrpProSerLeuProAlaAspLeuGlnAlaAlaTyrGluAsnProArgAspLysIle 340
984 TTCTGGCCATCTCTGCCAGCTGATCTGCAAGCTGCATACGAGAACCCAGAGATAAGATT 1043
341 LeuValPheLysAspGluAsnPheTrpMetIleArgGlyTyrAlaValLeuProAspTyr 360
1044 CTGGTTTTTAAAGATGAAGAACTTCTGTGATGATCAGAGATATGCTGCTTGCAGATTAT 1103
361 ProLysSerIleHisThrLeuGlyPheProGlyArgValLysLysIleAspAlaAlaVal 380
1104 CCCAATCCATCCATACATTAGGTTTTCCAGGACGCTGGAAGAAATAGATGCAGCCGTC 1163
381 CysAspLysThrThrArgLysThrTyrPhePheValGlyIleTrpCysTrpArgPheAsp 400
1164 TGTGATAAGACCAACAGAAAACCTACTTCTTTGTGGGCAATTTGGTCTGGAGGTTTGTAT 1223
401 GluMetThrGlnThrMetAspLysGlyPheProGlnArgValValLysHisPheProGly 420
1224 GAATGACCCAAACCATGGACAAAGGATTTCCGACAGAGTGTGTAAACACTTTCTTCTGGA 1283
421 IleSerIleArgValAspAlaAlaPheGlnTyrLysGlyPhePhePheSerArgGly 440
1284 ATCAGTATCCGTGTGTATGCTGCTTTCCAGTACAAAGGATTTCTTTTTCAGCCGTGGA 1343
441 SerLysGlnPheGluTyrAsnIleLysThrLysAsnIleThrArgIleMetArgThrAsn 460
1344 TCAAAGCAATTTGAATCAACATTAAGCAAAAGATATTATCCCGAATCATGAGAACTAAT 1403
461 ThrTrpPheGlnCysLysGluProLysAsnSerSerPheGlyPheAspIleAsnLysGlu 480
1404 ACTTGGTTTCAATCAAGAACCAAGAACTCCCTCATTTGGTTTGATATCAACAGAA 1463
481 LysAlaHisSerGlyGlyIleLysIleLysThrHisLysSerLeuSerLeuPheIlePhe 500
1464 AAGCACATTCAGGAGGCATAAAGATATTGTATCATAGAGTTTAAAGCTTGTATTATTTT 1523
501 GlyIleValHisLeuLeuLysAsnThrSerIleTyrGln 513
1524 GGTATTGTTTCAATTTGCTGAAACCACTTCTATTATCA 1562
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RESULT 10

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US-10-175-746-191
; Sequence 191, Application US/10175746
; Publication No. US20030027270A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Beresini, Maureen
; APPLICANT: DeForge, Laura
; APPLICANT: Desnoyers, Luc
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Sherwood, Steven
; APPLICANT: Smith, Victoria
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Watanabe, Colin K
; APPLICANT: Wood, William
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; TITLE OF INVENTION: ACIDS ENCODING THE SAME
; FILE REFERENCE: P3330R1C353
; CURRENT APPLICATION NUMBER: US/10/175,746
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; CURRENT FILING DATE: 2002-06-19
; Prior Application removed - See File Wrapper or Palm
; NUMBER OF SEQ ID NOS: 550
; SEQ ID NO 191
; LENGTH: 1647
; TYPE: DNA
; ORGANISM: Homo Sapien
US-10-175-746-191
Alignment Scores:
Pred. No.: 0 Length: 1647
Score: 2752.00 Matches: 512
Percent Similarity: 99.81% Conservative: 0
Best Local Similarity: 99.81% Mismatches: 1
Query Match: 99.60% Indels: 0
DB: 14 Gaps: 0
US-10-729-807-10 (1-513) x US-10-175-746-191 (1-1647)
QY 1 MetLysArgLeuLeuLeuLeuCysLeuPhePheIleThrPheSerSerAlaPheProLeu 20
Db 24 ATGAAGCGCCTTCTGCTTCTGTTTCTTTTATACATTTTCTTCTGCAATTCCTTCA 83
QY 21 ValArgMetThrGluAsnGluGluAsnMetGlnLeuAlaGlnAlaTyrLeuAsnGlnPhe 40
Db 84 GTCGGATGACGGAAATGAAGAAATATGCAACTGGCTCAGGCATATCTCAACCACTTC 143
QY 41 TyrSerLeuGluLeuGluGlyAsnHisLeuValGlnSerLysAsnArgSerLeuIleAsp 60
Db 144 TACTCTCTTGAAATAGAGGGAATCATCTTTGTTTCAAGCAAGATAGGAGTCTCATGAT 203
QY 61 AspLysIleArgGluMetGlnAlaPhePheGlyLeuThrValThrGlyLysLeuAspSer 80
Db 204 GACAAAATTCGGGAATGCAAGCAATTTTGGATTGACAGTACTGGAACTGGACTCA 263
QY 81 AsnThrLeuGluIleMetLysThrProArgCysGlyValProAspValGlyGlnTyrGly 100
Db 264 AACACCTTCAGATCATGAAGACACCCAGGTGTGGGTGCTGATGTGGGCCAGTATGGC 323
QY 101 TyrThrLeuProGlyTyrArgLysTyrAsnLeuThrTyrArgIleIleAsnTyrThrPro 120
Db 324 TACACCTCTCCGTGGTGGAGAAATACAACTCACCTACAGATTAATAAACTATACCTCG 383
QY 121 AspMetAlaArgAlaAlaValAspGluAlaIleGlnGluGlyLeuGluValTrpSerLys 140
Db 384 GATATGCGACGAGCTGCTGGATGAGGCTATCCAAAGAGTTTAGAAGTGTGGAGCAA 443
QY 141 ValThrProLysLysPheThrLysIleSerLysGlyIleAlaAspIleMetIleAlaPhe 160
Db 444 GTCACCTCACTAAAATTCACCAAGATTTCAAGGGGATTCAGACATCATGATGCTTT 503
QY 161 ArgThrArgValHisGlyArgCysProArgTyrPheAspGlyProLeuGlyValLeuGly 180
Db 504 AGGACTGAGTCCATGTCGTGCTGCTATTTTGTGCTCCCTTGGGAGTGTGCTGGC 563
QY 181 HisAlaPheProProGlyProGlyLysLeuGlyGlyAspThrHisPheAspGluAsn 200
Db 564 CATGCCCTTCTCTGCTCCGGTCCGGTGTGGTGTGCTCATCTATTGTGATGAGGATGAAAAC 623
QY 201 TrpThrLysAspGlyAlaGlyPheAsnLeuPheValAlaAlaHisGluPheGlyHis 220
Db 624 TGGACCAAGGATGGAGCAGGATTCAACTTGTGCTGCTGCTCATGAATTTGGTTCAT 683
QY 221 AlaLeuGlyLeuSerHisSerAsnAspGlnThrAlaLeuMetPheProAsnTyrValSer 240
Db 684 GCATGGGCTCTCTCTCACTCCATGATCAACACGCTTGATGTTCCCAAAATATGTCCTC 743
QY 241 LeuAspProArgLysTyrProLeuSerSerGlnAspIleAsnGlyIleGlnSerIleTyr 260
Db 744 CTGGATCCCAAGAAATACCCACTTTCTCAGGATGATATCAATGGAATCCAGTCCATCTAT 803
QY 261 GlyGlyLeuProLysValProAlaLysGluProThrIleProHisAlaCysAsp 280
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Db 804 GGAGGTCTGCCTAAGTACCTGCTAAGCCAAAGAACCCACTATACCCCATCGCTGTGAC 863
QY 281 ProAspLeuThrPheAspAlaIleThrThrPheArgArgGluValMetPhePheLysGly 300
Db 864 CTGACTCTGACCTTTTGACGCTATCAACTTTCCGACAGAGAGTATGTTCTTTAAAGC 923
QY 301 ArgHisLeuThrArgIleThrArgPheThrAspValGluPheGluLeuLeuAlaSer 320
Db 924 AGGCACCTAAGAGATCTATTATGATATCAGGATGTTGAGTTTGAATTAATGCTTCA 983
QY 321 PheTrpProSerLeuProAlaAspLeuGlnAlaAlaThrGluAsnProArgAspLysIle 340
Db 984 TTCTGGCCATCTCTGCAGCTGATCTGCAAGCTGCATACAGAACCCAGAGATAGATT 1043
QY 341 LeuValPheLysAspGluAsnPheTrpMetIleArgGlyThrAlaValLeuProAspTyr 360
Db 1044 CTGGTCTTTTAAAGATGAAAACTTCTGGATGATCAGAGGATATGCTGCTTGCAGATTAT 1103
QY 361 ProLysSerIleHisThrLeuGlyPheProGlyValGlyValLysLysIleAspAlaAlaVal 380
Db 1104 CCCAATCCATCCATACATAGTTTTCAGAGCTGTGAGAAATATAGATGACGCCGTC 1163
QY 381 CysAspLysThrThrArgLysThrThrPhePheValGlyIleTrpCysTrpArgPheAsp 400
Db 1164 TGTGATAAGACACACAAAGAAACCTACTTCTTTTGGGCATTTGGTGCTGGAGTTTGAT 1223
QY 401 GluMetThrGlnThrMetAspLysGlyPheProGlnArgValValLysHisPheProGly 420
Db 1224 GAAATGACCAACCACTGACAAAGGATTCGCCGACAGAGTGGTAAACACACTTTCCTGGA 1283
QY 421 IleSerIleArgValAspAlaAlaPheGlnThrLysGlyPhePhePhePheSerArgGly 440
Db 1284 ATCAGTATCCGTTGGTGAUGCTCTTCCAGTACAAGGATTCCTCTTTTACGCCGTGGA 1343
QY 441 SerLysGlnPheGluThrAsnIleLysThrLysAsnIleThrArgIleMetArgThrAsn 460
Db 1344 TCAAGACATTTGAATACAACTTAAGACAAAGATATTACCGAATCATGAGAACTAAT 1403
QY 461 ThrTrpPheGlnCysLysGluProLysAsnSerSerPheGlyPheAspIleAsnLysGlu 480
Db 1404 ACTTGCTTTCAATGCAAGAACCAAGAACTCCTCATTTTGGTTTGGATATCAACAAGGAA 1463
QY 481 LysAlaHisSerGlyGlyIleLysIleLeuThrLysHisLysSerLeuSerLeuPheIlePhe 500
Db 1464 AAAGCACATTCAGAGGCAATAAGATATTGTATCATAGAGTTTAAAGCTTTTATTTT 1523
QY 501 GlyIleValHisLeuLysAsnThrSerIleTyrGln 513
Db 1524 GGTATTGTTCAATTGCTGAAAAACACTTCTATTATCAAA 1562

RESULT 11

US-10-176-918-191
; Sequence 191, Application US/10176918
; Publication No. US20030027275A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Beresini, Maureen
; APPLICANT: Deforge, Laura
; APPLICANT: Desnoyers, Luc
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Sherwood, Steven
; APPLICANT: Smith, Victoria
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Watanabe, Colin K
; APPLICANT: Wood, William
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC

; TITLE OF INVENTION: ACIDS ENCODING THE SAME
; FILE REFERENCE: P3330R1C382
; CURRENT APPLICATION NUMBER: US/10/176,918
; PRIOR APPLICATION DATE: 2002-06-20
; Prior Application removed - See File Wrapper or Palm
; NUMBER OF SEQ ID NOS: 550
; SEQ ID NO 191
; LENGTH: 1647
; TYPE: DNA
; ORGANISM: Homo Sapien
; US-10-176-918-191
Alignment Scores:
Pred. No.: 0 Length: 1647
Score: 2752.00 Matches: 512
Percent Similarity: 99.81% Conservative: 0
Best Local Similarity: 99.81% Mismatches: 1
Query Match: 99.60% Indels: 1
DB: 14 Gaps: 0
US-10-729-807-10 (1-513) x US-10-176-918-191 (1-1647)

QY 1 MetLysArgLeuLeuLeuLeuCysLeuPhePheIleThrPheSerSerAlaPheProLeu 20
Db 24 ATGAAGCGCTTCTGCTTCTGTTTGTCTTTTAAACATTTTCTTCGATTTCCCTTA 83
QY 21 ValArgMetThrGluAsnGluAsnMetGlnLeuAlaGlnAlaTyrLeuAsnGlnPhe 40
Db 84 GTCCGGATGACGGAATAATGAAGAAATATGCAACTGGCTCAGGCATATCTCAACCATTC 143
QY 41 TyrSerLeuGluIleGlyValAsnHisLeuValGlnSerLysAsnArgSerLeuIleAsp 60
Db 144 TACTCTCTTGAATAGAGGGAATCATCTTGTCAAGCAAGANTAGGAGTCTCATAGAT 203
QY 61 AspLysIleArgGluMetGlnAlaPhePheGlyLeuThrValThrGlyLysLeuAspSer 80
Db 204 GACAAAATTCGGGAAATGCAAGCAATTTTGTGATTGACAGTCACCTGGAATACTGGACTCA 263
QY 81 AsnThrLeuGluIleMetLysThrProArgCysGlyValProAspValGlyGlnTyrGly 100
Db 264 AACACCTTTGAGATCATGAAGACACCCAGGTGTGGGTGCTGATGTGGCCAGTATGTC 323
QY 101 TyrThrLeuProGlyTyrArgLysTyrAsnLeuThrTyrArgIleIleAsnTyrThrPro 120
Db 324 TACACCTCTCCCTGGGTGGGAAAAATACACCTCCTACAGANTATATAACTATATCTCCG 383
QY 121 AspMetAlaArgAlaAlaValAspGluAlaIleGlnGluGlyLeuGluValTrpSerLys 140
Db 384 GATATGGCACGAGCTGCTGTGATGAGGCTATCCAAAGAGTTTAGAAGTGTGGAGCAAA 443
QY 141 ValThrProLeuLysPheThrLysIleSerLysGlyIleAlaAspIleMetIleAlaPhe 160
Db 444 GTCACCTCCACTAAAATTCCCAAGATTTCCAAAGGGGATTCAGACATCATGATTTGCTTT 503
QY 161 ArgThrArgValHisGlyValGlyArgCysProArgTyrPheAspGlyProLeuGlyValLeuGly 180
Db 504 AGGACTCGAGTCCATGGTGGTGTCTCGTATTATTGATGCTCCCTTGGAGAGTGTGGC 563
QY 181 HisAlaPheProProGlyProGlyLeuGlyGlyAspThrHisPheAspGluAspGluAsn 200
Db 564 CATGCTTTCTCTCTGGTCCGGGTCTGGGTGTGACACTCACTCACTTTTGTGAGGATGAAAAC 623
QY 201 TrpThrLysAspGlyAlaGlyPheAsnLeuPheLeuValAlaAlaHisGluPheGlyHis 220
Db 624 TGGACCAAGGATGAGACAGGATTCAACTTGTGTCTTGTGGCTGCTCATGAATTTGGTCA 683
QY 221 AlaLeuGlyLeuSerHisSerAsnAspGlnThrAlaLeuMetPheProAsnTyrValSer 240
Db 684 GCATGGGGCTCTCTCACTCCAATGATCAACAGCCTTGATGTTCCCAANTATGTCCTCC 743
QY 241 LeuAspProArgLysTyrProLeuSerGlnAspAspIleAsnGlyIleGlnSerIleTyr 260
Db 744 CTGGATCCCAAGAAATACCCACTTTTCTCAGGATGATATCAATGGAATCCAGTCCATCTAT 803

261 GlyClyLeuProLysValProAlaLysProLysGluProThrIleProHisAlaCysAsp 280
Db GGAGGCTGCTAGGTAAGCTGCTAAGCAAGAACCCATATACCCCTGCTGTGAC 863
281 ProAspLeuThrPheAspAlaIleThrPheArgGluValMetPhePheLysGly 300
Db CTGACTTGACTTTTGCGCTATCACACTTTCGCGAGAGATATGTTCTTTAAAGGC 923
301 ArgHisLeuTrpArgIleTyrTyrAspIleThrAspValGluPheGluLeuAlaSer 320
Db AGGCACCTATGAGGATCTATTATGATATACCGATGTGAGTTGATTAATTGCTTCA 983
321 PheTrpProSerLeuProAlaAspLeuGlnAlaLysGluAsnProArgAspLysIle 340
Db TTCTGGCCATCTCTGCCAGCTGATCTGCAAGCTCATACGAGAACCCCGAGATTAAGATT 1043
341 LeuValPheLysAspGluAsnPheTrpMetIleArgGlyTyrAlaValLeuProAspTyr 360
Db CTGCTTTTAAAGATGAACCTCTGGATGATCAGAGATATGCTGCTTGGCCAGATTAT 1103
361 ProLysSerIleHisThrLeuGlyPheProGlyArgValLysLysIleAspAlaVal 380
Db CCCAAATCCATCCATACATTAGGTTTCCAGAGCTGTGAAGAAATAGATGCAGCGCTC 1163
381 CysAspLysThrThrArgLysThrTyrPhePheValGlyIleTyrCysTrpArgPheAsp 400
Db TGTGATTAAGACCAACAAGAAACCTACTTCTTGTGGGCAATTTGGTGTGGAGTTTGAT 1223
401 GluMetThrGlnThrMetAspLysGlyPheProGlnArgValValLysHisPheProGly 420
Db GAATGACCCCAACCATGGACAAAGGATTCGCGAGAGGTGGTAAACACTTTCCTGGA 1283
421 IleSerIleArgValAspAlaAlaPheGlnTyrLysGlyPhePhePheSerArgGly 440
Db ATCAGTATCGGTGTGATGCTGCTTTCAGTACAAAGGATTTCTTTTTCAGCGGTGA 1343
441 SerLysGlnPheGluTyrAsnIleLysThrLysAsnIleThrArgIleMetArgThrAsn 460
Db TCAAGCAATTTGAATACACATTAAGCAAAAGATATATCCCGAATCATGAGAACTAAT 1403
461 ThrTrpPheGlnCysLysGluProLysAsnSerSerPheGlyPheAspIleAsnLysGlu 480
Db ACTTGGTTTCAATGCAAGAACCAAGAACTCTCTCAITTTGTTTGTATCAACAAGAA 1463
481 LysAlaHisSerGlyGlyIleLysIleLeuTyrHisLysSerLeuSerLeuPheIlePhe 500
Db AAAGCAATTCAGGAGGCATAAAGATATTTGATCATTAAGAGTTTAAAGCTTTGTTATTTT 1523
501 GlyIleValHisLeuLeuLysAsnThrSerIleTyrGln 513
Db GGTATTTGTTTCTTGTGTAAGAAACACTTCTATTTATCA 1562

RESULT 12

US-10-176-921-191

; Sequence 191, Application US/10176921

; Publication No US20030027276A1

; GENERAL INFORMATION:

; APPLICANT: Baker, Kevin P.

; APPLICANT: Beresini, Maureen

; APPLICANT: DeForge, Laura

; APPLICANT: Desnoyers, Luc

; APPLICANT: Filvaroff, Ellen

; APPLICANT: Gao, Wei-Qiang

; APPLICANT: Gerritsen, Mary E.

; APPLICANT: Goddard, Audrey

; APPLICANT: Godowski, Paul J.

; APPLICANT: Gurney, Austin L.

; APPLICANT: Sherwood, Steven

; APPLICANT: Smith, Victoria

; APPLICANT: Stewart, Timothy A.

; APPLICANT: Tumas, Daniel

; APPLICANT: Watanabe, Colin K

APPLICANT: Wood, William
APPLICANT: Zhang, Zemin
TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
FILE REFERENCE: P3330R1C288
CURRENT APPLICATION NUMBER: US/10/176,921
CURRENT FILING DATE: 2002-06-20
Prior Application removed - See File Wrapper or Palm
NUMBER OF SEQ ID NOS: 550
SEQ ID NO 191
LENGTH: 1647
TYPE: DNA
ORGANISM: Homo Sapien
US-10-176-921-191

Alignment Scores:

Pred. No.: 0 Length: 1647
Score: 2752.00 Matches: 512
Percent Similarity: 99.81% Conservative: 0
Best Local Similarity: 99.81% Mismatches: 1
Query Match: 99.60% Indels: 0
DB: 14 Gaps: 0

US-10-729-807-10 (1-513) x US-10-176-921-191 (1-1647)

Qy 1 MetLysArgLeuLeuLeuLeuLeuPhePheIleThrPheSerSerAlaPheProLeu 20
Db 24 ATGAAGCGCCTTCGCTCTGTTTCTTTATAACATTTCTTCGCAATTTCCCTTA 83
Qy 21 ValArgMetThrGluAsnGluGluAsnMetGlnLeuAlaGlnAlaTyrLeuAsnGlnPhe 40
Db 84 GTCGGATGACGGAATATGAAGAAATATGCACTGGCTCAGGCATATCTCAACAGTTC 143
Qy 41 TyrSerLeuGluIleGluGlyAsnHisLeuValGlnSerLysAsnArgSerLeuIleAsp 60
Db 144 TACTCTCTGAAATAGAGGGAATCATCTTGTTCAAAGCAAGATAGAGTCTCATAGAT 203
Qy 61 AspLysIleArgGluMetGlnAlaPhePheGlyLeuThrValThrGlyLysLeuAspSer 80
Db 204 GACAAAATTCGGGAAATGCAAGCAATTTTGGATGTAGAGTACTGGAAAACTGGACTCA 263
Qy 81 AsnThrLeuGluIleMetLysThrProArgCysGlyValProAspValGlyGlnTyrGly 100
Db 264 AACACCTTCAGATCATGAAGACACCCAGGTGTGGGTGCTGATGTGGCCAGTATGGC 323
Qy 101 TyrThrLeuProGlyTyrArgLysTyrAsnLeuThrTyrArgIleIleAsnTyrThrPro 120
Db 324 TACACCTCCCTCGGTGGAGAAAATACAACTCCTACACGATAATAAATACTACTCCG 383
Qy 121 AspMetAlaArgAlaAlaValAspGluAlaIleGlnGluGlyLeuGluValTrpSerLys 140
Db 384 GATATGGCAGAGCTGCTGTGGATGAGGCTATCCAAAGGTTTAGAAGTGTGGAGCAAA 443
Qy 141 ValThrProLysPheThrLysIleSerLysGlyIleAlaAspIleMetIleAlaPhe 160
Db 444 GTCACCTCCACTAAATTCACCAAGATTTCAAAGGGGATTCAGACATCATGATGCTTT 503
Qy 161 ArgThrArgValHisGlyArgCysProArgTyrPheAspGlyProLeuGlyValLeuGly 180
Db 504 AGGACTCGAGTCCATGGTGGTGCCTCTATTTTGTATGAGTGTGGAGTGTGGC 563
Qy 181 HisAlaPheProProGlyProGlyLeuGlyValAspThrHisPheAspGluAspGluAsn 200
Db 564 CATGCCCTTCTCTGCTCGGCTCTGGGTGGTGACACTCATTTTGTATGAGGATGAAAC 623
Qy 201 TrpThrLysAspGlyAlaGlyPheAsnLeuPheLeuValAlaHisGluPheGlyHis 220
Db 624 TGGACCAAGATGGAGCAGGATTCACCTGTTCTTGTGGCTGCTCATGAATTTGGTCAT 683
Qy 221 AlaLeuGlyLeuSerHisSerAsnAspGlnThrAlaLeuMetPheProAsnTyrValSer 240
Db 684 GCACCTGGGGCTCTCTCTACTCCATGATCAAAACAGCCCTGTATGTTCCCAAAATATGTCCTCC 743


```

QY 241 LeuAspProArgLysTyrProLeuSerGlnAspAspIleAsnGlyIleGlnSerIleTyr 260
DB 744 CTGATCCAGAAAATACCCACTTTCTCAGGATGATATCAATGGAAATCCAGTCCATCAT 803
QY 261 GlyGlyLeuProLysValProAlaLysProLysGluProThrIleProHisAlaCysAsp 280
DB 804 GGAGGTCTGCTAAGTACTCTTAAGCCAAAGAACCCACTATATCCCATCCCTGTGAC 863
QY 281 ProAspLeuThrPheAspAlaIleThrThrPheArgArgGluValMetPhePheLysGly 300
DB 864 CTGACTTGTACTTTGACGCTATCAAACTTTCCGACAGAGTAATGTTCTTTAAAGGC 923
QY 301 ArgHisLeuTrpArgIleTyrTyrAspIleThrAspValGluPheGluLeuIleAlaSer 320
DB 924 AGGCACCTATGAGGATCTATTATGATATACGGATGTTGAGTTTGAAATTAATGCTTCA 983
QY 321 PheTrpProSerLeuProAlaAspLeuGlnAlaIleTyrGluAsnProArgAspLysIle 340
DB 984 TTCTGGCCATCTCTGCCAGCTGATCTGCAAGCTGCATACGAGAACCCAGAGATAAGATT 1043
QY 341 LeuValPheLysAspGluAsnPheTrpMetIleArgGlyTyrAlaValLeuProAspTyr 360
DB 1044 CTGGTTTTAAAGATCAAACTTCTGGATGATCAGAGGATATGCTGCTTGCAGATTAT 1103
QY 361 ProLysSerIleHisThrIleGlyPheProGlyArgValLysLysIleAspAlaIleVal 380
DB 1104 CCCAAATCCATCCATACATTAGTTTTCAGGACGTTGAGAAATAGATGACCCGTC 1163
QY 381 CysAspLysThrThrArgLysThrTyrPhePheValGlyIleTrpCysTrpArgPheAsp 400
DB 1164 TGTGATAGACACCAAGAAAACCTACTTCTTTGTGGCATTTGGTCTGGAGTTTGAT 1223
QY 401 GluMetThrGlnThrMetAspLysGlyPheProGlnArgValLysHisPheProGly 420
DB 1224 GAATGACCCAAACCATGACAAAGGATTCGCGACAGAGTGGTAAACACATTTCTCTGA 1283
QY 421 IleSerIleArgValAspAlaIlePheGlnTyrLysGlyPhePhePheSerArgGly 440
DB 1284 ATCAGTATCCGTTGTATGCTCTTTCCAGTACAAGGATTTCTTTTTCAGCCGTGA 1343
QY 441 SerLysGlnPheGluTyrAsnIleLysThrLysAsnIleThrArgIleMetArgThrAsn 460
DB 1344 TCAGAGCAATTTGAATACACATTAAGACAAAGAAATATTACCGAATCATGAGAACTAAT 1403
QY 461 ThrTrpPheGlnCysLysGluProLysAsnSerSerPheGlyPheAspIleAsnLysGlu 480
DB 1404 ACTTGGTTTCAATGCAAGAACCAAGAACTCTCTCATTTGGTTTTGATATCAACAAGGAA 1463
QY 481 LysAlaHisSerGlyGlyIleLysIleLeuTyrHisLysSerLeuSerLeuPheIlePhe 500
DB 1464 AAAGCACATTCAGAGGCATAAGATTTGTATCATAGAGTTTAAGCTTGTATTTTTT 1523
QY 501 GlyIleValHisLeuLeuLysAsnThrSerIleTyrGln 513
DB 1524 GGTAATTGTTCATTTGCTGAAAAACACTTCTATTATCAAA 1562

```

RESULT 13

US-10-137-865-191

; Sequence 191, Application US/10137865

; Publication No. US20030032155A1

; GENERAL INFORMATION:

; APPLICANT: Baker, Kevin P.

; APPLICANT: Beresini, Maureen

; APPLICANT: DeForge, Laura

; APPLICANT: Desnoyers, Luc

; APPLICANT: Filvaroff, Ellen

; APPLICANT: Gao, Wei-Qiang

; APPLICANT: Gerritsen, Mary E.

; APPLICANT: Goddard, Audrey

; APPLICANT: Godowski, Paul J.

; APPLICANT: Gurney, Austin L.

; APPLICANT: Sherwood, Steven

; APPLICANT: Smith, Victoria

```

; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tamas, Daniel
; APPLICANT: Watanabe, Colin K
; APPLICANT: Wood, William
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P3330R1C154
; CURRENT APPLICATION NUMBER: US/10/137,865
; CURRENT FILING DATE: 2002-05-03
; Prior Application removed - See Palm or File Wrapper
; NUMBER OF SEQ ID NOS: 550
; SEQ ID NO 191
; LENGTH: 1647
; TYPE: DNA
; ORGANISM: Homo Sapien
; US-10-137-865-191

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Alignment Scores:

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Pred. No.: 0 Length: 1647
Score: 2752.00 Matches: 512
Percent Similarity: 99.81% Conservative: 0
Best Local Similarity: 99.81% Mismatches: 1
Query Match: 99.60% Indels: 0
DB: 14 Gaps: 0

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US-10-729-807-10 (1-513) x US-10-137-865-191 (1-1647)

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QY 1 MetLysArgLeuLeuLeuLeuCysLeuPhePheIleThrPheSerSerAlaPheProLeu 20
DB 24 ATGAAGCGCTTCTGCTTCTGTTTGTCTTTTGTCTTTTATAACATTTTCTTCGATTTCCCTTA 83
QY 21 ValArgMetThrGluAsnGluGluAsnMetGlnLeuAlaGlnAlaTyrLeuAsnGlnPhe 40
DB 84 GTCCGGATGACCGGAAATGAAGAAATATGCAACTGGCTCAGGCATATCTCAACAGTTC 143
QY 41 TyrSerLeuGluIleGluGlyAsnHisLeuValGlnSerLysAsnArgSerLeuIleAsp 60
DB 144 TACTCTTGAATAGAGGGAAATCATCTTGTTCAAAGCAAGATAGGAGTCTCATAGAT 203
QY 61 AspLysIleArgGluMetGlnAlaPhePheGlyLeuThrValThrGlyLysLeuAspSer 80
DB 204 GACAAAATTCGGGAAATGCAAGCAATTTTGTGATTTGACAGTCACTGGAAAACTGGACTCA 263
QY 81 AsnThrLeuGluIleMetLysThrProArgCysGlyValProAspValGlyGlnTyrGly 100
DB 264 AACACCTTGGATCATGAAGACACCCAGTGTGGGTGCTGTGATGTGGCCAGTATGCG 323
QY 101 TyrThrLeuProGlyTrpArgLysTyrAsnLeuThrTyrArgIleIleAsnTyrThrPro 120
DB 324 TACACCTCTCTGGTGGGAGAAATACAACTCACCTACAGAAATAATAAATACTATCTCCG 383
QY 121 AspMetAlaArgAlaAlaValAspGluAlaIleGlnGluGlyLeuGlnValTrpSerLys 140
DB 384 GATATGGCACGAGCTGCTGTGATGAGGTATCCAAAGAGGTTTAAAGTGGAGCAAA 443
QY 141 ValThrProLeuLysPheThrLysIleSerLysGlyIleAlaAspIleMetIleAlaPhe 160
DB 444 GTCATCTCCATAAATTCACCAAGATTTCAAGGGGATTTGCAGACATCATGATGCTTT 503
QY 161 ArgThrArgValHisGlyArgCysProArgTyrPheAspGlyProLeuGlyValLeuGly 180
DB 504 AGGACTCGAGTCCATGCTCGTCTGCTCTGCTATTTTGTGTTGGTGGAGTGTGGC 563
QY 181 HisAlaPheProProGlyProGlyLeuGlyGlyAspThrHisPheAspGluAsn 200
DB 564 CATGCCCTTCTCTCTGCTCGGTCCTGGGTGTGGTGTGGTGTGGTGTGGTGTGGTGTGG 623
QY 201 TrpThrLysAspGlyValaGlyPheAsnLeuPheLeuValAlaAlaHisGluPheGlyHis 220
DB 624 TGGACCAAGGATGGAGCAGATTCAACTTGTTCCTGTGCTGCTCATGAATTTGGTCAT 683
QY 221 AlaLeuGlyLeuSerHisSerAsnAspGlnThrAlaLeuMetPheProAsnTyrValSer 240

```


Db 624 TGGACCAAGGATGGAGCAGGATTCAACTGTGTTCTTGTGGCTGCTCATGAATTTGGTCAT 683
 QY 221 AlaLeuGlyLeuSerHisSerAsnAspGlnThrAlaLeuMetPheProAsnTyrValSer 240
 Db 684 GCACCTGGGCTCTCTCACTCCCAATGATCAACAGCCTTGATGTTCCCAAAATTAATGTCTCC 743
 QY 241 LeuAspProArgLysTyrProLeuSerGlnAspAspIleAsnGlyIleGlnSerIleTyr 260
 Db 744 CTGGATCCCAAGAAATACCCACTTTCTCAGGATGATATCAATGGAAATCCAGTCCATCAT 803
 QY 261 GlyGlyLeuProLysValProAlaLysProLysGluProThrIleProHisAlaCysAsp 280
 Db 804 GGAGCTCTGCCTTAAGTACCTCTAAGCAAGAACCCACTATACCCCATGCCCTGTGCAC 863
 QY 281 ProAspLeuThrPheAspAlaIleThrThrPheArgArgGluValMetPhePheLysGly 300
 Db 864 CTTGACTTGGCTTTGACGCTATCAACAATTTCCGACAGAGAAATTAATGCTTTAAAGGC 923
 QY 301 ArgHisLeuThrArgIleTyrTyrAspIleThrAspValGluPheGluLeuIleAlaSer 320
 Db 924 AGGCACCTATGAGGATCTATTATGATATCAACGGATGTGAGTTTGAATTAATGCTTCA 983
 QY 321 PheTrpProSerLeuProAlaAspLeuGlnAlaIleTyrGluAsnProArgAspLysIle 340
 Db 984 TTCTGGCCATCTCTCCAGCTGATCTGCNAGCTGCATACGAGAACCCACAGATTAAGATT 1043
 QY 341 LeuValPheLysAspGluAsnPheTrpMetIleArgGlyTyrAlaValLeuProAspTyr 360
 Db 1044 CTGGTTTTTAAAGATGAAAACCTCTTGATGATCAGAGGATATGCTGTCTGCCAGATTAT 1103
 QY 361 ProLysSerIleHisThrLeuGlyPheProGlyArgValLysLysIleAspAlaIleVal 380
 Db 1104 CCAAAATCCATCCATACATATAGTGTTCAGACGCTGTGAAGAAATAGATGACCGGTC 1163
 QY 381 CysAspLysThrThrArgLysThrTyrPheValGlyIleTyrCysTrpArgPheAsp 400
 Db 1164 TGTGATAAGCACACAGAAAACCTACTTCTTTGTGGGCAATTTGGTCTGGAGTTTGAT 1223
 QY 401 GluMetThrGlnThrMetAspLysGlyPheProGlnArgValValLysHisPheProGly 420
 Db 1224 GAATGACCAACCAATGACAAAGGATTTCCCGCAGAGAGTGTGTAACACACTTTCTCTGA 1283
 QY 421 IleSerIleArgValAspAlaIlePheGlnTyrLysGlyPhePhePheSerArgGly 440
 Db 1284 ATCAGTATCCGTGTTGATGCTGTTTCCAGTACAAAGAGATTTCTTTTTCAGCCGTGA 1343
 QY 441 SerLysGlnPheGluTyrAsnIleLysThrLysAsnIleThrArgIleMetArgThrAsn 460
 Db 1344 TCAAGCAATTTGAATACAACTTAAGAACAAAGAAATATACCGAATCATGAGAACTAAT 1403
 QY 461 ThrTrpPheGlnCysLysGluProLysAsnSerSerPheGlyPheAspIleAsnLysGlu 480
 Db 1404 ACTTGGTTTCAATGCAAGAACCAAGAACTCTCTCAATTTGTTTTCATATCAACAGGAA 1463
 QY 481 LysAlaHisSerGlyGlyIleLysIleLeuTyrHisLysSerLeuSerLeuPheIlePhe 500
 Db 1464 AAAGACATTCAGAGGCAATAAGATATTGTATCATAAAGAGTTTAAGCTTGTATTATTTT 1523
 QY 501 GlyIleValHisLeuLeuLysAsnThrSerIleTyrGln 513
 Db 1524 GGTAATGTTTCAATTTGCTGAAAAACATTTCTATTATTACAA 1562

RESULT 15

US-10-142-431-191
 ; Sequence 191, Application US/10142431
 ; Publication No. US20030036179A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Baker, Kevin P.
 ; APPLICANT: Beresini, Maureen
 ; APPLICANT: DeFoe, Laura
 ; APPLICANT: Desnoyers, Luc
 ; APPLICANT: Filvaroff, Ellen
 ; APPLICANT: Gao, Wei-Qiang

; APPLICANT: Gerritsen, Mary E.
 ; APPLICANT: Goddard, Audrey
 ; APPLICANT: Godowski, Paul J.
 ; APPLICANT: Gurney, Austin L.
 ; APPLICANT: Sherwood, Steven
 ; APPLICANT: Smith, Victoria
 ; APPLICANT: Stewart, Timothy A.
 ; APPLICANT: Tumas, Daniel
 ; APPLICANT: Watanabe, Colin K
 ; APPLICANT: Wood, William
 ; APPLICANT: Zhang, Zemin
 ; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
 ; FILE REFERENCE: P333081C251
 ; CURRENT FILING DATE: 2002-05-10
 ; Prior Application removed - See File Wrapper or Palm
 ; NUMBER OF SEQ ID NOS: 550
 ; SEQ ID NO 191
 ; LENGTH: 1647
 ; TYPE: DNA
 ; ORGANISM: Homo Sapien
 ; US-10-142-431-191

Alignment Scores:
 Pred. No.: 0 Length: 1647
 Score: 2752.00 Matches: 512
 Percent Similarity: 99.81% Conservative: 0
 Best Local Similarity: 99.81% Mismatches: 1
 Query Match: 99.60% Indels: 0
 DB: 14 Gaps: 0

US-10-729-807-10 (1-513) x US-10-142-431-191 (1-1647)

QY 1 MetLysArgLeuLeuLeuLeuCysLeuPhePheIleThrPheSerSerAlaPheProLeu 20
 Db 24 ATGAAGCGCTTCTGCTTCTGTTTGTCTTTATATAACATTTCTTCTGCAITTCCTTTA 83
 QY 21 ValArgMetThrGluAsnGluGluAsnMetGlnLeuAlaGlnAlaTyrLeuAsnGlnPhe 40
 Db 84 GTCCGGATGACGGAATAATGAAGAAATATGCAACTGGCTCAGGCATATCTCAACCAAGTTC 143
 QY 41 TyrSerLeuGluIleGluGlyAsnHisLeuValGlnSerLysAsnArgSerLeuIleAsp 60
 Db 144 TACTCTCTTGAATAGAGGGAATCATCTTGTCAAAGCAAGAAATAGGAGTCTCATAGAT 203
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 Db 204 GACAAAATTCGGGAAATGCAAGCATTTTGTGATTGACAGTGACTGGAATACTGGACTCA 263
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 QY 101 TyrThrLeuProGlyTyrArgLysTyrAsnLeuThrTyrArgIleIleAsnTyrThrPro 120
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 QY 121 AspMetAlaArgAlaAlaValAspGluAlaIleGlnGluGlyLeuGluValTyrSerLys 140
 Db 384 GATATGGCAGAGCTGCTGTGGATGAGGCTATCCAAAGAGGTTTAGAAGTGTGGAGCAAA 443
 QY 141 ValThrProLeuLysPheThrLysIleSerLysGlyIleAlaAspIleMetIleAlaPhe 160
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 QY 161 ArgThrArgValHisGlyArgCysProArgTyrPheAspGlyProLeuGlyValLeuGly 180
 Db 504 AGGACTCGAGTCCATGCTGGTGTCTCTCGTATTTTGTGGTCCCTTGGAGGTGCTTGGC 563
 QY 181 HisAlaPheProGlyProGlyLeuGlyGlyAspThrHisPheAspGluAspGluAsn 200
 Db 564 CATGCCCTTTCTCTCGTGGTCTCTGGGTGGTGACTCACTCATTTTGTATGAGGATGAAAC 623

QY 201 TrpThrLysAspGlyAlaGlyPheAsnLeuPheLeuValAlaAlaHisGluPheGlyHis 220
DB 624 TGGACCAAGGATGGAGCAGGATCAACTTGTCTTGTGGCTGCTCATGAATTTGGTCAT 683
QY 221 AlaLeuGlyLeuSerHisSerAspGlnThrAlaLeuMetPheProAsnTyrValSer 240
DB 684 GCACCTGGGGCTCTCTCACTCCAAATGATCAAAACAGCCTTGATGTTCCCAAATTAATGCTCC 743
QY 241 LeuAspProArgLysTyrProLeuSerGlnAspIleAsnGlyIleGlnSerIleTyr 260
DB 744 CTGGATCCAGAAATACCCCACTTCTCAGGATGATCAATGGAATCCAGTCCATCTAT 803
QY 261 GlyGlyLeuProLysValProAlaLysProLysGluProThrIleProHisAlaCysAsp 280
DB 804 GGAGGTCTGCTAAGGTACCTGCTAAGCCAAAGGACCCACTATACCCCATGCCCTGTGAC 863
QY 281 ProAspLeuThrPheAspAlaIleThrThrPheArgArgGluValMetPhePheLysGly 300
DB 864 CCTGACTTGACTTTTGAAGCTATCACAACTTTCGCGAGAGAGTAATGTTCTTTAAAGGC 923
QY 301 ArgHisLeuTrpArgIleTyrTyrAspIleThrAspValGluPheGluLeuIleAlaSer 320
DB 924 AGGCACCTATGGAGGATCTATTATGATATCAGGATGTTGAGTTTGAATTAATTTGCTTCA 983
QY 321 PheTrpProSerLeuProAlaAspLeuGlnAlaAlaTyrGluAsnProArgAspLysIle 340
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QY 341 LeuValPheLysAspGluAsnPheTrpMetIleArgGlyTyrAlaValLeuProAspTyr 360
DB 1044 CTGGTTTTTAAAGATGAAACTTCTGGATGATCAGAGGATATGCTGTTGCCAGATTAT 1103
QY 361 ProLysSerIleHisThrLeuGlyPheProGlyArgValLysLysIleAspAlaAlaVal 380
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QY 381 CysAspLysThrThrArgLysThrTyrPhePheValGlyIleTyrCysTyrArgPheAsp 400
DB 1164 TGTGATAAGACCAACAAAGAAACCTACTTCTTTGTGGCATTTGGTCTCGAGGTTTGAT 1223
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QY 421 IleSerIleArgValAspAlaAlaPheGlnTyrLysGlyPhePhePheSerArgGly 440
DB 1284 ATCAGTATCGTGTTGATGCTGTTTCCAGTACAAGGATCTCTTTTTCAGCCGTGA 1343
QY 441 SerLysGlnPheGluTyrAsnIleLysThrLysAsnIleThrArgIleMetArgThrAsn 460
DB 1344 TCAAAGCAATTTGAATACACATTAAAGACAAAGATATTACCCGATCATGAGACTAAT 1403
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QY 481 LysAlaHisSerGlyGlyIleLysIleLeuTyrHisLysSerLeuSerLeuPheIlePhe 500
DB 1464 AAAGCAGATTCAGAGGCATAAAGATATTGTATCATAGAGTTTAAAGCTTGTATTATTTT 1523
QY 501 GlyIleValHisLeuLeuLysAsnThrSerIleTyrGln 513
DB 1524 GGTATTGTTCAATTGCTGAAAAACACTTCTATTATCAAA 1562

Search completed: November 16, 2004, 00:46:28

Job time : 804 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2004 CompuGen Ltd.

OM protein - nucleic search, using frame_plus_p2n model

Run on: November 15, 2004, 21:08:13 ; Search time 4696 Seconds
(without alignments)
3980.746 Million cell updates/sec

Title: US-10-729-807-10

Perfect score: 2763

Sequence: 1 MKRLLLCLEPFFSSAPPL.....SLSLFIRGIVHLLKNVSIYQ 513

Scoring table:

BLOSUM62
Xgapop 10.0, Xgapext 0.5
Ygapop 10.0, Ygapext 0.5
Fgapop 6.0, Fgapext 7.0
Delop 6.0, Delext 7.0

Searched: 32822875 seqs, 18219865908 residues

Total number of hits satisfying chosen parameters: 65645750

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Maximum Match 0%

Listing first 45 summaries

Command line parameters:

-MODEL=frame+ p2n.model -DEV=xlh
-Q=/cgm2 1/USPTO.spool/US10729807/runat 15112004 131727 16851/app query.fasta_1.711
-DB=EST -QSWT=fastap -SUFFIX=rst -MINMATCH=0.1 -LOOPEXT=0 -LOOPS=human40.cdi -LIST=45
-UNITS=bits -START=1 -END=1 -MATRIX=blosum62 -TRANS=human40.cdi -ALIGN=15 -MODE=LOCAL
-DOCALIGN=200 -THR_SCORE=pct -THR_MAX=100 -THR_MIN=0 -ALIGN=15 -MODE=LOCAL
-OUTFMT=ptc -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=2000000000
-USER=US10729807.cgm 1 1 3437 @runat 15112004 131727 16851 -NCPU=6 -ICPU=3
-NO MMAP -LARGQUERY -NEG SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG
-DEV TIMEOUT=120 -WARN TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database : EST:
1: gb_est1.*
2: gb_est2.*
3: gb_hic.*
4: gb_est3.*
5: gb_est4.*
6: gb_est5.*
7: gb_est6.*
8: gb_gsl.*
9: gb_gsl2.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1322	47.8	731	5 BX102293	BX102293 BX102293
2	1243.5	45.0	1735	3 AK020292	AK020292 Mus muscu
3	1159	41.9	2223	3 AK089234	AK089234 Mus muscu
4	1154	41.8	2074	3 AK089516	AK089516 Mus muscu
5	1154	41.8	2426	3 AK089381	AK089381 Mus muscu
6	1149	41.6	755	4 BG189775	BG189775 RST8821 A
7	1146	41.5	2427	3 AK089336	AK089336 Mus muscu
8	1107	40.1	1784	3 CR603756	CR603756 full-length
9	1032.5	37.4	1798	3 AK089309	AK089309 Mus muscu

10	1030.5	37.3	2013	3 AK049552	AK049552 Mus muscu
11	1024.5	37.1	1800	3 AK090051	AK090051 Mus muscu
12	1023.5	37.0	1519	3 AK089523	AK089523 Mus muscu
13	1023.5	37.0	1798	3 AK089452	AK089452 Mus muscu
14	984.5	35.6	1449	9 AY420752	AY420752 Mus muscu
15	983.5	35.6	1452	9 AY420750	AY420750 Homo sapi
16	979.5	35.5	1453	3 AK089509	AK089509 Mus muscu
17	915	33.1	1416	9 AY418899	AY418899 Homo sapi
18	910	32.9	1850	3 CR645708	CR645708 Tetraodon
19	905	32.8	1419	9 AY418901	AY418901 Mus muscu
20	865	31.3	1330	9 AY420747	AY420747 Homo sapi
21	862.5	31.2	894	5 BU120858	BU120858 603144842
22	839.5	30.4	683	6 BY753385	BY753385 BY753385
23	821	29.7	632	5 BU402270	BU402270 604137994
24	819	29.6	1027	7 CN065546	CN065546 D09 Ag2 p
25	808	29.2	1261	9 AY420749	AY420749 Mus muscu
26	797	28.8	2895	3 CR608838	CR608838 full-length
27	792.5	28.7	1452	9 AY420751	AY420751 Pan trogl
28	770	27.9	771	7 CN052608	CN052608 Salamande
29	769	27.8	871	7 CN067389	CN067389 J10 Ag2 p
30	765.5	27.7	843	7 CN062082	CN062082 Ag2_p35 H
31	764.5	27.7	854	7 CN066791	CN066791 H10 Ag2 p
32	764.5	27.7	903	6 CA471366	CA471366 AGENCOURT
33	757.5	27.4	869	5 BU281887	BU281887 603602842
34	752.5	27.2	909	1 AU050632	AU050632 AU050632
35	747	27.0	832	7 CN060762	CN060762 A04 Ag2 p
36	746	27.0	746	1 AI436025	AI436025 th8g12.x
37	745.5	27.0	846	7 CN064495	CN064495 Ag2_p7 D8
38	743	26.9	928	5 BU382223	BU382223 603857156
39	741	26.8	593	4 BM440043	BM440043 pgr.in.pko
40	737	26.7	411	1 AA424347	AA424347 zv90e12.r
41	731.5	26.5	4346	3 BC047278	BC047278 Mus muscu
42	730	26.4	716	5 BU200410	BU200410 604158850
43	728.5	26.4	910	7 CN068049	CN068049 l12 Ag2 p
44	723	26.2	935	7 CO647474	CO647474 ILLUMIGEN
45	720	26.1	561	5 BX918107	BX918107 BX918107

ALIGNMENTS

RESULT 1

BX102293

LOCUS

BX102293 Soares NhMPu_S1 Homo sapiens cDNA clone IMAGE9980231887 ;
IMAGE:767086, mRNA sequence.

DEFINITION

ACCESSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

731 bp mRNA linear

EST 06-FEB-2003

IMAGE:767086, mRNA sequence.

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FEATURES
source

Location/Qualifiers

1. 731
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clones="IMAGp9980231887 ; IMAGE:767086"
/tissue_types="Pooled human melanocyte, fetal heart, and pregnant uterus"
/lab_host="DH10B"
/clone_lib="Soares NhMPu S1"
/note="Organ: mixed (see below); Vector: p773D-Pac (Pharmacia) with a modified polylinker; Site 1: Not I; Site 2: Eco RI; Equal amounts of plasmid DNA from three normalized libraries (melanocyte 2NBHM, pregnant uterus NBHPU, and fetal heart NBH19W) were mixed, and ss circles were made in vitro. Following HAP purification, this DNA was used as tracer in a subtractive hybridization reaction. The driver was PCR-amplified cDNAs from pools of 5,000 clones made from the same 3 libraries. The pools consisted of 1.M.A.G.E. clones 260232-265223, 340488-345479, and 484488-489479."

ORIGIN

Alignment Scores:

Pred. No.: 7.42e-143 Length: 731
Score: 1322.00 Matches: 241
Percent Similarity: 99.59% Conservative: 1
Best Local Similarity: 99.18% Mismatches: 1
Query Match: 47.85% Indels: 0
DB: 5 Gaps: 0

US-10-729-807-10 (1-513) x BX102293 (1-731)

Qy 244 ArgLysTyrProLeuSerGlnAspIleAsnGlylleGlnSerIleTyrGlyGlyLeu 263
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Db 1 AGAAATACCCATTCTTCAGGATGATATCAATGGAATCCAGTCCATCTATGAGGTCTG 60
| | | | |
Qy 264 ProLysValProAlaLysProLysGluProThrIleProHisAlaCysAspProAspLeu 283
| | | | |
Db 61 CCTAAGAACCTGCTAAGCAAGAACCCATATACCCATCCCTGTCACCTGACTTG 120
| | | | |
Qy 284 ThrPheAspAlaIleThrThrPheArgGluValMetPhePheLysGlyArgHisLeu 303
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Db 121 ACTTTGACGCTATCAACTTTCGACAGAGAGTATGTTCTTTAAAGCAGCGACCTA 180
| | | | |
Qy 304 TrpArgIleTyrTrsAspIleThrAspValGluPheGluLeuIleAlaSerPheTrpPro 323
| | | | |
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| | | | |
Qy 324 SerLeuProAlaAspLeuGlnAlaLysTyrGluAsnProArgAspLysIleLeuValPhe 343
| | | | |
Db 241 TCTCTGCCAGCTGAATCTGACGCTGATACGAGAACCCAGAGATAAGATTCTGGTTTT 300
| | | | |
Qy 344 LysAspGluAsnPheTrpMetIleArgGlyTyrAlaValLeuProAspTyrProLysSer 363
| | | | |
Db 301 AAAGATGAAACTTCCTGGATATCAGAGATATGCTGCTTGCAGATTATCCCAATCC 360
| | | | |
Qy 364 IleHisThrLeuGlyPheProGlyArgValLysIleAspAlaValCysAspLys 383
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Qy 384 ThrThrArgLysThrTyrPhePheValGlyIleTyrCysTrpArgPheAspGluMetThr 403
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Db 421 ACCCAAGAAAAACCTACTCTTTGTGGCAATTTGCTGGAGGTTTATGATGAATGACC 480
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Qy 404 GlnThrMetAspLysGlyPheProGlnArgValValLysHisPheProGlyIleSerIle 423
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Db 541 CGGTGTGATGCTGCTTTCAGTACAAAGGATTCTTCTTTTTCAGCGCTGGATCAAAGCAA 600
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Qy 444 PheGluTyrAsnIleLysThrLysAsnIleThrArgIleMetArgThrAsnThrTrpPhe 463
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Db 601 TTTGAATACGACATTAAGACAAAGATATTACCCGAATCATGAGAACTAATCTTGTTT 660
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Qy 464 GlnCysLysGluProLysAsnSerSerPheGlyPheAspIleAsnLysGluLysAlaHis 483
| | | | |
Db 661 CAATGCAAGAACCAAGAACTCTCTATTGGTTTGTATATCAACAAGGAAAAAGCAT 720
| | | | |
Qy 484 SerGlyGly 486
| | | | |
Db 721 TCAGGAGGC 729
| | | | |
RESULT 2
AK020292
LOCUS
DEFINITION
Mus musculus adult male cecum cDNA, RIKEN full-length enriched library, clone:9130404C19 product:matrix metalloproteinase 10, full insert sequence.
AK020292.1 GI:12860834
VERSION
HTC; CAP trapper.
KEYWORDS
Mus musculus (house mouse)
SOURCE
Mus musculus
ORGANISM
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE
1 Carninci, P. and Hayashizaki, Y.
TITLE High-efficiency full-length cDNA cloning
JOURNAL Meth. Enzymol. 303, 19-44 (1999)
MEDLINE 99279253
PUBMED 10349636
REFERENCE
2 Carninci, P., Shibata, Y., Hayatsu, N., Sugahara, Y., Shibata, K., Itoh, M., Konno, H., Okazaki, Y., Muramatsu, M. and Hayashizaki, Y.
TITLE Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes
JOURNAL Genome Res. 10 (10), 1617-1630 (2000)
MEDLINE 20493374
PUBMED 11042159
REFERENCE
3 Shibata, K., Itoh, M., Aizawa, K., Nagaoka, S., Sasaki, N., Carninci, P., Konno, H., Akiyama, J., Nishi, K., Kitsumai, T., Tashiro, H., Itoh, M., Sumi, N., Ishii, Y., Nakamura, S., Hazama, M., Nishine, T., Harada, A., Yamamoto, R., Matsumoto, H., Sakaguchi, S., Ikegami, T., Kashiwagi, K., Fujisawa, S., Inoue, K., Togawa, Y., Izawa, M., Ohara, E., Watahiki, M., Yoneda, Y., Ishikawa, T., Ozawa, K., Tanaka, T., Matsuura, S., Kawai, J., Okazaki, Y., Muramatsu, M., Inoue, Y., Kira, A. and Hayashizaki, Y.
TITLE RIKEN integrated sequence analysis (RISA) system--384-format sequencing pipeline with 384 multicapillary sequencer
JOURNAL Genome Res. 10 (11), 1757-1771 (2000)
MEDLINE 20530913
PUBMED 11076861
REFERENCE
4 The RIKEN Genome Exploration Research Group Phase II Team and the FANTOM Consortium
TITLE Functional annotation of a full-length mouse cDNA collection
JOURNAL Nature 409, 685-690 (2001)
PUBMED 11076861
REFERENCE
5 The FANTOM Consortium and the RIKEN Genome Exploration Research Group Phase I & II Team.
TITLE Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs
JOURNAL Nature 420, 563-573 (2002)
PUBMED 11076861
REFERENCE
6 (bases 1 to 1735)
JOURNAL Adachi, J., Aizawa, K., Akahira, S., Akimura, T., Arai, A., Aono, H., Arakawa, T., Bono, H., Carninci, P., Fukuda, S., Fukunishi, Y., Furuno, M., Hanagaki, T., Hara, A., Hayatsu, N., Hiramoto, K., Hiraoka, T., Hori, P., Imotani, K., Ishii, Y., Itoh, M., Izawa, M., Kasukawa, T., Kato, H., Kawai, J., Kojima, Y., Konno, H., Kouda, M., Koyu, S., Kurihara, C., Matsuyama, T., Miyazaki, A., Nishi, K., Nomura, K., Numazaki, R., Ohno, M., Okazaki, Y., Okido, T., Owa, C., Saito, H., Saito, R., Sakai, K., Sakai, K., Sano, H., Sasaki, D., Shibata, K., Shibata, Y., Shinagawa, A., Shiraki, T., Sogabe, Y.,

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Db	1182	ACTCTCGTTTCTCCACCGTGAAGAAGATTGATGCAGCTGTTTGAAGAAGAGAAG	1241
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Db	1242	AAGAAACAGTACTCTTTGTAGGGGCAAAATACCTGGAGATTGTGATGAGACAAGACATGTT	1301
Qy	406	MetAspLysGlyPheProGlnArgValIysHisPheProGlyIleSerIleArgVal	425
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Qy	426	AspAlaIaPheGlnTyrLysGlyPhePhePheSerArgGlySerLysGlnPheGlu	445
Db	1362	GATCTGTGTTACACGAATTTGGGTTTTTTTATTCTTCAGGATCATCACAGTTGCG	1421
Qy	446	TyrAsnIleLysThrLysAsnIleThrArgIleMetArgThrAsnThrTrpPheGlnCys	465
Db	1422	TTTGACCCCAATGCCAGCAGCGTGACACATACCTGAAGAGCAACAGCTGGCTGCTGTC	1481
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ACCESSION	AK089234.1	GI:26354353	
VERSION			
KEYWORDS	HTC; CAP trapper.		
SOURCE	Mus musculus (house mouse)		
ORGANISM	Mus musculus		
REFERENCE			
AUTHORS	Carninci, P. and Hayashizaki, Y.		
TITLE	High-efficiency full-length cDNA cloning		
JOURNAL	Meth. Enzymol. 303, 19-44 (1999)		
MEDLINE	9279253		
PUBMED	10349636		
REFERENCE			
AUTHORS	Carninci, P., Shibata, Y., Hayatsu, N., Sugahara, Y., Shibata, K., Itoh, M., Konno, H., Okazaki, Y., Muramatsu, M. and Hayashizaki, Y.		
TITLE	Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes		
JOURNAL	Nature Res. 10 (10), 1617-1630 (2000)		
MEDLINE	20499374		
PUBMED	11042159		
REFERENCE			
AUTHORS	Shibata, K., Itoh, M., Aizawa, K., Nagaoka, S., Sasaki, N., Carninci, P., Konno, H., Akiyama, J., Nishi, K., Kitsuai, T., Tashiro, H., Itoh, M., Sumi, N., Ishii, Y., Nakamura, S., Hazama, M., Nishine, T., Harada, A., Yamamoto, R., Matsumoto, H., Sakeguchi, S., Ikegami, T., Kashiwagi, K., Fujiwaki, S., Inoue, K., Ito, Y., Izawa, M., Tanaka, T., Kawai, M., Ikoneda, Y., Ishikawa, T., Ozawa, K., Tanaka, T., Matsura, S., Kawai, J., Okazaki, Y., Muramatsu, M., Inoue, Y., Kira, A. and Hayashizaki, Y.		
TITLE	RIKEN integrated sequence analysis (RISA) system--384-format sequencing pipeline with 384 multicapillary sequencer		
JOURNAL	Nature Res. 10 (11), 1757-1771 (2000)		
MEDLINE	20530913		
PUBMED	11076861		
REFERENCE			
AUTHORS	The RIKEN Genome Exploration Research Group Phase II Team and the FANTOM Consortium.		
TITLE	Functional annotation of a full-length mouse cDNA collection		
JOURNAL	Nature 409, 685-690 (2001)		
REFERENCE			
AUTHORS	The FANTOM Consortium and the RIKEN Genome Exploration Research Group Phase I & II Team.		
TITLE	Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs		
JOURNAL	Nature 420, 563-573 (2002)		


```

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Qy      41  TyrSerLeuGluIleGluGlyAsnHisLeuValGlnSerLysAsnArgSerLeuIleAsp 60
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Qy      61  AspLysIleArgGluMetGlnAlaPheGlyLeuThrValThrGlyLysLeuAspSer 80
Db      259  GAGAGCTTAAAGATGACGCGCTCTTCAGCTTAGCAGAGACCTGGGAAGTTAGATCA 318
Qy      81  AsnThrLeuGluIleMetLysThrProArgCysGlyValProAspValGlyGlnTyrGly 100
Db      319  GCTACAATGGGGAATTATGGAATGCTCGATGTGGAGTGCCTGACTCTGGTATTCTTG 378
Qy      101  TyrThr-----LeuProGlyTyrArgLysTyrAsnLeuThrTyrArgIleAsnTyr 118
Db      379  CTAACCCAGGGAAGTCCCAAGTGGACACACATAACCTGACCTACAGGATTATAAACCAT 438
Qy      119  ThrProAspMetAlaArgAlaValAlaAspGluAlaIleGlnGluGlyLeuGluValTrp 138
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Qy      139  SerLysValThrProLeuLysPheThrLysSerLysGlyLeuAlaAspIleMetIle 158
Db      499  AGTGTAGCATGCCCTGACCTTACCGAGATCTTACAGGGAAGACGACATCAACATT 558
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Db      559  GCTTTCGTCTCAAGACACCATGGTGCACATTTCTCCA-----TTTGATGGACCCCAATGGA 612
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Db      613  ATCCCTTGCCATGCCCTTCAACAGCCCAAGGATTTGGAGAGAGCTCATTTTGATTTCA 672
Qy      198  AspGluAsnTrpThrLysAspGlyAlaGlyPheAsnLeuPheLeuValAlaAlaHisGlu 217
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Qy      218  PheGlyHisAlaLeuGlyLeuSerHisSerAsnAspGlnThrAlaLeuMetPheProAsn 237
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Db      793  TATGCTTACAGGGAACCCAGCACCCTATTCACTACCTCAAGATGATATCAATGCATTCAG 852
Qy      258  SerIleTyrGlyLeuProLysValProAlaLysProLysGluProThrIleProHis 277
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Qy      278  AlaCysAspProAspLeuThrPheAspAlaIleThrThrPheArgArgGluValMetPhe 297
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Db      970  TTTAAAGACAAGTACTCTCGAGCGGCCTCCTCAGCTGAGAACAGTTGACCTCAATTTC 1029
Qy      318  IleAlaSerPheTrpProSerLeuProAlaAspLeuGlnAlaAlaTyrGluAsn---Pro 336
Db      1030  ATATCTCTGTCTGGCCCTCTTACCCACAGCTCTTCAGGCTGCTTATGAAGATTGAC 1089
Qy      337  ArgAspLysIleLeuValPheLysAspGluAsnPheTrpMetIleArgGlyTyrAlaVal 356
Db      1090  AGAGACCTAGTTTCTCTATTAAAGGACAGACGATCTGGGCTCTCAAGTGGCTATGACCTG 1149
Qy      357  LeuProAspTyrProLysSerIleHisThrLeuGlyPheProGlyArgValLysIle 376

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Db      1150  CAGCAAGGTTACCCAGAGATATATCAACTATGATTCCCAAGGAGTGTCCAGCCATT 1209
Qy      377  AspAlaIleValCysAspLysThrThrArgLysThrTyrPhePheValGlyIleTrpCys 396
Db      1210  GATCAGCTGTT-----TCCATAACGGGAAGACATACTTCTTCTATAAACACCAAGTGC 1263
Qy      397  TrpArgPheAspGluMetThrGlnThrMetAspLysGlyPheProGlnArgValValLys 416
Db      1264  TGGAGATATGACATCAAGAAGATCCATGACCCAGGTTACCCCAAAAGACATACCAAGC 1323
Qy      417  HisPheProGlyIleSerIleArgValAspAlaIlePheGlnTyrLysGlyPhePhePhe 436
Db      1324  ATGTTCCAGGAGTAAACTGTAGATCGATGCTGAGTTTTCCTCGAGGACTCCTCTTCTCCTC 1383
Qy      437  PheSerArgGlySerLysGlnPheGluTyrAsnIleLysThrLysAsnIleThrArgIle 456
Db      1384  TTCCTTCAGTGACCAACAATATTTTGCATTTTAATTTTGTTCAGTCACAGAGTCACTAGATT 1443
Qy      457  MetArgThrAsnThrTrpPheGlnCys 465
Db      1444  GCAGAGCAATTTATGCTTAACCTGT 1470

RESULT 4
LOCUS      AK089516          2074 bp      mRNA      linear      HTC 03-APR-2004
DEFINITION Mus musculus B6-derived CD11 +ve dendritic cells cDNA, RIKEN
full-length enriched library, clone:F730044H20 product:matrix
metalloproteinase 8, full insert sequence.
ACCESSION   AK089516
VERSION     AK089516.1 GI:26354565
KEYWORDS    HTC; CAP trapper.
SOURCE      Mus musculus (house mouse)
ORGANISM    Mus musculus
Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

1
Carninci, P. and Hayashizaki, Y.
High-efficiency full-length cDNA cloning
Meth. Enzymol. 303, 19-44 (1999)
99279253
10349636
2
Carninci, P., Shibata, Y., Hayatsu, N., Sugahara, Y., Shibata, K.,
Itoh, M., Konno, H., Okazaki, Y., Muramatsu, M. and Hayashizaki, Y.
Normalization and subtraction of cap-trapper-selected cDNAs to
prepare full-length cDNA libraries for rapid discovery of new genes
Genome Res. 10 (10), 1617-1630 (2000)
20499374
11042159
3
Shibata, K., Itoh, M., Aizawa, K., Nagaoka, S., Sasaki, N., Carninci, P.,
Konno, H., Akiyama, J., Nishi, K., Kitsuai, T., Tashiro, H., Itoh, M.,
Sumi, N., Ishii, Y., Nakamura, S., Hazama, M., Nishine, T., Harada, A.,
Yamamoto, R., Matsumoto, H., Sakaguchi, S., Ikegami, T., Kashiwagi, K.,
Fujiwara, S., Inoue, K., Togawa, Y., Izawa, M., Ohara, E., Watahiki, M.,
Yoneda, Y., Ishikawa, T., Ozawa, K., Tanaka, T., Matsura, S., Kawai, J.,
Okazaki, Y., Muramatsu, M., Inoue, Y., Kira, A. and Hayashizaki, Y.
RIKEN integrated sequence analysis (RISA) system--384-format
sequencing pipeline with 384 multicapillary sequencer
Genome Res. 10 (11), 1757-1771 (2000)
20530913
11076861
4
The RIKEN Genome Exploration Research Group Phase II Team and the
FANTOM Consortium.
Functional annotation of a full-length mouse cDNA collection
Nature 409, 685-690 (2001)
5
The FANTOM Consortium and the RIKEN Genome Exploration Research
Group Phase I & II Team.
Analysis of the mouse transcriptome based on functional annotation
of 60,770 full-length cDNAs
Nature 420, 563-573 (2002)

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US-10-729-807-10 (1-513) x AK089381 (1-2426)

[illegible]

D _b	1091	AGAGACCTAGTTTTCCTTAATTAAAGGCAGACAGTACTGGGCTCTTAAGTGCGCTATGACCTG	1150
Q _y	357	LeuProAspTyxPrOlysSerIleHisThrLeuGlyPheProGlyArgValLysIle	376
D _b	1151	CAGCAAGGTACCCTCCAGAGATATATCCAATACTGGGATTCACAAGGAGTGTCCAAGGCCATT	1210
Q _y	377	AspAlaAlaValCysAspLysThrThrArgLysThrTy-PhePheValGIyIleTrpCys	396
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Q _y	397	TrpArgPheAspGluMetThrGlnThrMetAspLysGlyPheProGlnArgValLys	416
D _b	1265	TGGAGATATGACAATCAAAGAAGATCCATGAACCCAGGTATACCCAAAAGCATACCAAGC	1324
Q _y	417	HisPheProGlyIleSerIleArgValAspAlaPheGlnTyrlsGlyPhePhe	436
D _b	1325	ATGTTCCCAGGATAAAGTCTAGAGTCGATGCAGTTTCTCTGCAGGACTCCTTCTCTCCCTC	1384
Q _y	437	PheSerArgGlySerLysGlnPheGluTyxAsnIleLysThrLysAsnIleThrArgIle	456
D _b	1385	TTCTTCAGTGGACCAATAATTTTGCATTAAATTTTGTTCAGTCACAGAGTCAC TAGATT	1444
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D _b	1445	GCAAGAAGCAATTTATGGCTTAACCTG	1471

RESULT 6	EG189775	755 bp	mRNA	linear	EST 21-APR-2001
LOCUS	EG189775				
DEFINITION	EST8421	Athersys RAGE Library	Homo sapiens	CDNA, mRNA	sequence.
ACCESSION	EG189775				
VERSION	EG189775.1	GI:13711462			
KEYWORDS	EST.				
SOURCE	Homo sapiens (human)				

ORGANISM	Homo sapiens
	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE	1 (bases 1 to 735)
AUTHORS	Harrington,J.J., Sherf,B., Rundlett,S., Jackson,P.D., Perry,R., Cain,S., Leventhal,C., Thornton,M., Ramachandran,R., Whittington,J., Lerner,L., Costanzo,D., McElligott,K., Bozer,S., Mays,R., Smith,E., Veloso,N., Klika,A., Hess,J., Cothren,K., Lo,K., Offenbacher,J., Danzig,J. and Ducar,M.
TITLE	Creation of genome-wide protein expression libraries using random activation of gene expression
JOURNAL	Nat. Biotechnol. 19 (5), 440-445 (2001)
MEDLINE	21227151
PUBMED	11329013
COMMENT	Contact: Scott J. Cain

atcersys, Inc.
3201 Carnegie Ave., Cleveland, OH 44115, USA
Tel: 216 431 9900
Fax: 216 361 9596
Email: scaine@atcersys.com
High quality sequence stop: 551

FEATURES source

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1. /755
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Libraries using Random Activation of Gene Expression',
Nature Biotechnology, in press. Note that even though the
cell type indicated is HT1080, since a random activation
method was used, these sequence tags are not necessarily
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ORIGIN

Alignment Scores:	
Pred. No.:	1.12e-122
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Length:	755
Matches:	226

Percent Similarity: 93.52%		Conservative: 5	
Best Local Similarity: 91.50%		Mismatches: 16	
Query Match: 41.59%		Indels: 5	
DB: 4		Gaps: 0	
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QY	229	AspGlnThrAlaLeuMetPheProAsnTyrValSerLeuAspProArgLysTyrProLeu	248
DB	69	GATCAACAGCCTTGATGTTCCCAATATATGTCCTCGATCCAGAAATACCCACTT	128
QY	249	SerGlnAspAlaAsnGlyIleGlnSerIleTyrGlyGlyLeuProLysValProAla	268
DB	129	TCTCAGGATGATATCAATGGAAATCCAGTCCATCTATGAGGTCTGCTTAAGGTACCTGCT	188
QY	269	LysProLysGluProThrIleProHisAlaCysAspProAspLeuThrPheAspAlaIle	288
DB	189	AAGCCAAAGGAACCACTATACCCCATGCTGTGACCTTGACTTTGACGCTATC	248
QY	289	ThrThrPheArgGluValMetPhePheLysGlyArgHisLeuTyrPArgIleTyrTyr	308
DB	249	ACAACCTTTCCGACAGAGTATGTTCTTTAAGCGACGACCATATGAGGATCTATTAT	308
QY	309	AspIleThrAspValGluPheGluLeuIleAlaSerPheTyrProSerLeuProAlaAsp	328
DB	309	GATATCAGCGATGTTGAGTTTGAATTAATGTTTCATCTGCGCATCTCTGCGACCTGAT	368
QY	329	LeuGlnAlaAlaTyrGluAsnProArgAspLysIleLeuValPheLysAspGluAsnPhe	348
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QY	349	TrpMetIleArgGlyTyrAlaValLeuProAspTyrProLysSerIleHisThrLeuGly	368
DB	429	TGGATGATCAGAGGATATGCTGTCTTGCCAGATTATCCCAATATCCATCATATTAGT	488
QY	369	PheProGlyArgValLysLysIleAspAlaAlaValCysAspLysThrThrArgLysThr	388
DB	489	TTTCCAGGACGTTGAGAAATAGATGACGCGCTGTGTGATAAGACCAACAGAAACCC	548
QY	389	TyrPhePheValGlyIleTyrCysTyrArgPheAspGluMetThrGlnThrMetAspLys	408
DB	549	TACTTCTTTGGGCATTTGGTCTGGAGTTTGTGATGAAATGACCCCAACCATGGACAAA	608
QY	409	GlyPheProGlnArgValValLysHisPheProGlyLysSerIleArgValAspAlaAla	428
DB	609	GGATTCCCGCACAGAGTGTG-AAACACTTTTGTGTGATC-AGGATACGTGTGGATGCTGT	665
QY	429	PheGlnTyrLysGlyPhePhePheSerArgGlySerLysGlnPheGluTyrAsnIle	448
DB	666	TTGGAATACAAAGGATTTTATTTTGTG-AGGCCTGGATCAAACTA-TTCTCATTTCCACCTT	723
QY	449	LysThrLysAsnIleThrArg	455
DB	724	AACACGAAGAATTTTCCCGA	744
RESULT 7	AK089336 2427 bp mRNA linear HTC 03-APR-2004		
LOCUS	Mus musculus B6-derived CD11 +ve dendritic cells cDNA, RIKEN		
DEFINITION	full-length enriched library, clone:F73008D09 product:matrix metalloproteinase 8, full insert sequence.		
ACCESSION	AK089336		
VERSION	AK089336.1 GI:26105213		
KEYWORDS	HTC; CAP trapper.		
SOURCE	Mus musculus (house mouse)		
ORGANISM	Mus musculus		
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.		
1			

Carninci, P. and Hayashizaki, Y. High-efficiency full-length cDNA cloning Meth. Enzymol. 303, 19-44 (1999) 99279253 10349636	
2 Carninci, P., Shibata, Y., Hayatsu, N., Sugahara, Y., Shibata, K., Itoh, M., Konno, H., Okazaki, Y., Muramatsu, M. and Hayashizaki, Y. Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes Genome Res. 10 (10), 1617-1630 (2000)	
20499374 11042159	
3 Shibata, K., Itoh, M., Aizawa, K., Nagaoka, S., Sasaki, N., Carninci, P., Konno, H., Akiyama, J., Nishi, K., Kitsuai, T., Tashiro, H., Itoh, M., Sumi, N., Ishii, Y., Nakamura, S., Hazama, M., Nishine, T., Harada, A., Yamamoto, R., Matsumoto, H., Sakaguchi, S., Ikegami, T., Kashiwagi, K., Fujiwaka, S., Inoue, K., Togawa, Y., Izawa, M., Ohara, E., Watahiki, M., Yoneda, Y., Ishikawa, T., Ozawa, K., Tanaka, T., Matsura, S., Kawai, J., Okazaki, Y., Muramatsu, M., Inoue, Y., Kira, A. and Hayashizaki, Y. RIKEN integrated sequence analysis (RISA) system--384-format sequencing pipeline with 384 multicapillary sequencer Genome Res. 10 (11), 1757-1771 (2000)	
20530913 11076861	
4 The RIKEN Genome Exploration Research Group Phase II Team and the FANTOM Consortium. Functional annotation of a full-length mouse cDNA collection Nature 409, 685-690 (2001)	
5 The PANTOM Consortium and the RIKEN Genome Exploration Research Group Phase I & II Team. Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs Nature 420, 563-573 (2002)	
6 (bases 1 to 2427) Adachi, J., Aizawa, K., Akimura, T., Arakawa, T., Bono, H., Carninci, P., Fukuda, S., Furuno, M., Hanagaki, T., Hara, A., Hashizume, W., Hayashida, K., Hayatsu, N., Hiramoto, K., Hiraoka, T., Hirozane, T., Hori, F., Imotani, K., Ishii, Y., Itoh, M., Kagawa, I., Kasukawa, T., Kato, H., Kawai, J., Kojima, Y., Kondo, S., Konno, H., Kouda, M., Koya, S., Kurihara, C., Matsuyama, T., Miyazaki, A., Murata, M., Nakamura, M., Nishi, K., Nomura, K., Numazaki, R., Ohno, M., Ohsato, N., Okazaki, Y., Saito, R., Saitoh, H., Sakai, C., Sakai, K., Sakazume, N., Sano, H., Sasaki, D., Shibata, K., Shinagawa, A., Shiraki, T., Sogabe, Y., Tagami, M., Tagawa, A., Takahashi, F., Takaku-Akahira, S., Takeda, Y., Tanaka, T., Tomaru, A., Toya, T., Yasunishi, A., Muramatsu, M. and Hayashizaki, Y. Direct Submission Submitted (16-APR-2002) Yoshihide Hayashizaki, The Institute of Physical and Chemical Research (RIKEN), Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center (GSC), RIKEN Yokohama Institute, 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan (E-mail: genome-res@sc.riken.jp, URL: http://genome.gsc.riken.jp/, Tel: 81-45-503-9222, Fax: 81-45-503-9216) cDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN. Division of Experimental Animal Research in Riken contributed to prepare mouse tissues. Tissues were provided by Dr. John Todd (Dept. of Medical Genetics Wellcome Trust Centre for Molecular Mechanisms in Disease Wellcome Trust/MRC building Addenbrookes Hospital Cambridge) whose assistance we gratefully acknowledge. Please visit our web site for further details. URL: http://genome.gsc.riken.jp/ URL: http://fantom.gsc.riken.jp/ Location/Qualifiers 1. .2427 /organism="Mus musculus"	

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ORIGIN

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Score:	226
Percent Similarity:	71
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	Length:
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1146.00	Conservative:
63.13%	Mismatches:
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41.48%	Gaps:
US-10-729-807-10 (1-513)	x AK089336 (1-2427)

US-10-729-807-10 (1-513) x AK089336 (1-2427)

QY	1	Met	lys	arg	g	leu	leu	leu	leu	cys	leu	phe	phe	ile	thr	phe	ser	ser	ala	phe	pro	leu	20
DB																						20	
QY	91	CTG	AAG	ACCT	TCC	CAAT	TACT	GTAT	CTCT	CAC	ACAC	CAC	AGCT	GTG	CAAA	TGC	CTT	CCC	CAG	TAA	150		
DB																					150		
QY	21	Val	arg	met	thr	glu	asn	glu	leu	asn	met	glu	leu	ala	glu	ala	tyr	leu	asn	gln	phe	40	
DB																					40		
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DB																		207					
QY	41	Tyr	ser	leu	glu	ile	glu	glu	lys	his	leu	val	gln	ser	lys	asn	arg	ser	leu	ile	asp	60	
DB																					60		
QY	208	TACA	ACTA	-----	CCA	AGCA	TCA	TAAT	CCG	TCTT	CGAG	AAAT	CGCC	AGAT	GTG	CA	261						
DB																	261						
QY	61	Asp	lys	ile	arg	glu	met	gln	ala	phe	phe	gly	leu	thr	val	thr	gly	lys	leu	asp	ser	80	
DB																					80		
QY	262	GAG	AAGCTT	AAAGAGAT	CGAC	GGTCTT	CTT	CACT	TAG	CAG	AGACT	GGGAAG	TTAGAT	GCA	321								
DB															321								
QY	81	Asn	thr	leu	glu	ile	met	lys	thr	pro	arg	cys	gly	val	pro	asp	val	gly	gln	tyr	gly	100	
DB																					100		
QY	322	GCT	ACAT	GGGAT	TAT	GGA	ATG	CCT	CGAT	GTG	AGT	GCCT	GAT	CTCT	GGT	GAT	TCT	CTG	381				
DB																					381		
QY	101	Tyr	thr	-----	Leu	pro	gly	tyr	trp	arg	lys	tyr	asn	leu	thr	tyr	arg	ile	ile	asn	tyr	118	
DB																					118		
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DB																					441		
QY	119	Thr	pro	asp	met	ala	arg	-	ala	ala	val	asp	glu	ala	ile	gln	glu	gly	leu	glu	val	138	
DB																					138		
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DB																					501		
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DB					</																		

RESULTS

CR603756	1784 bp	mRNA	linear	HTC 21-JUL-2004
LOCUS	full-length cDNA clone CS0DI002YD16 of Placenta Cot 25-normalized of Homo sapiens (human).			
DEFINITION				
ACCESSION	CR603756.1 GI:50484563			
VERSION	HTC; CNSLT_cDNA.			
KEYWORDS	Homo sapiens (human)			
SOURCE	Homo sapiens			
ORGANISM	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.			
REFERENCE	1 (bases 1 to 1784)			
AUTHORS	Li, W.B., Gruber, C., Jessee, J. and Polayes, D.			
TITLE	Full-length cDNA libraries and normalization			
JOURNAL	Unpublished			
REMARK	Contact : Feng Liang Email : fliang@lifetech.com URL : http://fulllength.invitrogen.com/ InvitroGen Corporation 1600 Paraday Avenue			
REFERENCE	2 (bases 1 to 1784)			
AUTHORS	Genoscope.			
TITLE	Direct Submission			
JOURNAL	Submitted (20-JUL-2004) Genoscope - Centre National de Séquençage			

QY	3	ArgLeuLeuLeuLeuLeuLeuLeuPhePhePheIleThrPheSerSerAlaPheProLeuValArg	22
Db	37	AAAGTTCTCTTAATAGCTCTCTCGAGCCCACTGCTTCTGGAGCTCTTCCCTCGAACAGC	96
QY	23	MetThrGluAsnGluGluAsnMetGlnLeu---AlaGlnAlaTyrLeuAsnGlnPheTyr	41
Db	97	TCTACAGCCCTGGAAGAAAATAAATGCTGCTATTTGGTGAAAGATACTTAGAAAAAATTTTAT	156
QY	42	SerLeuGluIleGluGlyAsnHisLeuValGlnSerLysAsnArg-----SerLeu	58
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QY	79	AspSerAsnThrLeuGluIleMetLysThrProArgCysGlyValProAspValGlyGln	98
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Db	388	AATAATATACACACCTGCATGAACCGTGAGGATGTGTGACTACGCATCCGGAAGCTTTC	447
QY	136	GluValTyrSerLysValThrProLeuLysPheThrLysIleSerLysGlyIleAlaAsp	155
Db	448	CAAGTATGGAGTAATGTATACCCCTTGAAATTCAGCAAGATTAAACACAGGCATGGCTGAC	507
QY	156	IleMetIleAlaPheArgThrArgValHisGlyArgCysProArgTyrPheAspGlyPro	175
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QY	176	LeuGlyValLeuGlyHisAlaPheProProGlyProGlyLeuGlyGlyAspThrHisPhe	195
Db	565	GGTGGAAATCCTACGCCCATGCTTTTGGACCTGGATCTGGCATTTGGAGGGATGCATTC	626
QY	196	AspGluAspGluAsnTyrThrLysAspGlyAlaGlyPheAsnLeuPheLeuValala	215
Db	625	GATGAGGACGAATTCGGACTACACATTGAGGGGCAC-CACCTTGTCTCTCACTGCTGTT	686
QY	216	HisGluPheGlyHisAlaLeuGlyLeuSerHisSerAsnAspGlnThrAlaLeuMetPhe	236

Qy 197 GluAspGluAsnTrpThrLysAspGlyAlaGlyPheAsnLeuPheLeuValAlaHis 216
 Db 627 GAGCAGAAACGTCGAGTAAAGATTTTCAAGGCACAAACCTCTCTCTGTGTGTCAT 686
 Qy 217 GluPheGlyHisAlaLeuGlyLeuSerHisSerAsnAspGlnThrAlaLeuMetPhePro 236
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 Qy 277 HisAla--CysAspProAspLeuThrPheAspAlaIleThrPheArgArgGluVal 295
 Db 867 TCAACTTCTGTACCAAGCTTGAGTTTGTATGCTGCACACAGTGGGAGAGAAATC 926
 Qy 296 MetPhePheLysGlyArgHisLeuTrpArgIleTyrTyrAspIleThrAspValGluPhe 315
 Db 927 TTTTCTTTAAAGACTGTTCTTCTGGTGAAGCTTCTCTGGAGTCCAGCCACCAACAT 986
 Qy 316 GluLeuIleAlaSerPheTrpProSerLeuProAlaAspLeuGlnAlaAlaTyrGlu--- 334
 Db 987 ACTTCTATTTCTCATATGCCAAGCATCCCATCTCGTATTCAGCTGCTTACGAAAT 1046
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 Db 1047 GAAAGCAGAAATCAACTTTCTTTTAAAGATGAGAGTACTGGTAAATAACAACATTA 1106
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 Qy 375 LysIleAspAlaAlaValCysAspLysThrThrArgLysThrTyrPhePheValGlyLe 394
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 Db 1407 AAAACATTGAAAGTACAGCTGGTTGTGTGTAGAA 1445
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 ACCESSION AK049552
 VERSION 1 GI:26340287
 KEYWORDS HTC; CAP trapper.
 SOURCE Mus musculus (house mouse)
 ORGANISM Mus musculus
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Eutelestomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 REFERENCE 1
 AUTHORS Carninci, P. and Hayashizaki, Y.
 TITLE High-efficiency full-length cDNA cloning
 JOURNAL Meth. Enzymol. 303, 19-44 (1999)

MEDLINE
PUBMED
REFERENCE

AUTHORS

TITLE

JOURNAL

MEDLINE

PUBMED

REFERENCE

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JOURNAL

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TITLE

JOURNAL

MEDLINE

PUBMED

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

FEATURES

source

99279253
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2

Carninci, P., Shibata, Y., Hayatsu, N., Sugahara, Y., Shibata, K., Itoh, M., Konno, H., Okazaki, Y., Muramatsu, M. and Hayashizaki, Y.

Normalization and subtraction of cap-trapper-selected cDNAs to

prepare full-length cDNA libraries for rapid discovery of new genes

Genome Res. 10 (10), 1617-1630 (2000)

20499374

11042159

3

Shibata, K., Itoh, M., Aizawa, K., Nagao, S., Sasaki, N., Carninci, P., Konno, H., Akiyama, J., Nishi, K., Kitsuina, T., Tashiro, H., Itoh, M., Sumi, N., Ishii, Y., Nakamura, S., Hazama, M., Nishine, T., Harada, A., Yamamoto, R., Matsumoto, H., Sakaguchi, S., Ikegami, T., Kashiwagi, K., Fujiwaka, S., Inoue, K., Togawa, Y., Izawa, M., Ohara, E., Watahiki, M., Yoneda, Y., Ishikawa, T., Ozawa, K., Tanaka, T., Matsuura, S., Kawai, J., Okazaki, Y., Muramatsu, M., Inoue, Y., Kira, A. and Hayashizaki, Y.

RIKEN integrated sequence analysis (RISA) system--384-format

sequencing pipeline with 384 multipillar sequencer

Genome Res. 10 (11), 1757-1771 (2000)

20530913

11076861

4

The RIKEN Genome Exploration Research Group Phase II Team and the

FANTOM Consortium.

Functional annotation of a full-length mouse cDNA collection

Nature 409, 685-690 (2001)

5

The FANTOM Consortium and the RIKEN Genome Exploration Research

Group Phase I & II Team.

Analysis of the mouse transcriptome based on functional annotation

of 60,770 full-length cDNAs

Nature 420, 563-573 (2002)

6

(Bases 1 to 2013)

Adachi, J., Aizawa, K., Akimura, T., Arakawa, T., Bono, H., Carninci, P., Fukuda, S., Furuno, M., Hanagaki, T., Hara, A., Hashizume, W., Hayashida, K., Hayatsu, N., Hiramoto, K., Hiraoka, T., Hirozane, T., Hori, F., Imotani, K., Ishii, Y., Itoh, M., Kagawa, I., Kasukawa, T., Katoh, H., Kawai, J., Kojima, Y., Kondo, S., Konno, H., Kouda, M., Koya, S., Kurihara, C., Matsuyama, T., Miyazaki, A., Murata, M., Nakamura, M., Nishi, K., Nomura, K., Numazaki, R., Ohno, M., Ohsato, N., Okazaki, Y., Saito, H., Saitoh, H., Sakai, C., Sakai, K., Sakazume, N., Sano, H., Sasaki, D., Shibata, K., Shinagawa, A., Shiraki, T., Sogabe, Y., Tagami, M., Tagawa, A., Takahashi, F., Takaku-Akahira, S., Takeda, Y., Tanaka, T., Tomaru, A., Toya, T., Yasunishi, A., Muramatsu, M. and Hayashizaki, Y.

Direct Submission

Submitted (16-JUL-2001) Yoshihide Hayashizaki, The Institute of

Physical and Chemical Research (RIKEN), Laboratory for Genome

Exploration Research Group, RIKEN Genomic Sciences Center (GSC),

RIKEN Yokohama Institute, 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama,

Kanagawa 230-0045, Japan (E-mail: genome-res@gsr.riken.jp,

URL: http://genome.gsc.riken.jp/, Tel: 81-45-503-9222,

Fax: 81-45-503-9216)

cDNA library was prepared and sequenced in Mouse Genome

Encyclopedia Project of Genome Exploration Research Group in Riken

Genomic Sciences Center and Genome Science Laboratory in RIKEN.

Division of Experimental Animal Research in Riken contributed to

prepare mouse tissues.

Please visit our web site for further details.

URL: http://genome.gsc.riken.jp/

URL: http://fantom.gsc.riken.jp/

Location/Qualifiers

1. .2013

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High-efficiency full-length cDNA cloning
Meth. Enzymol. 303, 19-44 (1999)
99279253
10349636

2
REFERENCE
AUTHORS
Carninci, P., Shibata, Y., Hayatsu, N., Sugahara, Y., Shibata, K., Itoh, M., Konno, H., Okazaki, Y., Muramatsu, M. and Hayashizaki, Y.

TITLE
Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes

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AUTHORS
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TITLE
RIKEN integrated sequence analysis (RISA) system--384-format sequencing pipeline with 384 multicapillary sequencer

JOURNAL
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Genome Res. 10 (11), 1757-1771 (2000)
20530913
11076861

4
REFERENCE
AUTHORS
The RIKEN Genome Exploration Research Group Phase II Team and the FANTOM Consortium.

TITLE
Functional annotation of a full-length mouse cDNA collection

JOURNAL
MEDLINE
PUBMED
Nature 409, 685-690 (2001)

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AUTHORS
The FANTOM Consortium and the RIKEN Genome Exploration Research Group Phase I & II Team.

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Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs

JOURNAL
MEDLINE
PUBMED
Nature 420, 563-573 (2002)
11076861

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REFERENCE
AUTHORS
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TITLE
Direct Submission

JOURNAL
MEDLINE
PUBMED
Submitted (16-APR-2002) Yoshihide Hayashizaki, The Institute of Physical and Chemical Research (RIKEN), Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center (GSC), RIKEN Yokohama Institute; 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan (E-mail: genome-res@gsc.riken.jp, URL: http://genome.gsc.riken.jp/, Tel: 81-45-503-9222, Fax: 81-45-503-9216)

COMMENT
cDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN. Division of Experimental Animal Research in Riken contributed to prepare mouse tissues.

URL: http://genome.gsc.riken.jp/
URL: http://fantom.gsc.riken.jp/
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/mol_type="mRNA"
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ORIGIN			
Alignment Scores:			
Pred. No.:		1.37e-107	1519
Score:		1023.50	206
Percent Similarity:		60.25%	Conservative: 79
Best Local Similarity:		43.55%	Mismatches: 173
Query Match:		37.04%	Indels: 15
DB:		3	Gaps: 7
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Qy	117	AsnTyrThrProAspMetAlaAlaArgAlaAlaValAspGluAlaIleGlnGlyLeuGlu	136
Db	390	AATTACACTCCGACATGAAGCTGAGGATGTAGATACATATTTTCAGAAAGCTTTCCAA	449
Qy	137	ValTrpSerLysValThrProLeuLysPheThrLysIleSerLysGlyIleAlaAspIle	156
Db	450	GTCTGAGTGATGTGACTCTCTTAAGATTTCAGAAAGCTTCATAAAGATGAGGCTGACAT	509
Qy	157	MetIleAlaPheArgThrArgValHisGlyArgCysProArgTyrPheAspGlyProLeu	176
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Db	567	GGTACACTAGCCCATGCTTTTATCTCGGACCTGTATTAACAGAGATGACATTTGAT	626
Qy	197	GluAspGluAsnTrpThrLysAspGlyAlaGlyPheAsnLeuPheLeuValAlaAlaHis	216
Db	627	GAGCAGAAACGTGAGCTATAAAGTTTCAAGGCACAAACCTCTCTCTTGTGTTCAT	686
Qy	217	GluPheGlyHisAlaLeuGlyLeuSerHisSerAsnAspGlnThrAlaLeuMetPhePro	236
Db	687	GAACTTGCCCATCTCTTGGGCTCGAGCATTCCAATAATCCAAAGTCAATATGTATACCC	746
Qy	237	AsnTyrValSerLeuAspProArgLysTyrProLeuSerGlnAspAspIleAsnGlyIle	256
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Db	807	CAGTCCCTCTATGAGCCCGACAGTGAACCCCATCTTGCACAAACCTAGCAGTCCACCA	866
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Qy	296	MetPhePheLysGlyArgHisLeuTrpArgIleTyrTyrAspIleThrAspValGluPhe	315
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Qy	316	GluLeuIleAlaSerPheTrpProSerLeuProAlaAspLeuGlnAlaAlaTyrGlu---	334
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LOCUS		Mus musculus B6-derived CD11 +ve dendritic cells cDNA, RIKEN	
DEFINITION		full-length enriched library, clone:F730032D10 product:MACROPHAGE	
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VERSION		AK089452.1 GI:26354521	
KEYWORDS		HTC; CAP trapper.	


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LOCUS Mus musculus MMP20 gene, VIRTUAL TRANSCRIPT, partial sequence,
DEFINITION

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genomic survey sequence.
AY420752
AY420752.1 GI:39776709
GSS.
Mus musculus (house mouse)
ORGANISM
REFERENCE
AUTHORS
Clark, A.G., Gnanowski, S., Nielson, R., Thomas, P., Kejarival, A.,
Todd, M.A., Tanenbaum, D.M., Civello, D.R., Lu, F., Murphy, B.,
Ferriera, S., Wang, G., Zheng, X.H., White, T.J., Sninsky, J.J.,
Adams, M.D. and Cargill, M.
Inferring nonneutral evolution from human-chimp-mouse orthologous
gene trios
Science 302 (5652), 1960-1963 (2003)
14671302
2 (bases 1 to 1449)
Clark, A.G., Gnanowski, S., Nielson, R., Thomas, P., Kejarival, A.,
Todd, M.A., Tanenbaum, D.M., Civello, D.R., Lu, F., Murphy, B.,
Ferriera, S., Wang, G., Zheng, X.H., White, T.J., Sninsky, J.J.,
Adams, M.D. and Cargill, M.
Direct Submission
Submitted (16-NOV-2003) Celera Genomics, 45 West Gude Drive,
Rockville, MD 20850, USA
This sequence as made by sequencing genomic exons and ordering them
based on alignment.
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Best Local Similarity: 43.43% Mismatches: 160
Query Match: 35.63% Indels: 23
DB: 9 Gaps: 13

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QY 87 LysThrProArgCysGlyValProAspValGlyGlnTyrGlyTyrThrLeuProGly--- 105
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Db 460 CTGAACCTTGTAAGATAAATCTGGGGAACAGATATCATGATATCTTTTGAACACTGGA 519
QY 164 ValHisGlyArgCysProArgTyr---PheAspGlyProLeuGlyValLeuGlyHisAla 182
Db 520 GATCATGGG-----GATTCCTACCATTTGATGGGCTCAGAGGACTGTGGCCATGCA 573
QY 183 PheProProGlyProGlyLeuGlyGlyAspThrHisPheAspGluAspGluAsnTrpThr 202
Db 574 TTTGCTCTGTGAGAAGGCTGGGAGAGACACATTCGACAATGCTGAGAAGTGGACT 633
QY 203 LysAspGlyAlaGlyPheAsnLeuPheLeuValAlaHisGluPheGlyHisAlaLeu 222
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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AUTHORS Clark,A.G., Glanowski,S., Nielson,R., Thomas,P., Kejariwal,A.,
Todd,M.A., Tanenbaum,D.M., Civeello,D.R., Lu,P., Murphy,B.,
Ferriera,S., Wang,G., Zheng,X.H., White,T.J., Sninsky,J.J.,
Adams,M.D. and Cargill,M.
TITLE Inferring nonneutral evolution from human-chimp-mouse orthologous
gene trios
JOURNAL Science 302 (5652), 1960-1963 (2003)
PUBMED 14671302
REFERENCE 2 (bases 1 to 1452)
AUTHORS Clark,A.G., Glanowski,S., Nielson,R., Thomas,P., Kejariwal,A.,
Todd,M.A., Tanenbaum,D.M., Civeello,D.R., Lu,P., Murphy,B.,
Ferriera,S., Wang,G., Zheng,X.H., White,T.J., Sninsky,J.J.,
Adams,M.D. and Cargill,M.
TITLE Direct Submission
JOURNAL Submitted (16-NOV-2003) Celera Genomics, 45 West Gude Drive,
Rockville, MD 20850, USA
COMMENT This sequence as made by sequencing genomic exons and ordering them
based on alignment.
FEATURES
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/db_xref="taxon:9606"
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/locus_tag="HCM7328"
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ORIGIN
Alignment Scores: 5.85e-103 Length: 1452
Pred. No.: 983.50 Matches: 205
Score: 61.54% Conservative: 91
Percent Similarity: 42.62% Mismatches: 160
Best Local Similarity: 35.60% Indels: 25
Query Match: 9 Gaps: 14
DB:
US-10-729-807-10 (1-513) x AY420750 (1-1452)
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GenCore version 5.1.6
Copyright (c) 1993 - 2004 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: November 15, 2004, 13:11:00 ; Search time 1693 Seconds

(without alignments)
35019.163 Million cell updates/sec

Title: US-10-729-807-28

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Scoring table: IDENTITY NUC

Gapop 10.0 , Gapext 1.0

Searched: 32822875 seqs, 18219865908 residues

Total number of hits satisfying chosen parameters: 65645750

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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2: gb_est2: *
3: gb_hic: *
4: gb_est3: *
5: gb_est4: *
6: gb_est5: *
7: gb_est6: *
8: gb_gss1: *
9: gb_gss2: *

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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3	482.2	29.6	746	1	AI436025	AI436025 th80gl2.x
4	437.8	26.9	683	6	BY753385	BY753385 BY753385
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7	386	23.7	2074	3	AK089516	AK089516 Mus muscu
8	386	23.7	2223	3	AK089234	AK089234 Mus muscu
9	385.8	23.7	561	5	EX918107	EX918107 BX918107
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24	314.2	19.3	1416	9	AY418899	AY418899 Homo sapi

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26	309.2	19.0	1419	9	AY418901	AY418901 Mus muscu
27	304.2	18.7	869	5	BUT281887	BUT281887 603602842
28	302.8	18.6	593	4	BM440043	BM440043 pgrln.pko
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34	277.8	17.1	926	6	CA487316	CA487316 AGENCOURT
35	275.4	16.9	1027	7	CN065546	CN065546 D09 Ag2.p
36	274.4	16.9	1449	9	AY420752	AY420752 Mus muscu
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38	270.2	16.6	935	7	CO647474	CO647474 ILLUMIGEN
39	266.4	16.4	871	7	CN067389	CN067389 J10 Ag2.p
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VERSION BX102293.1 GI:27845222
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SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
REFERENCE 1 (bases 1 to 731)
AUTHORS Ebert, L., Heil, O., Hennig, S., Neubert, P., Partsch, E., Peters, M., Radelof, J., Schneider, D. and Korn, B.
TITLE Human UnigeneSet - RZPD3
JOURNAL Unpublished (2003)
COMMENT Contact: Ina Rolfs
RZPD Deutsches Ressourcenzentrum fuer Genomforschung GmbH
Im Neuenheimer Feld 580, D-69120 Heidelberg, Germany
RZPD; IMAGE9980231887.
RZPDLIB; I.M.A.G.E. cDNA Clone Collection;
Human UnigeneSet - RZPD3 (RZPDLIB No.972)
http://www.rzpd.de/CloneCards/cgi-bin/showLib.pl/cgi/response?libNo=972 Contact: Ina Rolfs
RZPD Deutsches Ressourcenzentrum fuer Genomforschung GmbH
Heubnerweg 6, D-14059 Berlin, Germany
Tel: +49 30 32639 101
Fax: +49 30 32639 111
www.rzpd.de
This clone is available royalty-free from RZPD;
contact RZPD (clone@rzpd.de) for further information. Seq primer:
M13r, Primer sequence: TTTCACAGGAACAGCTATGAC.

FEATURES

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 sequence.
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 AI436025.1 GI:4307295
 VERSION
 EST.
 SOURCE
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 ORGANISM
 Homo sapiens
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 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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 National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
 Tumor Gene Index
 Unpublished (1997)
 Contact: Robert Strausberg, Ph.D.
 Email: cgapbs@mail.nih.gov
 This clone is available royalty-free through LLNL; contact the
 IMAGE Consortium (info@image.llnl.gov) for further information.
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 NhMpu, and fetal heart NhH19W) were mixed, and ss circles
 were made in vitro. Following HAP purification, this DNA
 was used as tracer in a subtractive hybridization
 reaction. The driver was PCR-amplified cDNAs from pools of
 5,000 clones made from the same 3 libraries. The pools
 consisted of I.M.A.G.E. clones 260232-265223,
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 Site 2: Eco RI; Equal amounts of plasmid DNA from three
 normalized libraries (melanocyte 2NBHM, pregnant uterus
 NhMpu, and fetal heart NhH19W) were mixed, and ss circles
 were made in vitro. Following HAP purification, this DNA
 was used as tracer in a subtractive hybridization
 reaction. The driver was PCR-amplified cDNAs from pools of
 5,000 clones made from the same 3 libraries. The pools
 consisted of I.M.A.G.E. clones 260232-265223,
 340488-345479, and 484488-489479."

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RESULT 4
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 DEFINITION
 musculus cDNA clone 1420007I11 5', mRNA sequence.
 ACCESSION
 BY753385
 BY753385.1 GI:27184783
 VERSION
 EST.
 SOURCE
 Mus musculus (house mouse)
 ORGANISM
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
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 Okazaki, Y., Furuno, M., Kasukawa, T., Adachi, J., Bono, H., Kondo, S.,
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 Yang, L., Yuan, Z., Zavolan, M., Zhu, Y., Zimmer, A., Carninci, P.,
 Hayatsu, N., Hirozane-Kishikawa, T., Konno, H., Nakamura, M.,
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Arakawa, T., Fukuda, S., Hara, A., Hashizume, M., Imotani, K., Ishii, Y., Itoh, M., Kagawa, I., Miyazaki, A., Sakai, K., Sasaki, D., Shibata, K., Shinagawa, A., Yasunishi, A., Yoshino, M., Waterston, R., Lander, E.S., Rogers, J., Birney, E. and Hayashizaki, Y.

Analysis of the mouse transcriptome based on functional annotation

of 60,770 full-length cDNAs

Nature 420, 563-573 (2002)

JOURNAL
MEDLINE
PubMed

COMMENT

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Fax: 81-45-503-9216

Email: genome-res@sc.riken.jp, URL: <http://genome.gsc.riken.jp/>
Adachi, J., Aizawa, K., Akimura, T., Arakawa, T., Carninci, P.,
Fukuda, S., Hashizume, M., Hayashida, K., Hirozane, T., Hori, F.,
Imotani, K., Ishii, Y., Itoh, M., Kagawa, I., Kawai, J., Kojima, Y.,
Kondo, S., Konno, H., Koya, S., Miyazaki, A., Murata, M., Nakamura, M.,
Nomura, K., Numazaki, R., Ohno, M., Ohsato, N., Salto, R., Sakazume, N.,
Sano, H., Sasaki, D., Sato, K., Shibata, K., Shiraki, T., Tagami, M.,
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Direct Submission

Computational Analysis of Full-length Mouse cDNAs Compared with
Human Genome Sequences Mamm. Genome. 12, 673-677 (2001)
Normalization and subtraction of cap-trapper-selected cDNAs to
prepare full-length cDNA libraries for rapid discovery of new
genes. Genome Res. 10 (10), 1617-1630 (2000)
RIKEN integrated sequence analysis (RISA) system--384-format
sequencing pipeline with 384 multicapillary sequencer. Genome Res.
10 (11), 1757-1771 (2000)

Computer-based methods for the mouse full-length cDNA
encyclopedia: real-time sequence clustering for construction of a
nonredundant cDNA library. Genome Res. 11 (2), 281-289 (2001)
cDNA library was prepared and sequenced in Mouse Genome
Encyclopedia Project of Genome Exploration Research Group in Riken
Genomic Sciences Center and Genome Science Laboratory in RIKEN.
Division of Experimental Animal Research in Riken contributed to
prepare mouse tissues.

Tissues were provided by Takashi Ishikawa (Department of Surgery
2 Yokohama City University 3-9 Fukuura, Kanazawa-ku, Yokohama
236-0004 Japan) whose assistance we gratefully acknowledge.

Please visit our web site (<http://genome.gsc.riken.go.jp/>) for
further details.

FEATURES
source

Location/Qualifiers
1. .683
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ORIGIN

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Best Local Similarity 83.2%; Pred. No. 8.7e-109;
Matches 510; Conservative 0; Mismatches 102; Indels 1; Gaps 1;

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RESULT 5
AA424347

LOCUS
DEFINITION

411 bp mRNA linear EST 16-OCT-1997
z990e12.r1 Soares NHMPu Sl Homo sapiens cDNA clone IMAGE:767086 5'
similar to SW:COG3_RABIT F28663 STROMELYSIN-1 PRECURSOR ;, mRNA
sequence.

ACCESSION
VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

Unpublished (1997)

Contact: Wilson RK

Washington University School of Medicine

4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108

Tel: 314 286 1800

Fax: 314 286 1810

Email: est@watson.wustl.edu

This clone is available royalty-free through LLNL ; contact the

IMAGE Consortium (info@image.llnl.gov) for further information.

Seq primer: -28ml3 rev2 EF from Amersham

High quality sequence stop: 405.

Location/Qualifiers

1. .411

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ORIGIN

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Matches 799; Conservative 0; Mismatches 535; Indels 36; Gaps 5;

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RESULT 7
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LOCUS
DEFINITION
Mus musculus B6-derived CD11 +ve dendritic cells cDNA, RIKEN
full-length enriched library, clone:F73004H20 product:matrix
metalloproteinase 8, full insert sequence.
AK089516
ACCESSION
AK089516.1 GI:26354565
VERSION
HTC; CAP trapper.
KEYWORDS
Mus musculus (house mouse)
SOURCE
Mus musculus
ORGANISM
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.

REFERENCE
1
Carninci, P., Shibata, Y., Hayatsu, N., Sugahara, Y., Shibata, K.,
Itoh, M., Kono, H., Okazaki, Y., Muramatsu, M. and Hayashizaki, Y.
Normalization and subtraction of cap-trapper-selected cDNAs to
prepare full-length cDNA libraries for rapid discovery of new genes
Genome Res. 10 (10), 1617-1630 (2000)
2

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MEDLINE PUBMED REFERENCE AUTHORS	20499374 11042159 3 Shibata, K., Itoh, M., Aizawa, K., Nagaoka, S., Sasaki, N., Carninci, P., Konno, H., Akiyama, J., Nishi, K., Kitsumai, T., Tashiro, H., Itoh, M., Sumi, N., Ishii, Y., Nakamura, S., Hazama, M., Nishine, T., Harada, A., Yamamoto, R., Matsumoto, H., Sakaguchi, S., Ikegami, T., Kashiwagi, K., Fujiwara, S., Inoue, K., Togawa, Y., Izawa, M., Ohara, E., Watahiki, M., Yoneda, Y., Ishikawa, T., Ozawa, K., Tanaka, T., Matsura, S., Kawai, J., Okazaki, Y., Muramatsu, M., Inoue, Y., Kira, A. and Hayashizaki, Y. RIKEN integrated sequence analysis (RISA) system - 384-format sequencing pipeline with 384 multicapillary sequencer Genome Res. 10 (11), 1757-1771 (2000) 20530913 11076861 4
TITLE JOURNAL MEDLINE PUBMED REFERENCE AUTHORS	THE RIKEN Genome Exploration Research Group Phase II Team and the FANTOM Consortium. Functional annotation of a full-length mouse cDNA collection Nature 409, 685-690 (2001) 5 The FANTOM Consortium and the RIKEN Genome Exploration Research Group Phase I & II Team. Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs Nature 420, 563-573 (2002) 6 (bases 1 to 2074) Adachi, J., Aizawa, K., Akimura, T., Arakawa, T., Bono, H., Carninci, P., Fukaya, S., Furuno, M., Hanagaki, T., Hara, A., Hashizume, M., Hayashida, K., Hayatsu, N., Hiramoto, K., Hiraoka, T., Hirozane, T., Hori, P., Imotani, K., Ishii, Y., Itoh, M., Kagawa, I., Kasukawa, T., Katoh, H., Kawai, J., Kojima, Y., Kondo, S., Konno, H., Kouda, M., Koya, S., Kurihara, C., Matsuyama, T., Miyazaki, A., Murata, M., Nakamura, M., Nishi, K., Nomura, K., Numazaki, R., Ohno, M., Ohsato, N., Okazaki, Y., Saito, R., Saitoh, H., Sakai, C., Sakai, K., Sakazume, N., Sano, H., Sasaki, D., Shibata, K., Shinagawa, A., Shiraki, T., Sogabe, Y., Tagami, M., Tagawa, A., Takahashi, F., Takaku-Akahira, S., Takeda, Y., Tanaka, T., Tomaru, A., Toya, T., Yasunishi, A., Muramatsu, M. and Hayashizaki, Y. Direct Submission Submitted (16-APR-2002) Yoshihide Hayashizaki, The Institute of Physical and Chemical Research (RIKEN), Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center (GSC), RIKEN Yokohama Institute, 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan (E-mail: genome-res@gsr.riken.jp, URL: http://genome.gsc.riken.jp/, Tel: 81-45-503-9222, Fax: 81-45-503-9216)
TITLE JOURNAL REFERENCE AUTHORS	cDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN. Division of Experimental Animal Research in Riken contributed to prepare mouse tissues. Tissues were provided by Dr. John Todd (Dept. of Medical Genetics Wellcome Trust Centre for Molecular Mechanisms in Disease Wellcome Trust/MRC building Addenbrookes Hospital Cambridge) whose assistance we gratefully acknowledge. Please visit our web site for further details. URL: http://genome.gsc.riken.jp/ URL: http://fantom.gsc.riken.jp/ Location/Qualifiers 1. 2074 /organism="Mus musculus" /mol_type="mRNA" /strain="C57BL/6J" /db_xref="FANTOM DB:F730044H20" /db_xref="taxon:10090" /clone="F730044H20" /cell_type="86-derived CD11 +ve dendritic cells" /note="unnamed protein product; matrix metalloproteinase 8 69. .1466 (MGI:1202395, GB NM_008611, evidence: BLASTN, 99%, match=1961)
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QY      1168  ATAAGACCACAGAAACCTACTCTTCTTGTGGCATTTGCTGCTGGAGTTTGATGAA 1227
Db      1216  ATAA-----CGGGAAGACATACCTCTTCATAAACCAACGAGTGTGGAGATATGCAATC 1269
QY      1228  TGACCCAAACCATGACAAAGGATTCCTGCGAGAGTGTGTAACACACTTTCCTGGAATCA 1287
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QY      1408  GGTTCATG 1417
Db      1450  GGTAACTG 1459

RESULT 8
AK089234
LOCUS
DEFINITION
Mus musculus NOD-derived CD11c +ve dendritic cells cDNA, RIKEN
full-length enriched library, clone:F630050H05 product:matrix
metalloproteinase 8, full insert sequence.
AK089234
VERSION
AK089234.1 GI:26354353
KEYWORDS
HTC; CAP trapper.
SOURCE
Mus musculus (house mouse)
ORGANISM
Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

REFERENCE
1
Carninci,P. and Hayashizaki,Y.
High-efficiency full-length cDNA cloning
Meth. Enzymol. 303, 19-44 (1999)
99279253
MEDLINE
10349636
PUBMED
10349636
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2
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Itoh,M., Konno,H., Okazaki,Y., Muramatsu,M. and Hayashizaki,Y.
Normalization and subtraction of cap-trapper-selected cDNAs to
prepare full-length cDNA libraries for rapid discovery of new genes
Genome Res. 10 (10), 1617-1630 (2000)
20499374
MEDLINE
11042159
PUBMED
11042159
REFERENCE
3
Shibata,K., Itoh,M., Aizawa,K., Nagaoka,S., Sasaki,N., Carninci,P.,
Konno,H., Akiyama,J., Nishi,K., Kitsuami,T., Tashiro,H., Itoh,M.,
Sumi,N., Ishii,Y., Nakamura,S., Hazama,M., Nishine,I., Harada,A.,
Yamamoto,K., Matsumoto,H., Sakaguchi,S., Ikegami,T., Kashiwagi,K.,
Fujiwara,S., Inoue,K., Togawa,Y., Izawa,M., Ohara,E., Watanabe,M.,
Yoneda,Y., Ishikawa,T., Ozawa,K., Tanaka,T., Matsura,S., Kawai,J.,
Okazaki,Y., Muramatsu,M., Inoue,Y., Kita,A. and Hayashizaki,Y.
RIKEN integrated sequence analysis (RISA) system--384-format
sequencing pipeline with 384 multipillar sequencer
Genome Res. 10 (11), 1757-1771 (2000)

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MEDLINE
PUBMED
REFERENCE
AUTHORS
TITLE
JOURNAL
REFERENCE
AUTHORS
TITLE
JOURNAL
REFERENCE
AUTHORS
TITLE
JOURNAL
COMMENT
FEATURES
source
CDS

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20530913
11076861
4
The RIKEN Genome Exploration Research Group Phase II Team and the
FANTOM Consortium.
Functional annotation of a full-length mouse cDNA collection
Nature 409, 685-690 (2001)
5
The FANTOM Consortium and the RIKEN Genome Exploration Research
Group Phase I & II Team.
Analysis of the mouse transcriptome based on functional annotation
of 60,770 full-length cDNAs
Nature 420, 563-573 (2002)
6
(bases 1 to 2223)
Adachi,J., Aizawa,K., Akimura,T., Arakawa,T., Bono,H., Carninci,P.,
Fukuda,S., Furuno,M., Hanagaki,T., Hara,A., Hashizume,W.,
Hayashida,K., Hayatsu,N., Hiramoto,K., Hiraoka,T., Hirozane,T.,
Hori,F., Imotani,K., Ishii,Y., Itoh,M., Kagawa,I., Kasukawa,T.,
Kato,H., Kawai,J., Kojima,Y., Kondo,S., Konno,H., Kouda,M.,
Koya,S., Kurihara,C., Matsuyama,T., Miyazaki,A., Murata,M.,
Nakamura,M., Nishi,K., Nomura,K., Numazaki,K., Ohno,M., Ohsato,N.,
Okazaki,Y., Saito,R., Saitoh,H., Sakai,C., Sakai,K., Sakazume,N.,
Sano,H., Sasaki,D., Shibata,K., Shinagawa,A., Shiraki,T.,
Sogabe,Y., Tagami,M., Tagawa,A., Takahashi,F., Takaku-Akahira,S.,
Takeda,Y., Tanaka,T., Tomaru,A., Toya,T., Yasunishi,A.,
Muramatsu,M. and Hayashizaki,Y.
Direct Submission
Submitted (16-APR-2002) Yoshihide Hayashizaki, The Institute of
Physical and Chemical Research (RIKEN), Laboratory for Genome
Exploration Research Group, RIKEN Genomic Sciences Center (GSC),
RIKEN Yokohama Institute; 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama,
Kanagawa 230-0045, Japan (E-mail: genome-res@gsc.riken.jp,
URL:http://genome.gsc.riken.jp/, Tel:81-45-503-9222,
Fax:81-45-503-9216)
cDNA library was prepared and sequenced in Mouse Genome
Encyclopedia Project of Genome Exploration Research Group in Riken
Genomic Sciences Center and Genome Science Laboratory in RIKEN.
Division of Experimental Animal Research in Riken contributed to
prepare mouse tissues.
Tissues were provided by Dr. John Todd (Dept. of Medical Genetics
Wellcome Trust Centre for Molecular Mechanisms in Disease Wellcome
Trust/MRC Building Addenbrookes Hospital Cambridge) whose
assistance we gratefully acknowledge.
Please visit our web site for further details.
URL:http://genome.gsc.riken.jp/
URL:http://fantom.gsc.riken.jp/.
Location/Qualifiers
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ORIGIN

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 QY 217 AAATGCAAGCATTTTTTGAATTCACAGTCACTGGAATACTGGACTCAACACCCCTTGAGA 276
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 DB 1460 GGCCTTAACCTG 1469

RESULT 9

BX918107 561 bp mRNA linear EST 07-MAY-2004
 LOCUS
 DEFINITION BX918107 Sus Scrofa library (scan) Sus scrofa cDNA clone
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ACCESSION BX918107 GI:41134926

VERSION

KEYWORDS

SOURCE

ORGANISM

Sus scrofa (pig)
 Sus scrofa
 Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.

REFERENCE 1 (bases 1 to 561)

AUTHORS Bonnet,A., Tosser-Klopp,G., Benne,F., Cabau,C., Villegier,S.,
 Soares,M., Bonaldo,F. and Hatey,F.

TITLE A Pig Normalised Multi-Tissue cDNA Library

JOURNAL Unpublished (2003)

COMMENT Contact: Tosser-Klopp G

Genetique Animale

Institut National

Chemin de Borde-Rouge - Auzeville BP27, 31326 Castanet-Tolosan

Cedex, FRANCE

Tel: 33 (0) 5 61 28 51 14

Fax: 33 (0) 5 61 28 53 08

Email: tosser@oulouse.inra.fr

Sequence cleaned of vector, adaptor and repetitions. Contact us

at eigenasupport@jouy.inra.fr to obtain the chromatogram of this

sequence.

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FEATURES

source

1. .561

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skin, spleen, thymus, placenta, pituitary gland, seminal

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gland, cerebral trunk, epididymis, female gonad,

gall-bladder, hippocampus, large intestine, male gonad,

melanocytes, stomach, udder"

ORIGIN

Query Match 23.7%; Score 385.8; DB 5; Length 561;
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 Matches 452; Conservative 0; Mismatches 92; Indels 1; Gaps 1;

[illegible]

of 60,770 full-length cDNAs
 Nature 420, 563-573 (2002)
 22354683
 MEDLINE
 PUBMED
 COMMENT
 Contact: Yoshihide Hayashizaki
 Laboratory for Genome Exploration Research Group, RIKEN Genomic
 Sciences Center (GSC), Yokohama Institute
 The Institute of Physical and Chemical Research (RIKEN)
 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan
 Tel: 81-45-503-9222
 Fax: 81-45-503-9216
 Email: genome-res@gs.riken.jp, URL: http://genome.gsc.riken.jp/
 Adachi, J., Aizawa, K., Akimura, T., Arakawa, T., Carninci, P.,
 Fukuda, S., Hashizume, W., Hayashida, K., Hirozane, T., Hori, F.,
 Imotani, K., Ishii, Y., Itoh, M., Kagawa, I., Kawai, J., Kojima, Y.,
 Kondo, S., Konno, H., Koya, S., Miyazaki, A., Murata, M., Nakamura, M.,
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 Sano, H., Sasaki, D., Sato, K., Shibata, K., Shiraki, T., Tagami, M.,
 Takeda, Y., Waki, K., Watahiki, A., Muramatsu, M. and Hayashizaki, Y.
 Direct Submission
 Computational Analysis of Full-length Mouse cDNAs Compared with
 Human Genome Sequences Mamm. Genome. 12, 673-677 (2001)
 Normalization and subtraction of cap-trapper-selected cDNAs to
 prepare full-length cDNA libraries for rapid discovery of new
 genes. Genome Res. 10 (10), 1617-1630 (2000)
 RIKEN integrated sequence analysis (RISA) system--384-Format
 sequencing pipeline with 384 multicapillary sequencer. Genome Res.
 10 (11), 1757-1771 (2000)

Computer-based methods for the mouse full-length cDNA
 encyclopedia: real-time sequence clustering for construction of a
 nonredundant cDNA library. Genome Res. 11 (2), 281-289 (2001)
 cDNA library was prepared and sequenced in Mouse Genome
 Encyclopedia Project of Genome Exploration Research Group in Riken
 Genomic Sciences Center and Genome Science Laboratory in RIKEN.
 Division of Experimental Animal Research in Riken contributed to
 prepare mouse tissues.
 Tissues were provided by Dr. John Todd (Dept. of Medical Genetics
 Wellcome Trust Centre for Molecular Mechanisms in Disease Wellcome
 Trust/MRC Building Addenbrookes Hospital Cambridge) whose
 assistance we gratefully acknowledge.
 Please visit our web site (http://genome.gsc.riken.go.jp) for
 further details.

FEATURES

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 REFERENCE 1 (bases 1 to 1784)
 AUTHORS Li, W.B., Gruber, C., Jessee, J. and Polayes, D.
 TITLE Full-length cDNA libraries and normalization
 JOURNAL Unpublished
 REMARK Contact: Feng Liang Email: fliang@lifetech.com URL :
 http://fulllength.invitrogen.com/ Invitrogen Corporation 1600
 Faraday Avenue
 REFERENCE 2 (bases 1 to 1784)
 AUTHORS Genoscope.
 TITLE Direct Submission
 JOURNAL Submitted (20-JUL-2004) Genoscope - Centre National de Sequencage :
 BP 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr
 - Web : www.genoscope.cns.fr)
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RESULT 13
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ACCESSION AK089336
 VERSION AK089336.1 GI:26105213
 KEYWORDS HTC; CAP trapper
 SOURCE Mus musculus (house mouse)
 ORGANISM Mus musculus

REFERENCE 1
 AUTHORS Carninci, P. and Hayashizaki, Y.
 TITLE High-efficiency full-length cDNA cloning
 JOURNAL Meth. Enzymol. 303, 19-44 (1999)
 MEDLINE 99279253
 PUBMED 10349636

REFERENCE 2
 AUTHORS Carninci, P., Shibata, Y., Hayatsu, N., Sugahara, Y., Shibata, K.,
 Itoh, M., Konno, H., Okazaki, Y., Muramatsu, M. and Hayashizaki, Y.
 TITLE Normalization and subtraction of cap-trapper-selected cDNAs to
 prepare full-length cDNA libraries for rapid discovery of new genes
 JOURNAL Genome Res. 10 (10), 1617-1630 (2000)
 MEDLINE 20499374
 PUBMED 11042159

REFERENCE 3
 AUTHORS Shibata, K., Itoh, M., Aizawa, K., Nagaoka, S., Sasaki, N., Carninci, P.,
 Konno, H., Akiyama, J., Nishi, K., Kitsumai, T., Tashiro, H., Itoh, M.,
 Sumi, N., Ishii, Y., Nakamura, S., Hazama, M., Nishine, T., Harada, A.,
 Yamamoto, R., Matsumoto, H., Sakaguchi, S., Ikegami, T., Kashiwagi, K.,
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 Yoneda, Y., Ishikawa, T., Ozawa, K., Tanaka, T., Matsuura, S., Kawai, J.,
 Okazaki, Y., Muramatsu, M., Inoue, Y., Kira, A. and Hayashizaki, Y.
 TITLE RIKEN integrated sequence analysis (RISA) system--384-format
 sequencing pipeline with 384 multicapillary sequencer
 JOURNAL Genome Res. 10 (11), 1757-1771 (2000)
 MEDLINE 20530913
 PUBMED 11076861

REFERENCE 4
 AUTHORS The RIKEN Genome Exploration Research Group Phase II Team and the
 FANTOM Consortium.
 TITLE Functional annotation of a full-length mouse cDNA collection
 JOURNAL Nature 409, 685-690 (2001)

REFERENCE 5
 AUTHORS The FANTOM Consortium and the RIKEN Genome Exploration Research
 Group Phase I & II Team.
 TITLE Analysis of the mouse transcriptome based on functional annotation
 of 60,770 full-length cDNAs
 JOURNAL Nature 420, 563-573 (2002)
 MEDLINE (bases 1 to 2427)
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Katoh, H., Kawai, J., Kojima, Y., Kondo, S., Konno, H., Kouda, M., Koya, S., Kurihara, C., Matsuyama, T., Miyazaki, A., Murata, M., Nakamura, M., Nishi, K., Nomura, K., Numazaki, R., Ohno, M., Ohsato, N., Okazaki, Y., Saito, R., Saitoh, H., Sakai, C., Sakai, K., Sakazume, N., Sano, H., Sasaki, D., Shibata, K., Shinagawa, A., Shiraki, T., Sogabe, Y., Tgam, M., Tagawa, A., Takahashi, F., Takaku-Akahira, S., Takeda, Y., Tanaka, T., Tomaru, A., Toya, T., Yasunishi, A., Muramatsu, M. and Hayashizaki, Y.

TITLE

JOURNAL

Submitted (16-APR-2002) Yoshihide Hayashizaki, The Institute of Physical and Chemical Research (RIKEN), Laboratory for Genome Exploration and Research Group, RIKEN Genomic Sciences Center (GSC), RIKEN Yokohama Institute; 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan [E-mail: genome-res@gsc.riken.jp, URL: http://genome.gsc.riken.jp/, Tel: 81-45-503-9222, Fax: 81-45-503-9216]

COMMENT

cDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN. Division of Experimental Animal Research in Riken contributed to prepare mouse tissues. Tissues were provided by Dr. John Todd (Dept. of Medical Genetics Wellcome Trust Centre for Molecular Mechanisms in Disease Wellcome Trust/MRC building Addenbrookes Hospital Cambridge) whose assistance we gratefully acknowledge. Please visit our web site for further details. URL: http://genome.gsc.riken.jp/ URL: http://fantom.gsc.riken.jp/

FEATURES

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Hillier, L., Allen, M., Bowles, L., Dubuque, T., Geisel, G., Jost, S.,
Kucaba, T., Lacy, M., Le, N., Lennon, G., Marra, M., Martin, J.,
Moore, B., Schellenberg, K., Steptoe, M., Tan, F., Theising, B.,
White, Y., Wyllie, T., Waterston, R. and Wilson, R.
WashU-Merck EST Project 1997
Unpublished (1997)
Contact: Wilson RK
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
Email: est@watson.wustl.edu
This clone is available royalty-free through LNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
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were made in vitro. Following HAP purification, this DNA
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1 Carninci, P. and Hayashizaki, Y.
 High-efficiency full-length cDNA cloning
 Meth. Enzymol. 303, 19-44 (1999)
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2
 Carninci, P., Shibata, Y., Hayatsu, N., Sugahara, Y., Shibata, K.,
 Itoh, M., Konno, H., Okazaki, Y., Muramatsu, M. and Hayashizaki, Y.
 Normalization and subtraction of cap-trapper-selected cDNAs to
 prepare full-length cDNA libraries for rapid discovery of new genes
 Genome Res. 10 (10), 1617-1630 (2000)
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3
 Shibata, K., Itoh, M., Aizawa, K., Nagaoka, S., Sasaki, N., Carninci, P.,
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 Okazaki, Y., Muramatsu, M., Inoue, Y., Kira, A. and Hayashizaki, Y.
 RIKEN integrated sequence analysis (RISA) system--384-format
 sequencing pipeline with 384 multicapillary sequencer
 Genome Res. 10 (11), 1757-1771 (2000)
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4
 The RIKEN Genome Exploration Research Group Phase II Team and the
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 Functional annotation of a full-length mouse cDNA collection
 Nature 409, 685-690 (2001)

5
 The FANTOM Consortium and the RIKEN Genome Exploration Research
 Group Phase I & II Team.
 Analysis of the mouse transcriptome based on functional annotation
 of 60,770 full-length cDNAs
 Nature 420, 563-573 (2002)
 6 (bases 1 to 1798)
 Adachi, J., Aizawa, K., Akimura, T., Arakawa, T., Bono, H., Carninci, P.,
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 AUTHORS

source

Muramatsu, M. and Hayashizaki, Y.

Submitted (16-Apr-2002)

Physical and Chemical Research (RIKEN), Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center (GSC), RIKEN Yokohama Institute; 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan (E-mail: genome-res@gs.riken.jp, URL: http://genome.gsc.riken.jp/, Tel: 81-45-503-9222, Fax: 81-45-503-9216)

CDNA library was prepared and sequenced in Mouse Genome

Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN. Division of Experimental Animal Research in Riken contributed to prepare mouse tissues.

Tissues were provided by Dr. John Todd (Dept. of Medical Genetics Wellcome Trust Centre for Molecular Mechanisms in Disease Wellcome Trust/MRC building Addenbrookes Hospital Cambridge) whose assistance we gratefully acknowledge.

Please visit our web site for further details.

URL: http://genome.gsc.riken.jp/

URL: http://fantom.gsc.riken.jp/

Location/Qualifiers

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GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.

OM protein - protein search, using sw model

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SUMMARIES

Result No.	Score	% Match	Query Match	Length	DB ID	Description
1	2763	100.0	513	3	AA90293	Human pep
2	2763	100.0	513	5	AAE14392	Human mat
3	2752	99.6	513	4	AAU12267	Human PRO
4	2752	99.6	513	4	AAU00469	Human TAN
5	2752	99.6	513	6	ABO17711	Novel hum
6	2752	99.6	513	6	ABU80965	Human PRO
7	2752	99.6	513	6	ABU66665	Human PRO
8	2752	99.6	513	6	ABO32578	Secreted
9	2752	99.6	513	6	ABU59746	Novel sec
10	2752	99.6	513	6	ABO24936	Human sec
11	2752	99.6	513	6	ABU66941	Human sec
12	2752	99.6	513	6	ADA45711	Novel hum
13	2752	99.6	513	6	ADA76142	Human PRO
14	2752	99.6	513	6	ADA18792	Human PRO
15	2752	99.6	513	6	ADA61415	Homo sapi
16	2752	99.6	513	6	ADB19200	Novel hum
17	2752	99.6	513	6	ADB27741	Human PRO
18	2752	99.6	513	6	ADA86220	Novel hum
19	2752	99.6	513	6	ADA15784	Human PRO
20	2752	99.6	513	6	ADA47570	Human PRO
21	2752	99.6	513	6	ADA67365	Human PRO
22	2752	99.6	513	6	ADB30372	Human PRO
23	2752	99.6	513	6	ADA85668	Novel hum
24	2752	99.6	513	6	ADA96880	Human PRO
25	2752	99.6	513	6	ADA79184	Human PRO

ALIGNMENTS

RESULT 1

AA90293
ID AAY90293 standard; protein; 513 AA.

XX AC AAY90293;

DT 24-OCT-2000 (first entry)

XX Human peptidase, HPEP-10 protein sequence.

XX Human; peptidase; cell proliferative disorder; arteriosclerosis;
psoriasis; myelofibrosis; cancer; autoimmune disorder; Crohn's disease;
inflammatory disorder; AIDS; anaemia; allergy; asthma; atherosclerosis;
Grave's disease; multiple sclerosis; scleroderma; infection; diabetes;
metabolic disorder; Addison's disease; cystic fibrosis; diagnosis;
glycogen storage disease; obesity; therapy; HPEP-10.

XX Homo sapiens.

XX WO200042201-A2.

XX 20-JUL-2000.

XX 11-JAN-2000; 2000WO-US000641.

XX 11-JAN-1999; 99US-0172247P.

XX 03-MAY-1999; 99US-0132253P.

XX 27-MAY-1999; 99US-0136653P.

XX (INCY-) INCYTE PHARM INC.

XX Bandman O, Hillman JL, Tang YT, Azimzai Y, Baughn MR, Lal P;
Yue H, Lu DAM;

XX WPI; 2000-482832/42.

XX N-PSDB; AAA37666.

XX An isolated polypeptide for diagnosis, prevention and treatment of cell
proliferative, autoimmune/ inflammatory and metabolic disorders comprises
a sequence encoding a human peptidase.

XX Claim 2; Page 100-101; 131pp; English.

XX This sequence represents a human peptidase, designated HPEP-10. The
invention relates to 18 human peptidases designated HPEP-1 to HPEP-18,
respectively. The peptidases can be used for treating a disease or
condition associated with decreased expression or over expression of
functional human peptidases. The diseases that can be diagnosed,

26	2752	99.6	513	6	ADA87323	Novel hum
27	2752	99.6	513	6	ADB16525	Human PRO
28	2752	99.6	513	6	ADA91617	Novel hum
29	2752	99.6	513	6	ADB14680	Human PRO
30	2752	99.6	513	6	ADB18641	Novel hum
31	2752	99.6	513	6	ADA93856	Human PRO
32	2752	99.6	513	6	ADB19752	Novel hum
33	2752	99.6	513	6	ADB13064	Human PRO
34	2752	99.6	513	6	ABO43244	Novel hum
35	2752	99.6	513	6	ADA74318	Human PRO
36	2752	99.6	513	6	ADB24551	Human PRO
37	2752	99.6	513	6	ADA82075	Human PRO
38	2752	99.6	513	6	ADA75038	Human PRO
39	2752	99.6	513	6	ADA85116	Human PRO
40	2752	99.6	513	6	ADA84564	Novel hum
41	2752	99.6	513	6	ADB29820	Human PRO
42	2752	99.6	513	6	ADA80348	Human PRO
43	2752	99.6	513	6	ADA75590	Human PRO
44	2752	99.6	513	6	ADA46815	Human PRO
45	2752	99.6	513	6	ADB25111	Human PRO

Db 361 PKSIHTLGFPRVKKIDAAVCDKTRKTYFVGIWCRWFDEMTQTMKGFQVRVXHPG 420
QY 421 ISIRVDAARQYKGFPSRSGKQFENYIKTKNITRIMRTNTWFOCKEPKNSSGFDINKE 480
Db 421 ISIRVDAARQYKGFPSRSGKQFENYIKTKNITRIMRTNTWFOCKEPKNSSGFDINKE 480
QY 481 KAHSGGKILYHKSLSLFIFGIHVHLLKNTSIYQ 513
Db 481 KAHSGGKILYHKSLSLFIFGIHVHLLKNTSIYQ 513
RESULT 3
AAU12267
ID AAU12267 standard; protein; 513 AA.
XX
AC AAU12267;
XX
DT 24-OCT-2001 (first entry)
XX
DE Human PRO5992 polypeptide sequence.
XX
KW Human secretory and transmembrane; PRO; mammalian; cancer; lung; breast;
KW prostate; cervical; tumour necrosis factor-alpha; TNF-alpha; cartilage;
KW ear; proliferation; glucose; free fatty acid; skeletal muscle; adipocyte;
KW A-peptide; factor VIIA; gene therapy.
XX
OS Homo sapiens.
XX
PN WO20010466-A2.
XX
PD 07-JUN-2001.
XX
PF 01-DEC-2000; 2000WO-US032678.
XX
PR 01-DEC-1999; 99WO-US028301.
PR 01-DEC-1999; 99WO-US028634.
PR 02-DEC-1999; 99WO-US028551.
PR 02-DEC-1999; 99WO-US028564.
PR 02-DEC-1999; 99WO-US028565.
PR 09-DEC-1999; 99US-0170262P.
PR 16-DEC-1999; 99WO-US030095.
PR 20-DEC-1999; 99WO-US030911.
PR 20-DEC-1999; 99WO-US030999.
PR 30-DEC-1999; 99WO-US031243.
PR 30-DEC-1999; 99WO-US031274.
PR 05-JAN-2000; 2000WO-US000219.
PR 06-JAN-2000; 2000WO-US000277.
PR 06-JAN-2000; 2000WO-US000376.
PR 11-FEB-2000; 2000WO-US003565.
PR 18-FEB-2000; 2000WO-US004341.
PR 18-FEB-2000; 2000WO-US004342.
PR 22-FEB-2000; 2000WO-US004414.
PR 24-FEB-2000; 2000WO-US004914.
PR 24-FEB-2000; 2000WO-US005004.
PR 01-MAR-2000; 2000WO-US005601.
PR 02-MAR-2000; 2000WO-US005841.
PR 03-MAR-2000; 2000US-0187202P.
PR 10-MAR-2000; 2000WO-US006319.
PR 15-MAR-2000; 2000WO-US006884.
PR 20-MAR-2000; 2000WO-US007377.
PR 21-MAR-2000; 2000WO-US007532.
PR 30-MAR-2000; 2000WO-US008439.
PR 17-MAY-2000; 2000WO-US013705.
PR 22-MAY-2000; 2000WO-US014042.
PR 30-MAY-2000; 2000WO-US014941.
PR 02-JUN-2000; 2000WO-US015264.
PR 05-JUN-2000; 2000US-0209832P.
PR 28-JUL-2000; 2000WO-US020710.
PR 11-AUG-2000; 2000WO-US022031.
PR 23-AUG-2000; 2000WO-US023522.
PR 24-AUG-2000; 2000WO-US023328.
PR 08-NOV-2000; 2000WO-US030952.

PR 10-NOV-2000; 2000WO-US030873.
XX (GETH) GENENTECH INC.
PA Baker KP, Beresini M, Deforge L, Desnoyers L, Filvaroff E, Gao W;
PI Gerritsen ME, Goddard A, Godowski PJ, Gurney AL, Sherwood S;
PI Smith V, Stewart TA, Tumas D, Watanabe CK, Wood WI, Zhang Z;
XX WPI; 2001-408281/43.
DR N-PSDB; AAS21339.
XX
XX Isolated , secretory and transmembrane PRO polypeptide used to detect
PT other PRO polypeptides, link bioactive molecules to cells expressing PRO
PT polypeptides, and detect the presence of mammalian tumors e.g. lung,
PT breast, prostate, cervical.
XX
XX Claim 12; Fig 192; 813pp; English.
PS
XX AAU12172-AAU12446 represent novel human secretory and transmembrane PRO
CC polypeptides. The PRO polypeptides are useful to detect other PRO
CC polypeptides, to link bioactive molecules to cells expressing PRO
CC polypeptides, to modulate biological activities of cells expressing PRO
CC polypeptides, and to detect the presence of mammalian lung, colon,
CC breast, prostate, rectal, cervical or liver tumours by comparing PRO
CC polypeptide expression in a cell sample to that in a control sample. Some
CC of the 275 sequences are also useful to stimulate the release of tumour
CC necrosis factor-alpha (TNF-alpha) from human blood, the proliferation or
CC differentiation of chondrocytes, the proliferation or gene expression in
CC pericyte cells, the release of proteoglycans from cartilage, the
CC proliferation of inner ear utricular supporting cells or of T-
CC lymphocytes, the release of a cytokine from peripheral blood monocytes
CC (PBMCs), or the proliferation of endothelial cells. Some of the PRO
CC polypeptides may modulate glucose or free fatty acid uptake by skeletal
CC muscle cells or by adipocytes; or inhibit binding of A-peptide to factor
CC VIIA. The PRO polypeptides can be used in assays to identify molecules
CC involved in binding interactions. The polynucleotides encoding PRO
CC polypeptides can be used to generate probes, antisense RNA/DNA,
CC transgenic or knock out animals and can be used in gene therapy
XX
SQ Sequence 513 AA;
Query Match 99.6%; Score 2752; DB 4; Length 513;
Best Local Similarity 99.8%; Pred. No. 4, 1e-261;
Matches 512; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1 MKRLLLCLFFITFSSAPFLVRMTENENMQAAYLNQFYSLETEGNHLVQSKRSLID 60
Db 1 MKRLLLCLFFITFSSAPFLVRMTENENMQAAYLNQFYSLETEGNHLVQSKRSLID 60
QY 61 DKIREMQAFGLTVTKLDSNTLEIMTKPRCGVDPVQGYTLPGWRKYNLYRIINYP 120
Db 61 DKIREMQAFGLTVTKLDSNTLEIMTKPRCGVDPVQGYTLPGWRKYNLYRIINYP 120
QY 121 DMARAAVDEAIQEGLEVWMSKVTPLKFTKISKGIADIMIAFRTRVHRCRCPRYDGLGVLG 180
Db 121 DMARAAVDEAIQEGLEVWMSKVTPLKFTKISKGIADIMIAFRTRVHRCRCPRYDGLGVLG 180
QY 181 HAPPPGPGGLGGDTHFDEDENWTKDAGFNLFLVAAHEFGHALGSLHSDQATALMPFNYS 240
Db 181 HAPPPGPGGLGGDTHFDEDENWTKDAGFNLFLVAAHEFGHALGSLHSDQATALMPFNYS 240
QY 241 LDPRKYPVLSQDDINGIQSIYGGLPKVPAPKPEPTPHACDDPLTDATITTFREVMFPKG 300
Db 241 LDPRKYPVLSQDDINGIQSIYGGLPKVPAPKPEPTPHACDDPLTDATITTFREVMFPKG 300
QY 301 RHLWRIYYDITDVEFELIASFWPSLPADLQAAAYENPRDKILVFKDENFMWIRGAVLPDY 360
Db 301 RHLWRIYYDITDVEFELIASFWPSLPADLQAAAYENPRDKILVFKDENFMWIRGAVLPDY 360
QY 361 PKSIHTLGFPRVKKIDAAVCDKTRKTYFFVGIWCRWFDEMTQTMKGFQVRVXHPG 420
Db 361 PKSIHTLGFPRVKKIDAAVCDKTRKTYFFVGIWCRWFDEMTQTMKGFQVRVXHPG 420

QY 421 ISIRVDAAFQYKGFPPSRGSKQFEYNKTKNITRMTNTWFOCKEPKNSFGFDINKE 480
 Db 421 ISIRVDAAFQYKGFPPSRGSKQFEYNKTKNITRMTNTWFOCKEPKNSFGFDINKE 480
 QY 481 KAHSGGKILYHKLSLSLFIIGIVHLLKNTSIYQ 513
 Db 481 KAHSGGKILYHKLSLSLFIIGIVHLLKNTSIYQ 513

RESULT 4
 AAU00469
 ID AAU00469 standard; protein; 513 AA.
 XX
 AC AAU00469;
 XX
 DT 04-JUL-2001 (first entry)
 XX
 DE Human TANGO 210 protein.
 XX
 KW Human; TANGO 210; clone jthke034a06; TANGO 364; TANGO 366; INTERCEPT 394;
 KW INTERCEPT 400; TANGO 405; cellular process regulator; gene therapy;
 KW MMP-8; matrix metalloproteinase-8; proteinase activity;
 KW extracellular matrix; kidney disorder; bone marrow disorder;
 KW skin disorder; vascular hypertension; metastatic cancer.
 XX
 OS Homo sapiens.
 XX
 FH Key Location/Qualifiers
 FT Peptide 1..17
 FT /label= Signal peptide
 FT /note= "Specifically claimed"
 FT Protein 18..513
 FT /label= Mature TANGO_210 protein
 FT /note= "Specifically claimed"
 FT Domain 18..488
 FT /note= "Optionally in alternative form #1 this domain is
 FT extracellular or in alternative form #2 this domain is
 FT intracellular. Specifically claimed"
 FT Domain 489..506
 FT /label= Transmembrane domain
 FT /note= "Specifically claimed"
 FT Domain 507..513
 FT /note= "Optionally in alternative form #1 this domain is
 FT intracellular or in alternative form #2 this domain is
 FT extracellular. Specifically claimed"
 XX
 FN WO200118016-A1.
 XX
 PD 15-MAR-2001.
 XX
 PF 30-JUN-2000; 2000WO-US018174.
 XX
 PR 10-SEP-1999; 98US-00393996.
 XX
 PA (MILL-) MILLENNIUM PHARM INC.
 XX
 PI Fraser CC, Sharp JD, Wrighton N, Myers PS, Goodearl ADJ;
 XX
 DR WPI; 2001-183280/18.
 DR N-PSDB; AAS01367.
 XX
 PT Isolated nucleic acid molecules encoding proteins useful as modulating
 PT agents in regulating a variety of cellular processes are used for
 PT treating e.g. cancer and autoimmune disorders.
 XX
 PS Claim 9; Fig 1A-ID; 326pp; English.
 XX
 CC The present sequence representing human TANGO 210 protein is isolated
 CC from cDNA clone jthke034a06 from a human foetal skin cDNA library. It is
 CC 1 of 6 novel human proteins which include TANGO 364 (AAU00471), TANGO 366
 CC (AAU00472), INTERCEPT 394 (AAU00473), INTERCEPT 400 (AAU00476), and TANGO
 CC 405 (AAU00479). Novel sequences for murine TANGO 210 (AAU00470),
 CC INTERCEPT 400 (AAU00477), TANGO 405 (AAU00480) and a rat INTERCEPT 400

CC (AAU00478) sequence are also described. The nucleic acids encoding these
 CC novel proteins are useful as modulating agents in regulating a variety of
 CC cellular processes and can be used to express the proteins in a host cell
 CC in gene therapy applications. Human TANGO 210 shows sequence homology to
 CC human MMP-8 (matrix metalloproteinase-8). TANGO 210 exhibits proteinase
 CC activity used to degrade one or more proteinaceous components of the
 CC extracellular matrix and can be used to prevent, diagnose or treat
 CC kidney, bone marrow or skin disorders e.g. vascular hypertension, acute
 CC renal failure and metastatic cancers. Note: This sequence has residues
 CC 309-513 missing in the sequence ID listing but the complete sequence is
 CC found in Fig1A-ID
 XX
 XX Sequence 513 AA;

Query Match 99.6%; Score 2752; DB 4; Length 513;
 Best Local Similarity 99.8%; Pred. No. 4.le-261;
 Matches 512; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 1 MKRLLLLCLFFITPSSAPPLVRMTENEENMQLAQAYLNQFYSLEIEGNHLVQSKNRSLLID 60
 Db 1 MKRLLLLCLFFITPSSAPPLVRMTENEENMQLAQAYLNQFYSLEIEGNHLVQSKNRSLLID 60
 QY 61 DKIREMAAFGLTVTGKLDNTLEIMKTPRCGVPDVGQYGTLLPGWKYNLYIINYP 120
 Db 61 DKIREMAAFGLTVTGKLDNTLEIMKTPRCGVPDVGQYGTLLPGWKYNLYIINYP 120
 QY 121 DMAAAVDEAIOEGLEVSKVTPPLKFTKISKGIADIMAFRTRVHGRCPRYDFDGLGVIG 180
 Db 121 DMAAAVDEAIOEGLEVSKVTPPLKFTKISKGIADIMAFRTRVHGRCPRYDFDGLGVIG 180
 QY 181 HAFPPGGLGGDTHFDEDEENWTKDAGFNFLVAAHEFGHALGSHNSDQALMFPNYS 240
 Db 181 HAFPPGGLGGDTHFDEDEENWTKDAGFNFLVAAHEFGHALGSHNSDQALMFPNYS 240
 QY 241 LDPKPYLSQDDINGIOSIYGLPKVPAPKEPTIPHACDDPLDFDAITTFRRVMPFKG 300
 Db 241 LDPKPYLSQDDINGIOSIYGLPKVPAPKEPTIPHACDDPLDFDAITTFRRVMPFKG 300
 QY 301 RHLWRIYDITDVEFELIASFWPSLPADLQAAVENPRDKILVFXDENFWFMRGVAVLDPY 360
 Db 301 RHLWRIYDITDVEFELIASFWPSLPADLQAAVENPRDKILVFXDENFWFMRGVAVLDPY 360
 QY 361 PKSHTLTGFPGRVKKIDAAVCDTKTRTYFFVGVWCWRFDEMTQTMDFKPPQVRVKKPPG 420
 Db 361 PKSHTLTGFPGRVKKIDAAVCDTKTRTYFFVGVWCWRFDEMTQTMDFKPPQVRVKKPPG 420
 QY 421 ISIRVDAAFQYKGFPPSRGSKQFEYNKTKNITRMTNTWFOCKEPKNSFGFDINKE 480
 Db 421 ISIRVDAAFQYKGFPPSRGSKQFEYNKTKNITRMTNTWFOCKEPKNSFGFDINKE 480
 QY 481 KAHSGGKILYHKLSLSLFIIGIVHLLKNTSIYQ 513
 Db 481 KAHSGGKILYHKLSLSLFIIGIVHLLKNTSIYQ 513

RESULT 5

ABO17711
 ID ABO17711 standard; protein; 513 AA.
 XX
 AC ABO17711;
 XX
 DT 26-AUG-2003 (first entry)
 XX
 DE Novel human secreted and transmembrane protein PRO5992.
 XX
 KW Human; secreted and transmembrane protein; PRO; antiinflammatory;
 KW antiarteriosclerotic; cardiant; anti-infertility; anti-HIV; cytostatic;
 KW antidiabetic; gene therapy; tumour necrosis factor (TNF)-alpha release;
 KW TNF-alpha release; cell proliferation; cell differentiation;
 KW gene expression modulator; proteoglycan release; cytokine release;
 KW tumour; inflammatory disease; organ failure; atherosclerosis;
 KW cardiac injury; infertility; birth defect; premature aging; AIDS;
 KW acquired immunodeficiency syndrome; cancer; diabetic complication;

CC diagnostics, biosensors or bioreactors. Both are useful in tissue typing.
CC This is the amino acid sequence of a novel human secreted and
CC transmembrane PRO polypeptide
XX
SQ Sequence 513 AA;

Query Match 99.6%; Score 2752; DB 6; Length 513;
Best Local Similarity 99.8%; Pred. No. 4.1e-261;
Matches 512; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 MKRLLLCLFPIITSSAPFLVRMTENENMQLAQAYLNQFYSLEIEGHNHLVQSKNRLSLID 60
DB 1 MKRLLLCLFPIITSSAPFLVRMTENENMQLAQAYLNQFYSLEIEGHNHLVQSKNRLSLID 60
QY 61 DKIREMAQFGLTVTKGLDNTLSEIMTKPRCGVDPVQGYGTLPGWRKYNLTIRIINYP 120
DB 61 DKIREMAQFGLTVTKGLDNTLSEIMTKPRCGVDPVQGYGTLPGWRKYNLTIRIINYP 120
QY 121 DMARAAVDEAIOEGLEWVSKVTPLEKFTKISGDIADIMAFRTRVHGRCPRYFDGPLGVLG 180
DB 121 DMARAAVDEAIOEGLEWVSKVTPLEKFTKISGDIADIMAFRTRVHGRCPRYFDGPLGVLG 180
QY 181 HAPPPGCLGDTDFEDENWTKDAGFNFLVAHFEFGHALGSHSNDQTALMFNPVVS 240
DB 181 HAPPPGCLGDTDFEDENWTKDAGFNFLVAHFEFGHALGSHSNDQTALMFNPVVS 240
QY 241 LDPKPYLSQDINGISYIGGLPKVPKPKPEPTIPHACDPLDFTDAITFRFVMPFKG 300
DB 241 LDPKPYLSQDINGISYIGGLPKVPKPKPEPTIPHACDPLDFTDAITFRFVMPFKG 300
QY 301 RHLWRIYDIIDVFELIASFWPSLPADLQAAAYENPRDKILVFDENFWMIRGVAVLPDY 360
DB 301 RHLWRIYDIIDVFELIASFWPSLPADLQAAAYENPRDKILVFDENFWMIRGVAVLPDY 360
QY 361 PKSIHTLGFPGVRKKIDAAVCDKTRTKTYFFVGICWRFDEMTQTMKGFPQVRVVKHPPG 420
DB 361 PKSIHTLGFPGVRKKIDAAVCDKTRTKTYFFVGICWRFDEMTQTMKGFPQVRVVKHPPG 420
QY 421 ISIRVDAAFQYKGFPPFSRSGSQFEYNIKTNIIRIMTNTWFOCKEPKNSFGFDINKE 480
DB 421 ISIRVDAAFQYKGFPPFSRSGSQFEYNIKTNIIRIMTNTWFOCKEPKNSFGFDINKE 480
QY 481 KAHSGGIKILYKLSLFIIGVHLLKNTSIYQ 513
DB 481 KAHSGGIKILYKLSLFIIGVHLLKNTSIYQ 513

RESULT 6

ABU80965
ID ABU80965 standard; protein; 513 AA.
XX AC ABU80965;
XX AC
DT 23-JUN-2003 (first entry)
XX AC
DE Human PRO polypeptide #96.
XX AC
KW Human; PRO polypeptide; secreted and transmembrane protein;
KW anti-PRO antibody; diagnostic assay; gene expression; diabetes;
KW bone disorder; cartilage disorder; rheumatoid arthritis; obesity;
KW sports injury; osteoarthritis; hyper-insulinaemia; hypo-insulinaemia;
KW hearing loss; coagulation disorder; stroke; heart attack; cardiac;
KW antidiabetic; anorectic; vulnery; antiarthritic; osteopathic;
KW antirheumatic; auditory; cerebroprotective; angiogenic.
OS Homo sapiens.
XX AC
EN US2003004311-A1.
XX AC
PD 02-JAN-2003.
XX AC
PF 19-DEC-2001; 2001US-00028072.
XX AC

PR 18-JUN-1997; 97US-0049911P.
PR 26-AUG-1997; 97US-0056974P.
PR 17-SEP-1997; 97US-0059113P.
PR 17-SEP-1997; 97US-0059115P.
PR 17-SEP-1997; 97US-0059117P.
PR 17-SEP-1997; 97US-0059122P.
PR 18-SEP-1997; 97US-0059184P.
PR 18-SEP-1997; 97US-0059263P.
PR 19-SEP-1997; 97US-0059352P.
PR 19-SEP-1997; 97US-0059588P.
PR 24-SEP-1997; 97US-0059836P.
PR 17-OCT-1997; 97US-0062250P.
PR 17-OCT-1997; 97US-0062285P.
PR 17-OCT-1997; 97US-0062287P.
PR 17-OCT-1997; 97US-0063755P.
PR 24-OCT-1997; 97US-0062814P.
PR 24-OCT-1997; 97US-0062816P.
PR 24-OCT-1997; 97US-0063045P.
PR 24-OCT-1997; 97US-0063082P.
PR 24-OCT-1997; 97US-0063127P.
PR 27-OCT-1997; 97US-0063327P.
PR 27-OCT-1997; 97US-0063329P.
PR 28-OCT-1997; 97US-0063550P.
PR 28-OCT-1997; 97US-0063561P.
PR 28-OCT-1997; 97US-0063704P.
PR 29-OCT-1997; 97US-0063733P.
PR 29-OCT-1997; 97US-0063735P.
PR 29-OCT-1997; 97US-0063738P.
PR 03-NOV-1997; 97US-0064248P.
PR 07-NOV-1997; 97US-0064809P.
PR 12-NOV-1997; 97US-0065186P.
PR 17-NOV-1997; 97US-0065846P.
PR 21-NOV-1997; 97US-0065636P.
PR 24-NOV-1997; 97US-0066453P.
PR 24-NOV-1997; 97US-0066511P.
PR 24-NOV-1997; 97US-0066770P.
PR 11-DEC-1997; 97US-0069212P.
PR 11-DEC-1997; 97US-0069278P.
PR 16-DEC-1997; 97US-0069334P.
PR 16-DEC-1997; 97US-0069694P.
PR 23-JAN-1998; 98US-0072320P.
PR 04-FEB-1998; 98US-0073612P.
PR 09-FEB-1998; 98US-0074086P.
PR 09-FEB-1998; 98US-0074092P.
PR 12-MAR-1998; 98US-0077791P.
PR 20-MAR-1998; 98US-0078910P.
PR 25-MAR-1998; 98US-0079294P.
PR 27-MAR-1998; 98US-0079663P.
PR 31-MAR-1998; 98US-0080165P.
PR 12-JUN-1998; 98US-008012456.
PR 28-AUG-1998; 98US-008017888.
PR 10-SEP-1998; 98US-008018824.
PR 14-SEP-1998; 98US-008019093.
PR 14-SEP-1998; 98US-008019094.
PR 16-SEP-1998; 98US-008019177.
PR 16-SEP-1998; 98US-008019330.
PR 17-SEP-1998; 98US-008019437.
PR 07-OCT-1998; 98US-008021141.
PR 29-OCT-1998; 98US-008022991.
PR 29-OCT-1998; 98US-008022992.
PR 20-NOV-1998; 98US-008024855.
PR 01-DEC-1998; 98US-008025108.
PR 05-JAN-1999; 99US-008000106.
PR 08-MAR-1999; 99US-008005028.
PR 10-MAR-1999; 99US-008005190.
PR 20-APR-1999; 99US-008008615.
PR 14-MAY-1999; 99US-008010733.
PR 02-JUN-1999; 99US-008012252.
PR 01-SEP-1999; 99US-008020111.
PR 08-SEP-1999; 99US-008020594.
PR 13-SEP-1999; 99US-008020944.

PR 15-SEP-1999; 99WO-US021090.
 PR 15-SEP-1999; 99WO-US021547.
 PR 15-OCT-1999; 99WO-US023089.
 PR 29-NOV-1999; 99WO-US028214.
 PR 30-NOV-1999; 99WO-US028313.
 PR 30-NOV-1999; 99WO-US028409.
 PR 01-DEC-1999; 99WO-US028301.
 PR 01-DEC-1999; 99WO-US028634.
 PR 02-DEC-1999; 99WO-US028551.
 PR 02-DEC-1999; 99WO-US028564.
 PR 02-DEC-1999; 99WO-US028565.
 PR 16-DEC-1999; 99WO-US030095.
 PR 20-DEC-1999; 99WO-US030911.
 PR 20-DEC-1999; 99WO-US030999.
 PR 30-DEC-1999; 99WO-US031243.
 PR 30-DEC-1999; 99WO-US031274.
 PR 05-JAN-2000; 2000WO-US000219.
 PR 06-JAN-2000; 2000WO-US000277.
 PR 06-JAN-2000; 2000WO-US000376.
 PR 11-FEB-2000; 2000WO-US0003565.
 PR 18-FEB-2000; 2000WO-US004341.
 PR 18-FEB-2000; 2000WO-US004342.
 PR 22-FEB-2000; 2000WO-US004414.
 PR 24-FEB-2000; 2000WO-US004914.
 PR 24-FEB-2000; 2000WO-US005004.
 PR 01-MAR-2000; 2000WO-US005601.
 PR 02-MAR-2000; 2000WO-US005746.
 XX
 PA (GETH) GENENTECH INC.
 XX
 PI Baker KP, Beresini M, Deforge L, Desnoyers L, Filvaroff E, Gao W;
 PI Gerritsen ME, Goddard A, Godowski PJ, Gurney AL, Sherwood S;
 PI Smith V, Stewart TA, Tumas D, Watanabe CK, Wood WI, Zhang Z;
 DR WPI; 2003-352836/33.
 DR N-PSDB; ACA67089.
 XX
 PT New isolated PRO polypeptide useful for treating diabetes, rheumatoid
 PT arthritis, sports injuries, obesity, hearing loss in mammals, stroke, or
 PT heart attack.
 XX
 PS Claim 12; Fig 192; 643pp; English.
 XX
 CC The present invention relates to the isolation of novel human PRO
 CC polypeptides, and the polynucleotide sequences encoding them. The PRO
 CC polypeptides are secreted and transmembrane proteins. The PRO
 CC polypeptides and polynucleotides are useful for preparing a medicament
 CC useful in the treatment of diabetes, bone and/or cartilage disorders
 CC (e.g. rheumatoid arthritis, sports injuries, osteoarthritis), obesity,
 CC hyper- or hypo-insulinaemia, hearing loss, and coagulation disorders
 CC (e.g. stroke, heart attack). Anti-PRO antibodies are useful in diagnostic
 CC assays for PRO, by detecting its expression in specific cells, tissues or
 CC serum, and for affinity purification of PRO from recombinant cell culture
 CC or natural sources. ABU0870-ABU81144 represent the human PRO
 CC polypeptides of the invention. Note: The sequence data for this patent
 CC was obtained in electronic format directly from the USPTO web site at
 CC seqdata.uspto.gov/psipsiDentry.html
 XX
 SQ Sequence 513 AA;
 Query Match 99.6%; Score 2752; DB 6; Length 513;
 Best Local Similarity 99.8%; Pred. No. 4.1e-261;
 Matches 512; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 1 MKRLLLCFFITFSSAPFLVRMTNEENMQLAQAYLNQFYSLEIEGHNHVSQKNSRLID 60
 DB 1 MKRLLLCFFITFSSAPFLVRMTNEENMQLAQAYLNQFYSLEIEGHNHVSQKNSRLID 60
 QY 61 DKIREMQAFGLTVTKLDSNILEIMKTPRCGVDPVGVQGYTLPGWRKKNLYRIINYP 120
 DB 61 DKIREMQAFGLTVTKLDSNILEIMKTPRCGVDPVGVQGYTLPGWRKKNLYRIINYP 120
 QY 121 DMARAADVDEAIOEGLEVWSKVTPLEKTKISKGDIAMIAFRTRVHGRCPRYEDGPIGVLG 180

DB 121 DMARAADVDEAIOEGLEVWSKVTPLEKTKISKGDIAMIAFRTRVHGRCPRYEDGPIGVLG 180
 QY 181 HAFPPGPGGLGGDTHEDEENWTKGAGFNLFVAAHEFGHALGSHSNDQTALMPFNYS 240
 DB 181 HAFPPGPGGLGGDTHEDEENWTKGAGFNLFVAAHEFGHALGSHSNDQTALMPFNYS 240
 QY 241 LDPRKYPISQDDINGIQSIYGGLPKVPAPKPKPTIPHACDPLDTFDAITTRREVWFFKG 300
 DB 241 LDPRKYPISQDDINGIQSIYGGLPKVPAPKPKPTIPHACDPLDTFDAITTRREVWFFKG 300
 QY 301 RHLWRIYDIITDVEFELIASFWPSLPADLQAAAYENPRDKILVFKDENFWMIRGYAVLPDY 360
 DB 301 RHLWRIYDIITDVEFELIASFWPSLPADLQAAAYENPRDKILVFKDENFWMIRGYAVLPDY 360
 QY 361 PKSIHTLGFPGRVKKIDAAVCDKTRKTYFFVGIWCVRPDEMTQTMKGFPPORVVKHFFG 420
 DB 361 PKSIHTLGFPGRVKKIDAAVCDKTRKTYFFVGIWCVRPDEMTQTMKGFPPORVVKHFFG 420
 QY 421 ISIRVDAAFQYKGGFFFSRSGSKQFYNIKTNITRMTNTWFOCKEPKNSFFGFDINKE 480
 DB 421 ISIRVDAAFQYKGGFFFSRSGSKQFYNIKTNITRMTNTWFOCKEPKNSFFGFDINKE 480
 QY 481 KAHSGGKILYHKSLSLFIFGIVHLLKNTSIYQ 513
 DB 481 KAHSGGKILYHKSLSLFIFGIVHLLKNTSIYQ 513
 RESULT 7
 ABU66665
 ID ABU66665 standard; protein; 513 AA.
 XX
 AC ABU66665;
 XX
 DT 23-MAY-2003 (first entry)
 XX
 DE Human PRO polypeptide #96.
 XX
 KW Human; PRO polypeptide; secreted and transmembrane protein;
 KW tumour necrosis factor-alpha; TNF-alpha; blood; proliferation;
 KW differentiation; chondrocyte; tumour; genetic disorder; cytostatic.
 XX
 OS Homo sapiens.
 XX
 PN US2003036180-A1.
 XX
 PD 20-FEB-2003.
 XX
 PF 09-MAY-2002; 2002US-00143114.
 XX
 PR 31-MAR-1997; 97WO-US005230.
 PR 12-JUN-1998; 98WO-US012456.
 PR 14-JUL-1998; 98WO-US014552.
 PR 28-AUG-1998; 98WO-US017888.
 PR 10-SEP-1998; 98WO-US018824.
 PR 14-SEP-1998; 98WO-US019093.
 PR 14-SEP-1998; 98WO-US019094.
 PR 14-SEP-1998; 98WO-US019177.
 PR 16-SEP-1998; 98WO-US019330.
 PR 17-SEP-1998; 98WO-US019437.
 PR 07-OCT-1998; 98WO-US021141.
 PR 29-OCT-1998; 98WO-US022991.
 PR 29-OCT-1998; 98WO-US022992.
 PR 20-NOV-1998; 98WO-US024855.
 PR 01-DEC-1998; 98WO-US025108.
 PR 05-JAN-1999; 99WO-US000106.
 PR 08-MAR-1999; 99WO-US005028.
 PR 10-MAR-1999; 99WO-US005190.
 PR 20-APR-1999; 99WO-US008615.
 PR 14-MAY-1999; 99WO-US010733.
 PR 02-JUN-1999; 99WO-US012252.
 PR 01-SEP-1999; 99WO-US020111.
 PR 08-SEP-1999; 99WO-US020594.

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PR 13-SEP-1999; 99WO-US020944.
PR 15-SEP-1999; 99WO-US021090.
PR 15-SEP-1999; 99WO-US021147.
PR 05-OCT-1999; 99WO-US023089.
PR 29-NOV-1999; 99WO-US028214.
PR 30-NOV-1999; 99WO-US028313.
PR 30-NOV-1999; 99WO-US028409.
PR 01-DEC-1999; 99WO-US028301.
PR 01-DEC-1999; 99WO-US028634.
PR 02-DEC-1999; 99WO-US028551.
PR 02-DEC-1999; 99WO-US028564.
PR 02-DEC-1999; 99WO-US028565.
PR 16-DEC-1999; 99WO-US030095.
PR 20-DEC-1999; 99WO-US030311.
PR 20-DEC-1999; 99WO-US030399.
PR 22-DEC-1999; 99WO-US030720.
PR 30-DEC-1999; 99WO-US031243.
PR 30-DEC-1999; 99WO-US031274.
PR 05-JAN-2000; 2000WO-US000219.
PR 06-JAN-2000; 2000WO-US000277.
PR 06-JAN-2000; 2000WO-US000376.
PR 11-FEB-2000; 2000WO-US003365.
PR 18-FEB-2000; 2000WO-US004341.
PR 18-FEB-2000; 2000WO-US004342.
PR 22-FEB-2000; 2000WO-US004414.
PR 24-FEB-2000; 2000WO-US004314.
PR 24-FEB-2000; 2000WO-US005004.
PR 01-MAR-2000; 2000WO-US005601.
PR 02-MAR-2000; 2000WO-US005746.
PR 02-MAR-2000; 2000WO-US005841.
PR 10-MAR-2000; 2000WO-US006319.
PR 15-MAR-2000; 2000WO-US006884.
PR 20-MAR-2000; 2000WO-US007377.
PR 21-MAR-2000; 2000WO-US007532.
PR 30-MAR-2000; 2000WO-US008439.
PR 17-MAY-2000; 2000WO-US013705.
PR 22-MAY-2000; 2000WO-US014042.
PR 30-MAY-2000; 2000WO-US014941.
PR 02-JUN-2000; 2000WO-US015264.
PR 28-JUL-2000; 2000WO-US020710.
PR 11-AUG-2000; 2000WO-US020321.
PR 23-AUG-2000; 2000WO-US023522.
PR 24-AUG-2000; 2000WO-US023328.
PR 08-NOV-2000; 2000WO-US030952.
PR 10-NOV-2000; 2000WO-US030873.
PR 01-DEC-2000; 2000WO-US032878.
PR 20-DEC-2000; 2000US-00747259.
PR 28-FEB-2001; 2001US-0034956.
PR 28-FEB-2001; 2001US-00796498.
PR 01-MAR-2001; 2001WO-US006520.
PR 03-MAR-2001; 2001US-00802706.
PR 14-MAR-2001; 2001US-00808689.
PR 22-MAR-2001; 2001US-00816744.
PR 05-APR-2001; 2001US-00828366.
PR 10-MAY-2001; 2001US-00854208.
PR 18-MAY-2001; 2001US-00854280.
PR 25-MAY-2001; 2001US-00860216.
PR 25-MAY-2001; 2001US-00866028.
PR 25-MAY-2001; 2001US-00866034.
PR 01-JUN-2001; 2001WO-US017092.
PR 01-JUN-2001; 2001US-00872035.
PR 01-JUN-2001; 2001WO-US017800.
PR 05-JUN-2001; 2001US-00874503.
PR 14-JUN-2001; 2001US-00882836.
PR 19-JUN-2001; 2001US-00886342.
PR 20-JUN-2001; 2001WO-US019692.
PR 21-JUN-2001; 2001US-00887879.
PR 22-JUN-2001; 2001WO-US020116.
PR 29-JUN-2001; 2001WO-US021066.
PR 09-JUL-2001; 2001WO-US021735.
PR 18-JUL-2001; 2001US-00908827.
PR 06-AUG-2001; 2001US-00924419.

PR 09-AUG-2001; 2001US-00927796.
PR 16-AUG-2001; 2001US-00931836.
PR 19-DEC-2001; 2001US-00028072.
XX (GETH ) GENENTECH INC.
XX Baker KP, Beresini M, Deforge L, Desnoyers L, Filvaroff E, Gao W;
PI Gerritsen ME, Goddard A, Godowski PJ, Gurney AL, Sherwood S;
PI Smith V, Stewart TA, Tumas D, Watanabe CK, Wood WI, Zhang Z;
XX WPI; 2003-332040/31.
DR N-PSDB; ACA03698.
XX
PT New secreted and transmembrane PRO nucleic acids, useful for gene
PT therapy, in chromosome and gene mapping, as chromosome markers, in tissue
PT typing, and in chromosome identification.
XX
PS Claim 12; Fig 192; 660pp; English.
XX
CC The present invention relates to the isolation of novel human PRO
CC polypeptides, and the polynucleotide sequences encoding them. The PRO
CC polypeptides are secreted and transmembrane proteins. The PRO
CC polypeptides are useful for detecting other PRO polypeptides, for linking
CC bioactive molecules to cells expressing PRO polypeptides, and for
CC biological activities of cells expressing PRO polypeptides, and for
CC identifying agonists or antagonists. The PRO polypeptides are useful for
CC stimulating the release of tumour necrosis factor (TNF)-alpha from
CC human blood, for stimulating the proliferation or differentiation of
CC chondrocytes, and detecting the presence of tumours. The polynucleotide
CC sequences encoding PRO polypeptides are useful as hybridisation probes,
CC in chromosome and gene mapping, in the generation of antisense RNA and
CC DNA, in the preparation of PRO polypeptides, for generating transgenic
CC animals or knockout animals, for the genetic analysis of individuals with
CC genetic disorders, and in gene therapy. AB066570-AB066844 represent the
CC human PRO polypeptides of the invention. Note: the sequence data for this
CC patent was obtained in electronic format directly from the USPTO web site
CC at seqdata.uspto.gov/psipsDIDentry.html
XX
SQ Sequence 513 AA;
Query Match 99.6%; Score 2752; DB 6; Length 513;
Best Local Similarity 99.8%; Pred. No. 4.1e-261;
Matches 512; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1 MKRLILLCLFFITFSSAPPLVRMTENEENMLQAQVLYNQFYSLEIEGNHLVQSKNSLID 60
DB 1 MKRLILLCLFFITFSSAPPLVRMTENEENMLQAQVLYNQFYSLEIEGNHLVQSKNSLID 60
QY 61 DKIREMOAFFGLTVTGKLDNSTLLEIMKTPRCGVPDVQGYGYTLPGWKYKNTLYRIINYP 120
DB 61 DKIREMOAFFGLTVTGKLDNSTLLEIMKTPRCGVPDVQGYGYTLPGWKYKNTLYRIINYP 120
QY 121 DMARAAVDEAIQEGLEWWSKVTPKFTKISKGIADIMAFRTRVHGRCPRYFGPLGVLG 180
DB 121 DMARAAVDEAIQEGLEWWSKVTPKFTKISKGIADIMAFRTRVHGRCPRYFGPLGVLG 180
QY 181 HAPPPGGLGGDTHFDEDEENWTKDGAGFNLFVAHAHFGHALGSHNSDQALMFFNYVS 240
DB 181 HAPPPGGLGGDTHFDEDEENWTKDGAGFNLFVAHAHFGHALGSHNSDQALMFFNYVS 240
QY 241 LDPRKYP LSQDDINGIQSIYGLPKVPAKPKETIPHACDPDLTFFDAITTFREVMFPFKG 300
DB 241 LDPRKYP LSQDDINGIQSIYGLPKVPAKPKETIPHACDPDLTFFDAITTFREVMFPFKG 300
QY 301 RHLWRIYDITDVEFELIASFWPSLPADLQAAYENPRDKILVFKDENFWMIRGAVLPDY 360
DB 301 RHLWRIYDITDVEFELIASFWPSLPADLQAAYENPRDKILVFKDENFWMIRGAVLPDY 360
QY 361 PKSHTLGPGRVKKIDAAVCDKTRTKTYFVGLWCWRFDEMTOTMDKGPQRVVKHPPG 420
DB 361 PKSHTLGPGRVKKIDAAVCDKTRTKTYFVGLWCWRFDEMTOTMDKGPQRVVKHPPG 420
QY 421 ISIRVDAAFQYKGGFFFSRSGSKQFEVNIKTNITRINTWTFCKEFPKNSFGFDINKE 480
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||||| 421 ISIRVDAAFQYKGFPPFSGKQPEYNIKTNNITIMTNTWFOCKEPKNSSGFDINKE 480
 ||||| 481 KAHSGGIKILYHKSLSLFIFGIVHLLKNTSIYQ 513
 ||||| 481 KAHSGGIKILYHKSLSLFIFGIVHLLKNTSIYQ 513

RESULT 8
 ABO32578
 ID ABO32578 standard; protein; 513 AA.
 XX AC ABO32578;
 XX 17-SEP-2003 (first entry)

Secreted polypeptide-related protein #40.
 XX Human; TANGO; INTERCEPT; secreted polypeptide; immune disorder;
 KW hormonal disorder; proliferative disorder; cancer; thyroid disorder;
 KW diabetes; multiple sclerosis; lupus; neurological disorder; anaemia;
 KW Alzheimer's disease; Parkinson's disease; cardiovascular disorder;
 KW myocardial infarction; congestive heart disease; blood platelet disorder;
 KW thrombocytopenia; blood vessel; atherosclerosis; vasculitis.
 XX Homo sapiens.
 XX OS
 XX US2003022279-A1.
 XX PD
 XX 30-JAN-2003.
 XX PF 12-JAN-2001; 2001US-00759130.
 XX PR 14-JUN-1999; 99US-00333159.
 XX PR 29-JUN-1999; 99US-00342364.
 XX PR 10-SEP-1999; 99US-00393996.
 XX PR 19-OCT-1999; 99US-00420707.
 XX PR 07-JAN-2000; 2000US-00479249.
 XX PR 27-APR-2000; 2000US-00559497.
 XX PR 24-MAY-2000; 2000US-00578063.
 XX PR 16-JUN-2000; 2000US-00596194.
 XX PR 23-JUN-2000; 2000US-00602871.
 XX PR 30-JUN-2000; 2000US-00608452.
 XX (FRAS/) FRASER C C.
 PA (BARN/) BARNES T M.
 PA (SHAR/) SHARP J D.
 PA (KIRS/) KIRST S J.
 PA (MYER/) MYERS P S.
 PA (LEIB/) LEIBY K R.
 PA (HOLT/) HOLTZMAN D A.
 PA (MCCA/) MCCARTHY S A.
 PA (WRIG/) WRIGHTON N.
 PA (MACK/) MACKAY C R.
 PA (GOOD/) GOODEARL A D J.
 XX Fraser CC, Barnes TM, Sharp JD, Kirst SJ, Myers PS, Leiby KR;
 PI Holtzman DA, McCarthy SA, Wrighton N, Mackay CR, Goodearl ADJ;
 XX WPI; 2003-456290/43.
 DR N-PSDB; ACD66739, ACD66740.
 XX New nucleic acid molecule encoding a secreted protein (e.g. TANGO 202,
 PT TANGO 210 or INTERCEPT 217), useful for diagnosing, preventing or
 PT treating disorders such as cancer, diabetes or atherosclerosis, and in
 PT forensic biology.
 XX Claim 9; Fig 15A-15D; 482pp; English.
 PS The invention relates to secreted polypeptide-related proteins and
 CC nucleic acids (TANGO and INTERCEPT proteins and nucleic acids). The
 CC nucleic acids, proteins and antibodies specific to the proteins are
 CC useful in screening assays, predictive medicine (e.g. diagnostic assays,

CC prognostic assays, monitoring clinical trials and pharmacogenetics) and
 CC prophylactic and therapeutic methods. The sequences are used in
 CC diagnosing, preventing or treating proliferative disorders (e.g.
 CC cancers), hormonal disorders (e.g. diabetes or thyroid disorders), immune
 CC disorders (e.g. multiple sclerosis or lupus), neurological disorders
 CC (e.g. Alzheimer's disease or Parkinson's disease), cardiovascular
 CC disorders (e.g. myocardial infarction or congestive heart disease), blood
 CC platelet disorders (e.g. thrombocytopenia or anaemia) and disorders
 CC involving blood vessels (e.g. atherosclerosis or vasculitis). The nucleic
 CC acids may also be used in chromosome mapping, tissue typing and forensic
 CC biology, and as surrogate markers. This sequence represents a secreted
 CC polypeptide-related protein of the invention. Note: The sequence data for
 CC this patent was obtained in electronic format directly from USPTO at
 CC seqdata.uspto.gov/sequence.html
 XX
 SQ Sequence 513 AA;
 Query Match 99.6%; Score 2752; DB 6; Length 513;
 Best Local Similarity 99.8%; Pred. No. 4.1e-261;
 Matches 512; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 1 MKRLLLLCLFITSSAPFLVRMTENEENMQLAQAYLNQFYSLEIEGHLVQSKRSLID 60
 DB 1 MKRLLLLCLFITSSAPFLVRMTENEENMQLAQAYLNQFYSLEIEGHLVQSKRSLID 60
 QY 61 DKIREMQAFGLTVTGKLDNSTLEIMKTPRCGVPDVGQYGLPGWRKYNLTIRIINTP 120
 DB 61 DKIREMQAFGLTVTGKLDNSTLEIMKTPRCGVPDVGQYGLPGWRKYNLTIRIINTP 120
 QY 121 DMARAAVDEAIQEGLEVMSKVTPFKTKISKGIADIMIAFRTRVHGRCPRYFDGVLG 180
 DB 121 DMARAAVDEAIQEGLEVMSKVTPFKTKISKGIADIMIAFRTRVHGRCPRYFDGVLG 180
 QY 181 HAPFPGGLGGDTHFDEDEENWTKDAGNLFVAAHEFGHALGSHSNDQTALMPFNYS 240
 DB 181 HAPFPGGLGGDTHFDEDEENWTKDAGNLFVAAHEFGHALGSHSNDQTALMPFNYS 240
 QY 241 LDPKRYPLSQDDINGIQSIYGLPKVPKPKPTPIHACDPLDTFDAITTFREVMFFKG 300
 DB 241 LDPKRYPLSQDDINGIQSIYGLPKVPKPKPTPIHACDPLDTFDAITTFREVMFFKG 300
 QY 301 RHLWRIYYDITDVEPELIASFWSLPADLQAAAYENPRDKILVFKDENFMIRGVAVLDPY 360
 DB 301 RHLWRIYYDITDVEPELIASFWSLPADLQAAAYENPRDKILVFKDENFMIRGVAVLDPY 360
 QY 361 PKSHTLPGPRVKKIDAAVCDKTRTKYFFVGIWCFWDEMTQTMKGFPQVVVKHPFG 420
 DB 361 PKSHTLPGPRVKKIDAAVCDKTRTKYFFVGIWCFWDEMTQTMKGFPQVVVKHPFG 420
 QY 421 ISIRVDAAFQYKGFPPFSGKQPEYNIKTNNITIMTNTWFOCKEPKNSSGFDINKE 480
 DB 421 ISIRVDAAFQYKGFPPFSGKQPEYNIKTNNITIMTNTWFOCKEPKNSSGFDINKE 480
 QY 481 KAHSGGIKILYHKSLSLFIFGIVHLLKNTSIYQ 513
 DB 481 KAHSGGIKILYHKSLSLFIFGIVHLLKNTSIYQ 513

RESULT 9
 ABO59746
 ID ABO59746 standard; protein; 513 AA.
 XX AC ABO59746;
 XX 13-MAY-2003 (first entry)
 XX Novel secreted and transmembrane protein PRO5992.
 XX Human; PRO; hypertrophy of neonatal heart; angiogenesis; wound healing;
 KW cardiac insufficiency disorder; cancer; tumour; immune response;
 KW adrenal cortical capillary endothelial growth; c-fos induction;
 KW vascular endothelial growth factor inhibition; VEGF inhibition;
 KW endothelial cell growth inhibitor; T-lymphocytes stimulation;

KW retinal neurons cell survival; rod photoreceptor cell survival;
KW retinal disorder; retinitis pigmentosum; kidney disorder;
KW mammalian kidney mesangial cell proliferation; Berger disease;
KW dermatitis; herpeticiformis; Crohn's disease; chondrocyte proliferation;
XX chondrocyte redifferentiation; sports injury; arthritis.

OS Homo sapiens.

PN US2003017563-A1.

XX 23-JAN-2003.

XX 07-MAY-2002; 2002US-00140808.

XX 31-MAR-1997; 97WO-US005230.
PR 12-JUN-1998; 98WO-US012456.
PR 14-JUL-1998; 98WO-US014552.
PR 28-AUG-1998; 98WO-US017888.
PR 10-SEP-1998; 98WO-US018824.
PR 14-SEP-1998; 98WO-US019093.
PR 14-SEP-1998; 98WO-US019094.
PR 14-SEP-1998; 98WO-US019177.
PR 16-SEP-1998; 98WO-US019330.
PR 17-SEP-1998; 98WO-US019437.
PR 07-OCT-1998; 98WO-US021141.
PR 29-OCT-1998; 98WO-US022991.
PR 29-OCT-1998; 98WO-US022992.
PR 20-NOV-1998; 98WO-US024855.
PR 01-DEC-1998; 98WO-US025108.
PR 05-JAN-1999; 99WO-US000106.
PR 08-MAR-1999; 99WO-US005028.
PR 10-MAR-1999; 99WO-US005190.
PR 20-APR-1999; 99WO-US008615.
PR 14-MAY-1999; 99WO-US010733.
PR 02-JUN-1999; 99WO-US012252.
PR 01-SEP-1999; 99WO-US020111.
PR 08-SEP-1999; 99WO-US020594.
PR 13-SEP-1999; 99WO-US020944.
PR 15-SEP-1999; 99WO-US021090.
PR 15-SEP-1999; 99WO-US021547.
PR 03-OCT-1999; 99WO-US023089.
PR 29-NOV-1999; 99WO-US028214.
PR 30-NOV-1999; 99WO-US028313.
PR 30-NOV-1999; 99WO-US028409.
PR 01-DEC-1999; 99WO-US028301.
PR 01-DEC-1999; 99WO-US028634.
PR 02-DEC-1999; 99WO-US028551.
PR 02-DEC-1999; 99WO-US028564.
PR 02-DEC-1999; 99WO-US028565.
PR 16-DEC-1999; 99WO-US030095.
PR 20-DEC-1999; 99WO-US030911.
PR 20-DEC-1999; 99WO-US030999.
PR 22-DEC-1999; 99WO-US030720.
PR 30-DEC-1999; 99WO-US031243.
PR 30-DEC-1999; 99WO-US031274.
PR 05-JAN-2000; 2000WO-US000219.
PR 06-JAN-2000; 2000WO-US000377.
PR 06-JAN-2000; 2000WO-US000376.
PR 11-FEB-2000; 2000WO-US000365.
PR 18-FEB-2000; 2000WO-US000431.
PR 18-FEB-2000; 2000WO-US000432.
PR 22-FEB-2000; 2000WO-US000441.
PR 24-FEB-2000; 2000WO-US004914.
PR 24-FEB-2000; 2000WO-US005004.
PR 01-MAR-2000; 2000WO-US005001.
PR 02-MAR-2000; 2000WO-US005046.
PR 02-MAR-2000; 2000WO-US005941.
PR 10-MAR-2000; 2000WO-US006319.
PR 15-MAR-2000; 2000WO-US006884.
PR 20-MAR-2000; 2000WO-US007377.
PR 21-MAR-2000; 2000WO-US007532.
PR 30-MAR-2000; 2000WO-US008439.
PR 17-MAY-2000; 2000WO-US013705.

PR 22-MAY-2000; 2000WO-US014042.
PR 30-MAY-2000; 2000WO-US014941.
PR 02-JUN-2000; 2000WO-US015264.
PR 28-JUL-2000; 2000WO-US020710.
PR 11-AUG-2000; 2000WO-US022031.
PR 23-AUG-2000; 2000WO-US023522.
PR 24-AUG-2000; 2000WO-US023328.
PR 08-NOV-2000; 2000WO-US030952.
PR 10-NOV-2000; 2000WO-US030873.
PR 01-DEC-2000; 2000WO-US032678.
PR 20-DEC-2000; 2000US-00747259.
PR 20-DEC-2000; 2000WO-US034956.
PR 28-FEB-2001; 2001US-00796498.
PR 28-FEB-2001; 2001WO-US006520.
PR 01-MAR-2001; 2001WO-US006666.
PR 09-MAR-2001; 2001US-00802706.
PR 14-MAR-2001; 2001US-00808689.
PR 22-MAR-2001; 2001US-00816744.
PR 05-APR-2001; 2001US-00828366.
PR 10-MAY-2001; 2001US-00854208.
PR 10-MAY-2001; 2001US-00854280.
PR 18-MAY-2001; 2001US-00860216.
PR 25-MAY-2001; 2001US-00866028.
PR 25-MAY-2001; 2001US-00866034.
PR 25-MAY-2001; 2001WO-US017092.
PR 01-JUN-2001; 2001US-00872035.
PR 01-JUN-2001; 2001WO-US017800.
PR 05-JUN-2001; 2001US-00874503.
PR 14-JUN-2001; 2001US-00882636.
PR 19-JUN-2001; 2001US-00886342.
PR 20-JUN-2001; 2001WO-US019692.
PR 21-JUN-2001; 2001US-00887879.
PR 22-JUN-2001; 2001WO-US020116.
PR 29-JUN-2001; 2001WO-US021066.
PR 09-JUL-2001; 2001WO-US021735.
PR 18-JUL-2001; 2001US-00908827.
PR 06-AUG-2001; 2001US-00924419.
PR 09-AUG-2001; 2001US-00927796.
PR 16-AUG-2001; 2001US-00931836.
PR 19-DEC-2001; 2001US-00028072.

(GETH) GENENTECH INC.

Baker KP, Beresini M, Deforge L, Desnoyers L, Filvaroff E, Gao W;
Garritsen ME, Goddard A, Godowski PJ, Gurney AL, Sherwood S;
Smith V, Stewart TA, Tumas D, Watanabe CK, Wood WI, Zhang Z;

WPI; 2003-148238/14.
N-PSDB; ABX89236.

Two hundred and seventy five nucleic acids encoding PRO polypeptides,
useful for treating pericyte-associated tumors, diabetes and various bone
and/or cartilage disorders, e.g. arthritis.

Claim 12; Fig 192; 659pp; English.

The invention describes an isolated human PRO polypeptide. The PRO
polypeptides are useful in detecting PRO polypeptides in a sample, in
linking a bioactive molecule to a cell expressing a PRO polypeptide, and
in modulating at least one biological activity of a cell expressing a PRO
polypeptide. PRO1312 stimulates hypertrophy of neonatal heart and is thus
useful for treating cardiac insufficiency disorders. PRO1154 and PRO1186
stimulate adrenal cortical capillary endothelial growth, and PRO536,
PRO943, PRO828, PRO826, PRO1068 or PRO535, PRO826, PRO819, PRO1126,
PRO1360 and PRO1387 induce c-fos in endothelial cells, and are thus
useful for treating conditions or disorders where angiogenesis would be
beneficial, e.g. wound healing and antagonist of this polypeptide are
useful for treating cancerous tumors. PRO812 inhibits vascular
endothelial growth factor (VEGF) stimulated proliferation of endothelial
cells and is thus useful for inhibiting endothelial cell growth in
mammals which would be beneficial in inhibiting tumour growth. PRO826,
PRO1068, PRO1184, PRO1346 and PRO1375 stimulate proliferation of
stimulated T-lymphocytes and are therapeutically useful for enhancing

CC immune response. PRO828, PRO826, PRO1068 or PRO1132 enhance survival of
CC retinal neurons cells (PRO1132 is also enhances survival/proliferation of
CC rod photoreceptor cells) and therefore are useful for treating retinal
CC disorders of injuries, e.g. retinitis pigmentosa, AMD. PRO819, PRO813
CC and PRO1066 induce proliferation of mammalian kidney mesangial cells,
CC and therefore are useful for treating kidney disorders associated with,
CC decreased mesangial cell function such as Berger disease or other
CC nephropathies associated with dermatitis, herpeticiformis or Crohn's
CC disease. PRO1310, PRO844, PRO1312, PRO1192 and PRO1387 induce the
CC proliferation and/or redifferentiation of chondrocytes in culture and are
CC thus useful for treating sports injuries, and arthritis. This is the
CC amino acid sequence of a novel human PRO protein
XX Sequence 513 AA;
SQ

Query Match 99.6%; Score 2752; DB 6; Length 513;
Best Local Similarity 99.8%; Pred. No. 4,1e-261;
Matches 512; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1 MKRLLLGLFFITFSSAPLVMTENEENMQLAQAYLNQFYSLTEGHNHLSVSKRSLLID 60
Db 1 MKRLLLGLFFITFSSAPLVMTENEENMQLAQAYLNQFYSLTEGHNHLSVSKRSLLID 60
QY 61 DKIREMQAFFGLTVTGKLDNLTLEIMKTPRCGVPDVGQGYTLPGWRKYNLTIRIINYP 120
Db 61 DKIREMQAFFGLTVTGKLDNLTLEIMKTPRCGVPDVGQGYTLPGWRKYNLTIRIINYP 120
QY 121 DMARAADVAEIOEGLEWMSKVTPFKTKISKGIADIMIAFRTRVHGRCPRYFDGGLVGLG 180
Db 121 DMARAADVAEIOEGLEWMSKVTPFKTKISKGIADIMIAFRTRVHGRCPRYFDGGLVGLG 180
QY 181 HAPPPGPGGGTHFDEENWTKDAGENLFLVAAHEFGHALGSHNDQTALMPFNYS 240
Db 181 HAPPPGPGGGTHFDEENWTKDAGENLFLVAAHEFGHALGSHNDQTALMPFNYS 240
QY 241 LDPRKPLSQDDINGITQSYGGLPKVPKPKPTTIPHACDPLDTDAITTFRRVVFVK 300
Db 241 LDPRKPLSQDDINGITQSYGGLPKVPKPKPTTIPHACDPLDTDAITTFRRVVFVK 300
QY 301 RHLWRIYDITDVEBELIASFWPSLPADLQAAAYENPRDKILVFKDENFWIRGYAVLPDY 360
Db 301 RHLWRIYDITDVEBELIASFWPSLPADLQAAAYENPRDKILVFKDENFWIRGYAVLPDY 360
QY 361 PKSIHTLGPGRVKKIDRAVCCKTKTKYFFVGICWREDEMTQMDKGFPORVVKHFG 420
Db 361 PKSIHTLGPGRVKKIDRAVCCKTKTKYFFVGICWREDEMTQMDKGFPORVVKHFG 420
QY 421 ISIRVDAAFQYKGFYFFSRGSKQFEYNIKTKNITRIMTNTWFOCKEPKNSFGFDINKE 480
Db 421 ISIRVDAAFQYKGFYFFSRGSKQFEYNIKTKNITRIMTNTWFOCKEPKNSFGFDINKE 480
QY 481 KAHSGGKILYHKSLSLFTFGIVHLLKNTSIYQ 513
Db 481 KAHSGGKILYHKSLSLFTFGIVHLLKNTSIYQ 513

RESULT 10

ABO24936
ID ABO24936 standard; protein; 513 AA.

XX AC

XX AC ABO24936;

XX DT 05-SEP-2003 (first entry)

XX DE Human secreted/transmembrane protein (PRO) #96.

XX KW Human; PRO; secreted protein; transmembrane protein; tumour; cytostatic;

XX KW gene therapy; tumour necrosis factor-alpha; TNF-alpha; blood;

XX KW proteoglycan; cartilage; cytokine; peripheral blood mononuclear cell;

XX KW PBMC; glucose uptake; FFA; skeletal muscle cell; adipocyte cell;

XX KW chondrocyte cell proliferation; chondrocyte cell differentiation;

XX KW pericyte cell; inner ear utricular supporting cell; T-lymphocyte cell;

XX KW endothelial cell; A-peptide; factor VIIA.

XX Homo sapiens.
OS US2003036179-A1.
XX 20-FEB-2003.
XX 10-MAY-2002; 2002US-00142431.
XX 31-MAR-1997; 97WO-US005230.
XX 12-JUN-1998; 98WO-US012456.
XX 14-JUL-1998; 98WO-US014552.
XX 28-AUG-1998; 98WO-US017888.
XX 10-SEP-1998; 98WO-US018824.
XX 14-SEP-1998; 98WO-US019093.
XX 14-SEP-1998; 98WO-US019094.
XX 14-SEP-1998; 98WO-US019177.
XX 16-SEP-1998; 98WO-US019330.
XX 17-SEP-1998; 98WO-US019437.
XX 07-OCT-1998; 98WO-US021141.
XX 29-OCT-1998; 98WO-US022991.
XX 29-OCT-1998; 98WO-US022992.
XX 20-NOV-1998; 98WO-US024855.
XX 01-DEC-1998; 98WO-US025108.
XX 05-JAN-1999; 99WO-US000106.
XX 08-MAR-1999; 99WO-US005028.
XX 10-MAR-1999; 99WO-US005190.
XX 20-APR-1999; 99WO-US008615.
XX 14-MAY-1999; 99WO-US010733.
XX 02-JUN-1999; 99WO-US012252.
XX 01-SEP-1999; 99WO-US020111.
XX 08-SEP-1999; 99WO-US020594.
XX 13-SEP-1999; 99WO-US020944.
XX 15-SEP-1999; 99WO-US021090.
XX 15-SEP-1999; 99WO-US021547.
XX 05-OCT-1999; 99WO-US023089.
XX 29-NOV-1999; 99WO-US028214.
XX 30-NOV-1999; 99WO-US028313.
XX 30-NOV-1999; 99WO-US028409.
XX 01-DEC-1999; 99WO-US028301.
XX 01-DEC-1999; 99WO-US028634.
XX 02-DEC-1999; 99WO-US028551.
XX 02-DEC-1999; 99WO-US028564.
XX 02-DEC-1999; 99WO-US028565.
XX 16-DEC-1999; 99WO-US030095.
XX 20-DEC-1999; 99WO-US030911.
XX 20-DEC-1999; 99WO-US030999.
XX 22-DEC-1999; 99WO-US030720.
XX 30-DEC-1999; 99WO-US031243.
XX 05-JAN-2000; 99WO-US031274.
XX 06-JAN-2000; 2000WO-US000219.
XX 06-JAN-2000; 2000WO-US000277.
XX 11-FEB-2000; 2000WO-US000376.
XX 18-FEB-2000; 2000WO-US003565.
XX 18-FEB-2000; 2000WO-US004341.
XX 22-FEB-2000; 2000WO-US004342.
XX 24-FEB-2000; 2000WO-US004914.
XX 24-FEB-2000; 2000WO-US004914.
XX 01-MAR-2000; 2000WO-US005004.
XX 02-MAR-2000; 2000WO-US005601.
XX 02-MAR-2000; 2000WO-US005746.
XX 10-MAR-2000; 2000WO-US005841.
XX 15-MAR-2000; 2000WO-US006319.
XX 21-MAR-2000; 2000WO-US006884.
XX 21-MAR-2000; 2000WO-US007377.
XX 30-MAR-2000; 2000WO-US007532.
XX 17-MAY-2000; 2000WO-US008439.
XX 22-MAY-2000; 2000WO-US013705.
XX 30-MAY-2000; 2000WO-US014042.
XX 02-JUN-2000; 2000WO-US014941.
XX 28-JUL-2000; 2000WO-US015264.
XX 11-AUG-2000; 2000WO-US020710.
XX 11-AUG-2000; 2000WO-US022031.

PR	23-AUG-2000;	2000WO-US0235252.
PR	24-AUG-2000;	2000WO-US0233328.
PR	28-NOV-2000;	2000WO-US030952.
PR	10-NOV-2000;	2000WO-US030873.
PR	10-DEC-2000;	2000WO-US032678.
PR	20-DEC-2000;	2000UTS-00747259.
PR	20-DEC-2000;	2000WO-US034956.
PR	28-FEB-2001;	2001US-00796498.
PR	28-FEB-2001;	2001WO-US006522.
PR	1-MAR-2001;	2001WO-US006666.
PR	14-MAR-2001;	2001US-00802706.
PR	19-MAR-2001;	2001US-00809689.
PR	22-MAR-2001;	2001US-00816744.
PR	05-APR-2001;	2001US-00828365.
PR	10-MAY-2001;	2001US-00854208.
PR	10-MAY-2001;	2001US-00854280.
PR	18-MAY-2001;	2001US-00860216.
PR	25-MAY-2001;	2001US-00866028.
PR	25-MAY-2001;	2001US-00866034.
PR	01-JUN-2001;	2001WO-US017092.
PR	15-JUN-2001;	2001US-00872035.
PR	01-JUN-2001;	2001WO-US017800.
PR	05-JUN-2001;	2001US-00874503.
PR	14-JUN-2001;	2001US-00882636.
PR	19-JUN-2001;	2001US-00886342.
PR	20-JUN-2001;	2001WO-US019692.
PR	21-JUN-2001;	2001US-00887879.
PR	22-JUN-2001;	2001WO-US020116.
PR	29-JUN-2001;	2001WO-US021065.
PR	09-JUL-2001;	2001WO-US021735.
PR	18-JUL-2001;	2001US-00908827.
PR	06-AUG-2001;	2001US-00924419.
PR	09-AUG-2001;	2001US-00927796.
PR	16-AUG-2001;	2001US-00931836.
PR	19-DEC-2001;	2001US-00928072.

(GETH) GENENTECH INC.

Baker KP, Bersini M, Deforge L, Desnoyers L, Filvaroff E, Gao W, Gerritsen ME, Goddard A, Godowski PJ, Gurney AL, Sherwood S, Smith V, Stewart TA, Tumas D, Watanabe CK, Wood WI, Zhang Z; WPI; 2003-466355/44.
N-PSNR: ACD41890

New isolated nucleic acid encoding a PRO polypeptide, e.g. PRO1114 or PRO4978, useful in molecular biology, chromosome and gene mapping, in generating antisense RNA and DNA, and in gene therapy.

Claim 12; Fig 192; 659pp; English.

The invention relates to an isolated nucleic acid comprising at least 80% sequence identity to a PRO (secreted and transmembrane protein) cDNA comprising a nucleic acid (a) encoding a PRO polypeptide, or its extracellular domain (with or without its associated signal peptide), which comprises any of the 275 120-850 residue amino acid sequences, given in the specification; (b) comprising any of the 275 300-3500 nucleotide sequences, given in the specification; or (c) comprising the full-length coding sequence of the nucleotide sequences given in the specification, or of the DNA deposited under any of the American Type Culture Collection (ATCC) Accession Numbers listed in the specification. Also included are a vector comprising the novel nucleic acid, a host cell comprising the vector, producing a PRO polypeptide, the isolated PRO polypeptides detailed above, a chimeric molecule comprising the PRO polypeptide of fused to a heterologous amino acid sequence, an anti-PRO antibody, detecting a PRO polypeptide in a sample suspected of containing a PRO polypeptide, linking a bioactive molecule to a cell expressing a PRO polypeptide, modulating at least one biological activity of a cell expressing a PRO polypeptide, stimulating the release of tumour necrosis factor- α (TNF- α) from human blood, (or proteoglycans from cartilage or cytokine from peripheral blood mononuclear cells (PBMC)), modulating the uptake of glucose or FFA by skeletal muscle cells or adipocyte cells, stimulating the proliferation or differentiation of

chondrocyte cells (or proliferation of or gene expression in pericyte cells), stimulating the proliferation of inner ear utricular supporting cells (or of T-lymphocyte cells, or of endothelial cells), inhibiting the binding of A-peptide to factor VIIA, or differentiation of adipocyte cells, detecting the presence of a tumour in a mammal and an oligonucleotide probe derived from any of the nucleotide sequences given in the specification. The polynucleotide is useful in molecular biology, including uses as hybridisation probes, in chromosome and gene mapping, in generating antisense RNA and DNA, and in gene therapy. The polynucleotide may also be used in preparing PRO polypeptides by recombinant techniques, and in generating either transgenic animals or knock-out animals which, in turn, are useful in the development and screening of therapeutically useful reagents. The PRO polypeptide or the antibody is used in preparing a medicament for treating a condition responsive to the polypeptide or antibody, such as tumours, and in various diagnostic assays. The present sequence represents a PRO polypeptide

Sequence 513 AA:
xx
xx
xx

Sequence 513 AA:

Query Match	99.6%;	Score 2752;	DB 6;	Length 513;
Best Local Similarity	99.8%;	Pred. No. 4.1e-261;		
Matches 512;	Conservative 0;	Mismatches 1;	Indels 0;	Gaps 0;
QY 1	MKRLLLLCLEFFITFSSAFFLVVRMTENENMQLAQAYLNQFYSLIEGHNHLVQSKNRS	60		
DB 1	MKRLLLLCLEFFITFSSAFFLVVRMTENENMQLAQAYLNQFYSLIEGHNHLVQSKNRS	60		
QY 61	DKIREMOAFFGLTVTGKLDNLTLEIMKTPRCGVDPVGGYGTLPQWRKYNLTIRIIN	120		
DB 61	DKIREMOAFFGLTVTGKLDNLTLEIMKTPRCGVDPVGGYGTLPQWRKYNLTIRIIN	120		
QY 121	DMARAAVDEAIQEGLEWVSKVTPLPKFTKISKGIIADIMIAFTRVHGRCPRYDGP	180		
DB 121	DMARAAVDEAIQEGLEWVSKVTPLPKFTKISKGIIADIMIAFTRVHGRCPRYDGP	180		
QY 181	HAPPPGGLGGDTHFDEDEENWKDGAGFNLPVAAHFGHAGLSHSDQATALMPNV	240		
DB 181	HAPPPGGLGGDTHFDEDEENWKDGAGFNLPVAAHFGHAGLSHSDQATALMPNV	240		
QY 241	LDPKPYLSODDINGIOSIYGGLPKVPAPKPEPTIPHACDDPLTDAITTFRRV	300		
DB 241	LDPKPYLSODDINGIOSIYGGLPKVPAPKPEPTIPHACDDPLTDAITTFRRV	300		
QY 301	RHLWRYYDITDVEFELIASFWPSLPADLQAAAYENPRDKILVPKDNFWMIRG	360		
DB 301	RHLWRYYDITDVEFELIASFWPSLPADLQAAAYENPRDKILVPKDNFWMIRG	360		
QY 361	PKSIHTLGPGRVKKIDAAACDKTTRKTYFVGIWCMWRFDEMTQTMKGFPQR	420		
DB 361	PKSIHTLGPGRVKKIDAAACDKTTRKTYFVGIWCMWRFDEMTQTMKGFPQR	420		
QY 421	ISIRVDAAFQYKGGFFFSRGSKQPEYNIKTNITRIMRTNFWOCKEPKNS	480		
DB 421	ISIRVDAAFQYKGGFFFSRGSKQPEYNIKTNITRIMRTNFWOCKEPKNS	480		
QY 481	KAHSGGKILYHKSLSLFIFGIVHLLKNVTSIYQ	513		
DB 481	KAHSGGKILYHKSLSLFIFGIVHLLKNVTSIYQ	513		

RESULT 11

RESOLUTION
ABU66941

ABU666941
ID ABU66941 standard; protein; 513 AA.

AC ABU66941;

XX
DT 27-MAY-2003 (first entry)

Human secreted/transmembrane. PRO. protein SEO ID 192.

Human: secreted protein. transmembrane protein: PRO: XX KW

KW Human; secreted protein; transmembrane protein; PRU; inflammatory disease; organ failure; atherosclerosis; cardiac injury;

KW infertility; birth defects; premature aging; AIDS; biosensor;
 KW acquired immunodeficiency syndrome; cancer; diabetic complication;
 XX bioactor; tumour.

OS Homo sapiens.

XX US2003032155-A1.

PN

XX 13-FEB-2003.

XX 03-MAY-2002; 2002US-00137865.

XX 31-MAR-1997; 97WO-US005230.

PR 12-JUN-1998; 98WO-US012456.

PR 14-JUL-1998; 98WO-US014552.

PR 28-AUG-1998; 98WO-US017888.

PR 10-SEP-1998; 98WO-US018824.

PR 14-SEP-1998; 98WO-US019093.

PR 14-SEP-1998; 98WO-US019094.

PR 14-SEP-1998; 98WO-US019177.

PR 16-SEP-1998; 98WO-US019330.

PR 17-SEP-1998; 98WO-US019437.

PR 07-OCT-1998; 98WO-US021141.

PR 29-OCT-1998; 98WO-US022991.

PR 29-OCT-1998; 98WO-US022992.

PR 20-NOV-1998; 98WO-US024855.

PR 01-DEC-1998; 98WO-US025108.

PR 05-JAN-1999; 99WO-US000106.

PR 08-MAR-1999; 99WO-US005028.

PR 10-MAR-1999; 99WO-US005130.

PR 20-APR-1999; 99WO-US008615.

PR 14-MAY-1999; 99WO-US010733.

PR 02-JUN-1999; 99WO-US012252.

PR 01-SEP-1999; 99WO-US020111.

PR 08-SEP-1999; 99WO-US020594.

PR 13-SEP-1999; 99WO-US020944.

PR 15-SEP-1999; 99WO-US021090.

PR 15-SEP-1999; 99WO-US021547.

PR 05-OCT-1999; 99WO-US023089.

PR 29-NOV-1999; 99WO-US028214.

PR 30-NOV-1999; 99WO-US028313.

PR 30-NOV-1999; 99WO-US028409.

PR 01-DEC-1999; 99WO-US028301.

PR 01-DEC-1999; 99WO-US028634.

PR 02-DEC-1999; 99WO-US028551.

PR 02-DEC-1999; 99WO-US028564.

PR 02-DEC-1999; 99WO-US028565.

PR 16-DEC-1999; 99WO-US030095.

PR 20-DEC-1999; 99WO-US030911.

PR 20-DEC-1999; 99WO-US030999.

PR 22-DEC-1999; 99WO-US030720.

PR 30-DEC-1999; 99WO-US031243.

PR 05-JAN-2000; 2000WO-US000219.

PR 06-JAN-2000; 2000WO-US000277.

PR 11-FEB-2000; 2000WO-US000376.

PR 18-FEB-2000; 2000WO-US0003565.

PR 18-FEB-2000; 2000WO-US004341.

PR 22-FEB-2000; 2000WO-US004342.

PR 24-FEB-2000; 2000WO-US004414.

PR 24-FEB-2000; 2000WO-US004914.

PR 01-MAR-2000; 2000WO-US005004.

PR 02-MAR-2000; 2000WO-US005601.

PR 02-MAR-2000; 2000WO-US005746.

PR 10-MAR-2000; 2000WO-US005841.

PR 10-MAR-2000; 2000WO-US006319.

PR 15-MAR-2000; 2000WO-US006884.

PR 20-MAR-2000; 2000WO-US007377.

PR 21-MAR-2000; 2000WO-US007532.

PR 30-MAR-2000; 2000WO-US008439.

PR 17-MAY-2000; 2000WO-US013705.

PR 22-MAY-2000; 2000WO-US014042.

PR 30-MAY-2000; 2000WO-US014941.

PR 02-JUN-2000; 2000WO-US015264.
 PR 28-JUL-2000; 2000WO-US020710.
 PR 11-AUG-2000; 2000WO-US022031.
 PR 23-AUG-2000; 2000WO-US023522.
 PR 24-AUG-2000; 2000WO-US023328.
 PR 08-NOV-2000; 2000WO-US030952.
 PR 10-NOV-2000; 2000WO-US030873.
 PR 01-DEC-2000; 2000WO-US032678.
 PR 20-DEC-2000; 2000US-00747259.
 PR 20-DEC-2000; 2000WO-US034956.
 PR 28-FEB-2001; 2001US-00796498.
 PR 01-MAR-2001; 2001WO-US006666.
 PR 09-MAR-2001; 2001US-00802706.
 PR 14-MAR-2001; 2001US-00808689.
 PR 22-MAR-2001; 2001US-00816744.
 PR 05-APR-2001; 2001US-00828366.
 PR 10-MAY-2001; 2001US-00854208.
 PR 10-MAY-2001; 2001US-00854280.
 PR 18-MAY-2001; 2001US-00860216.
 PR 25-MAY-2001; 2001US-00866028.
 PR 25-MAY-2001; 2001US-00866034.
 PR 25-MAY-2001; 2001WO-US017092.
 PR 01-JUN-2001; 2001US-00872035.
 PR 01-JUN-2001; 2001WO-US017800.
 PR 05-JUN-2001; 2001US-00874503.
 PR 14-JUN-2001; 2001US-00882636.
 PR 19-JUN-2001; 2001US-00886342.
 PR 20-JUN-2001; 2001WO-US019692.
 PR 21-JUN-2001; 2001US-00887879.
 PR 22-JUN-2001; 2001WO-US020116.
 PR 29-JUN-2001; 2001WO-US021066.
 PR 09-JUL-2001; 2001WO-US021735.
 PR 18-JUL-2001; 2001US-00908827.
 PR 06-AUG-2001; 2001US-00924419.
 PR 09-AUG-2001; 2001US-00927796.
 PR 16-AUG-2001; 2001US-00931836.
 PR 19-DEC-2001; 2001US-00028072.
 XX (GETH) GENENTECH INC.

PA Baker KP, Beresini M, Deforge L, Desnoyers L, Filvaroff E, Gao W;

XX Gerritsen ME, Goddard A, Godowski PJ, Gurney AL, Sherwood S;
 PI Smith V, Stewart TA, Tumas D, Watanabe CK, Wood WI, Zhang Z;

XX WPI; 2003-331925/31.

DR N-PSDB; ACA04119.

XX New secreted and transmembrane nucleic acids and polypeptides, designated
 PT as PRO, useful for treating inflammation, organ failure, atherosclerosis,
 PT cardiac injury, infertility, birth defects, premature aging, AIDS, or
 PT cancer.

XX Claim 12; Fig 192; 659pp; English.

XX The invention relates to an isolated nucleic acid comprising, or which is
 CC at least 80% identical to, or the full-length coding sequence of, any of
 CC the 275 nucleotide sequences, encoding the corresponding PRO polypeptide
 CC (one of 275 secreted or transmembrane proteins). The nucleic acid further
 CC comprises the full-length coding sequence of the DNA deposited under
 CC American Type Culture Collection (ATCC) accession number in a list given
 CC in the specification. Also included are vectors and host cells for
 CC producing PRO proteins, PRO fusion proteins, anti-PRO antibodies, PRO
 CC extracellular domains and mature sequences, methods of detecting PRO
 CC proteins, methods for stimulating the release of TNF-alpha (tumour
 CC necrosis factor alpha) from human blood, (and the proliferation of
 CC differentiation of chondrocyte cells, the proliferation of, or gene
 CC expression in pericyte cells, the release or proteoglycans from
 CC cartilage, proliferation of inner ear utricular supporting cells, the
 CC proliferation of T-lymphocyte cells, the release of a cytokine from
 CC peripheral blood mononuclear cells (PBMC), or the proliferation of
 CC endothelial cells), a method for modulating the uptake of glucose or free
 CC fatty acid (FFA) by skeletal muscle cells, a method for inhibiting the

CC binding of A-peptide to factor VIIA, or the differentiation of adipocyte
 CC cells, a method for detecting the presence of a tumour in a mammal and an
 CC oligonucleotide probe derived from any of the nucleotide sequences cited
 CC above. The nucleic acids and polypeptides are useful for treating
 CC inflammatory diseases, organ failure, atherosclerosis, cardiac injury,
 CC infertility, birth defects, premature aging, AIDS (acquired
 CC immunodeficiency syndrome), cancer, or diabetic complications. The
 CC nucleic acids are useful as hybridisation probes, in chromosome and gene
 CC mapping, and in generating antisense RNA or DNA. The polypeptides are
 CC useful as pharmaceuticals, diagnostics, biosensors or bioreactors. Both
 CC are useful in tissue typing. The present sequence represents a PRO
 CC protein of the invention
 XX
 SQ Sequence 513 AA;

Query Match 99.6%; Score 2752; DB 6; Length 513;
 Best Local Similarity 99.8%; Pred. No. 4.1e-261;
 Matches 512; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 1 MKRLLLCLFETESSAPPLVRMTENENMQLAQYLNQFVSLIEGHNHLVQSKNRSLLID 60
 Db 1 MKRLLLCLFETESSAPPLVRMTENENMQLAQYLNQFVSLIEGHNHLVQSKNRSLLID 60
 QY 61 DKIREMAQFGLTGTGLDSNTLIMKTPTGCGVDVGQGYTLPGWKKYMLTYRIINYP 120
 Db 61 DKIREMAQFGLTGTGLDSNTLIMKTPTGCGVDVGQGYTLPGWKKYMLTYRIINYP 120
 QY 121 DMARAAVDEAIQEGLEWVSKVTPKTKISKGIADIMAFRTRVHGRCPRYFDGFLGVLG 180
 Db 121 DMARAAVDEAIQEGLEWVSKVTPKTKISKGIADIMAFRTRVHGRCPRYFDGFLGVLG 180
 QY 181 HAPPPGGLGDTHTFDEENWKDGAGFNPLVAHFEFGALGSHNDQTALMFPNYS 240
 Db 181 HAPPPGGLGDTHTFDEENWKDGAGFNPLVAHFEFGALGSHNDQTALMFPNYS 240
 QY 241 LDPKRYPLSQDDINGISYIGLPGKVPKPKKEPTIPHACDPDLTFTDAITFRREVMPFKG 300
 Db 241 LDPKRYPLSQDDINGISYIGLPGKVPKPKKEPTIPHACDPDLTFTDAITFRREVMPFKG 300
 QY 301 RHLWRIYDITDVEFELIASFWPSLPADLQAAYENPRDKILVFKDENFWMIRGVAVLPDY 360
 Db 301 RHLWRIYDITDVEFELIASFWPSLPADLQAAYENPRDKILVFKDENFWMIRGVAVLPDY 360
 QY 361 PKSHTLGFGRVKKIDAAVCDKTKTRTPYVGVWCFWREDEMTQDKGPPQVRVKPPG 420
 Db 361 PKSHTLGFGRVKKIDAAVCDKTKTRTPYVGVWCFWREDEMTQDKGPPQVRVKPPG 420
 QY 421 ISIRVDAAFQYKGFPPFSRSGSKQFEYNKTKNITRMTNTWFOCKEPKNSSGFGDINKE 480
 Db 421 ISIRVDAAFQYKGFPPFSRSGSKQFEYNKTKNITRMTNTWFOCKEPKNSSGFGDINKE 480
 QY 481 KAHSGGKILYKHSLSLFIQVHLLKNTSIYQ 513
 Db 481 KAHSGGKILYKHSLSLFIQVHLLKNTSIYQ 513

RESULT 12

ADA45711
 ID ADA45711 standard; protein; 513 AA.

XX
 AC ADA45711;

XX
 DT 20-NOV-2003 (first entry)

XX
 DE Novel human secreted and transmembrane protein PRO5992.

XX Human; secreted and transmembrane protein; PRO;
 KW Tumour necrosis factor alpha release; TNF-alpha release;
 KW glucose uptake modulator; FFA uptake modulator;
 KW cell proliferation stimulator; cell differentiation stimulator;
 KW cell differentiation inhibitor; cytokine release stimulator; tumour;
 KW lung tumour; colon tumour; breast tumour; prostate tumour; rectal tumour;
 KW cervical tumour; liver tumour; chromosome mapping; gene mapping;

KW gene therapy; chromosome identification; chromosome marker.
 XX Homo sapiens.
 OS US2003022328-A1.
 XX 30-JAN-2003.
 PD
 PF 16-APR-2002; 2002US-00123904.
 XX 31-MAR-1997; 97WO-US005230.
 PR 12-JUN-1998; 98WO-US012456.
 PR 14-JUL-1998; 98WO-US014552.
 PR 28-AUG-1998; 98WO-US017888.
 PR 10-SEP-1998; 98WO-US018824.
 PR 14-SEP-1998; 98WO-US019093.
 PR 14-SEP-1998; 98WO-US019094.
 PR 14-SEP-1998; 98WO-US019177.
 PR 16-SEP-1998; 98WO-US019330.
 PR 17-SEP-1998; 98WO-US019437.
 PR 07-OCT-1998; 98WO-US021141.
 PR 29-OCT-1998; 98WO-US022991.
 PR 20-NOV-1998; 98WO-US024855.
 PR 01-DEC-1998; 98WO-US025108.
 PR 05-JAN-1999; 99WO-US000106.
 PR 08-MAR-1999; 99WO-US005028.
 PR 10-MAR-1999; 99WO-US005190.
 PR 20-APR-1999; 99WO-US008615.
 PR 14-MAY-1999; 99WO-US010733.
 PR 02-JUN-1999; 99WO-US012252.
 PR 01-SEP-1999; 99WO-US020111.
 PR 08-SEP-1999; 99WO-US020594.
 PR 15-SEP-1999; 99WO-US020944.
 PR 15-SEP-1999; 99WO-US021090.
 PR 15-SEP-1999; 99WO-US021547.
 PR 05-OCT-1999; 99WO-US023089.
 PR 29-NOV-1999; 99WO-US028214.
 PR 30-NOV-1999; 99WO-US028313.
 PR 30-NOV-1999; 99WO-US028409.
 PR 01-DEC-1999; 99WO-US028301.
 PR 01-DEC-1999; 99WO-US028634.
 PR 02-DEC-1999; 99WO-US028551.
 PR 02-DEC-1999; 99WO-US028564.
 PR 02-DEC-1999; 99WO-US028565.
 PR 16-DEC-1999; 99WO-US030095.
 PR 20-DEC-1999; 99WO-US030911.
 PR 20-DEC-1999; 99WO-US030999.
 PR 22-DEC-1999; 99WO-US030720.
 PR 30-DEC-1999; 99WO-US031243.
 PR 30-DEC-1999; 99WO-US031274.
 PR 03-JAN-2000; 2000WO-US000219.
 PR 06-JAN-2000; 2000WO-US000277.
 PR 06-JAN-2000; 2000WO-US000376.
 PR 11-FEB-2000; 2000WO-US003565.
 PR 18-FEB-2000; 2000WO-US004341.
 PR 18-FEB-2000; 2000WO-US004342.
 PR 22-FEB-2000; 2000WO-US004414.
 PR 24-FEB-2000; 2000WO-US004914.
 PR 24-FEB-2000; 2000WO-US005004.
 PR 01-MAR-2000; 2000WO-US005601.
 PR 02-MAR-2000; 2000WO-US005746.
 PR 02-MAR-2000; 2000WO-US005841.
 PR 10-MAR-2000; 2000WO-US006319.
 PR 15-MAR-2000; 2000WO-US006884.
 PR 20-MAR-2000; 2000WO-US007377.
 PR 21-MAR-2000; 2000WO-US007532.
 PR 30-MAR-2000; 2000WO-US008439.
 PR 17-MAY-2000; 2000WO-US013705.
 PR 22-MAY-2000; 2000WO-US014042.
 PR 30-MAY-2000; 2000WO-US014941.
 PR 02-JUN-2000; 2000WO-US015264.
 PR 28-JUL-2000; 2000WO-US020710.

PR 11-AUG-2000; 2000WO-US022031.
 PR 23-AUG-2000; 2000WO-US023522.
 PR 24-AUG-2000; 2000WO-US023328.
 PR 08-NOV-2000; 2000WO-US030952.
 PR 10-NOV-2000; 2000WO-US030873.
 PR 01-DEC-2000; 2000WO-US032678.
 PR 20-DEC-2000; 2000US-00747259.
 PR 20-DEC-2000; 2000WO-US034956.
 PR 28-FEB-2001; 2001US-00796498.
 PR 28-FEB-2001; 2001WO-US006520.
 PR 01-MAR-2001; 2001WO-US006666.
 PR 09-MAR-2001; 2001US-00802706.
 PR 14-MAR-2001; 2001US-00808689.
 PR 22-MAR-2001; 2001US-00816744.
 PR 05-APR-2001; 2001US-00828366.
 PR 10-MAY-2001; 2001US-00854208.
 PR 18-MAY-2001; 2001US-00854280.
 PR 25-MAY-2001; 2001US-00860216.
 PR 25-MAY-2001; 2001US-00866028.
 PR 25-MAY-2001; 2001US-00866034.
 PR 25-MAY-2001; 2001WO-US017092.
 PR 01-JUN-2001; 2001US-00872035.
 PR 01-JUN-2001; 2001WO-US017800.
 PR 05-JUN-2001; 2001US-00874503.
 PR 14-JUN-2001; 2001US-00882636.
 PR 19-JUN-2001; 2001US-00886342.
 PR 20-JUN-2001; 2001WO-US019692.
 PR 21-JUN-2001; 2001US-00887879.
 PR 22-JUN-2001; 2001WO-US020116.
 PR 29-JUN-2001; 2001WO-US021066.
 PR 09-JUL-2001; 2001WO-US021735.
 PR 18-JUL-2001; 2001US-00908827.
 PR 06-AUG-2001; 2001US-00924419.
 PR 09-AUG-2001; 2001US-00927796.
 PR 16-AUG-2001; 2001US-00931836.
 PR 19-DEC-2001; 2001US-00028072.
 PR (GETH) GENENTECH INC.
 XX
 PI Baker KP, Beresini M, Deforge L, Desnoyers L, Filvaroff E, Gao W;
 PI Gerritsen ME, Goddard A, Godowski PJ, Gurney AL, Sherwood S;
 PI Smith V, Stewart TA, Tumas D, Watanabe CK, Wood WI, Zhang Z;
 XX
 DR WPI; 2003-584997/55.
 DR N-PSDB; ADA45710.
 XX
 PT Novel secreted and transmembrane polypeptide for modulating biological
 PT activity of cell expressing the polypeptide, identifying agonists or
 PT antagonists of polypeptide, and as molecular weight markers.
 XX
 PS Claim 12; Fig 192; 659pp; English.

XX The invention describes 305 nucleic acids encoding PRO (secreted and
 CC transmembrane) polypeptides (I). (I) is useful for stimulating the
 CC release of TNF-alpha from human blood, for modulating the uptake of
 CC glucose or FFA by skeletal muscle cells or adipocyte cells, for
 CC stimulating the proliferation or differentiation of chondrocyte cells,
 CC for stimulating the proliferation of or gene expression in pericyte
 CC cells, for stimulating the release of proteoglycans from cartilage, for
 CC stimulating the proliferation of inner ear utricular supporting cells,
 CC for stimulating the proliferation of T-lymphocyte cells, for stimulating
 CC the release of a cytokine from PBMC cells, for inhibiting the binding of
 CC A-peptide to factor VIIa, for inhibiting the differentiation of adipocyte
 CC cells, for stimulating proliferation of endothelial cells, for detecting
 CC the presence of tumour in a mammal. The tumour is lung, colon, breast,
 CC prostate, rectal, cervical or liver tumour. The oligonucleotide probes
 CC are useful for isolating genomic and cDNA nucleotide sequences or
 CC antisense probes. (I) is also useful as therapeutic agent. PRO is useful
 CC in assays to identify other proteins or molecules involved in binding
 CC interaction. A polynucleotide (II) encoding (I) is useful in chromosome
 CC and gene mapping, in generation of antisense RNA and DNA, in the
 CC preparation of PRO polypeptide, for generating transgenic animals or
 CC knockout animals which in turn are useful in the development and

CC screening of therapeutically useful reagents, in gene therapy, for
 CC chromosome identification, as chromosome marker, and for generating
 CC probes. An anti-(I)-antibody is useful in diagnostic assays for PRO, e.g.
 CC detecting its expression in specific cells, tissues or serum, and for
 CC affinity purification of PRO from recombinant cell culture or natural
 CC sources. (I) and (II) are useful for tissue typing. This is the amino
 CC acid sequence of a novel human secreted and transmembrane PRO
 CC polypeptide.

XX Sequence 513 AA;

SQ Query Match 99.6%; Score 2752; DB 6; Length 513;
 Best Local Similarity 99.8%; Pred. No. 4.1e-261;
 Matches 512; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 MKRLLLCFLFFITSSAPPLVRMTENENMQLAQAYLNQFYSLEIGHNLVQSKNRSLLID 60
 DB 1 MKRLLLCFLFFITSSAPPLVRMTENENMQLAQAYLNQFYSLEIGHNLVQSKNRSLLID 60
 QY 61 DKIREMQAFFGLTVTGKLDNSTLEIMKTPRGVDPVGGYVTLPGWRKXNLYTYRIINYP 120
 DB 61 DKIREMQAFFGLTVTGKLDNSTLEIMKTPRGVDPVGGYVTLPGWRKXNLYTYRIINYP 120
 QY 121 DMARAAVDEAIOEGLEVMSKVTPKFTKISKGIADIMIAFTRVHGRCPRYFDGGLVIG 180
 DB 121 DMARAAVDEAIOEGLEVMSKVTPKFTKISKGIADIMIAFTRVHGRCPRYFDGGLVIG 180
 QY 181 HAPFPGGLGGDTHFDEDENTKDGAGNLFVAHAHEFGHALGSHSNDQALMFPNVYS 240
 DB 181 HAPFPGGLGGDTHFDEDENTKDGAGNLFVAHAHEFGHALGSHSNDQALMFPNVYS 240
 QY 241 LDPRKYPUSQDDINGIQSIYGLPKVPKPKPTIPHACDPLDFTDAITTFRRVWFFKG 300
 DB 241 LDPRKYPUSQDDINGIQSIYGLPKVPKPKPTIPHACDPLDFTDAITTFRRVWFFKG 300
 QY 301 RHLMRIYYDITDVEFELIASFWPSLPADLQAAYENPRDKILVFKDENFWMIRGVAVLDPY 360
 DB 301 RHLMRIYYDITDVEFELIASFWPSLPADLQAAYENPRDKILVFKDENFWMIRGVAVLDPY 360
 QY 361 PKSIHTLFGPGRVKIDAAVCDKTRTKYFFVGVWCFWCFDEMTQTMDFQFQVVKHPPG 420
 DB 361 PKSIHTLFGPGRVKIDAAVCDKTRTKYFFVGVWCFWCFDEMTQTMDFQFQVVKHPPG 420
 QY 421 ISIRVDAAFOYKGFPPFSGSGSKQFENIKTNITRIMTNTWTFQCKEPKNSFGFDINKE 480
 DB 421 ISIRVDAAFOYKGFPPFSGSGSKQFENIKTNITRIMTNTWTFQCKEPKNSFGFDINKE 480
 QY 481 KAHSGGKILYHKLSLFIPIGIVHLLKNTSIYQ 513
 DB 481 KAHSGGKILYHKLSLFIPIGIVHLLKNTSIYQ 513

RESULT 13
 ADA76142
 ID ADA76142 standard; protein; 513 AA.
 XX
 AC ADA76142;
 XX
 DT 20-NOV-2003 (first entry)
 DE Human PRO polypeptide #96.
 XX
 KW Human; PRO; secreted polypeptide; transmembrane polypeptide;
 KW tumour necrosis factor-alpha; TNF-alpha; chondrocyte cell; tumour;
 KW cancer; adrenal; lung; colon; breast; prostate; kidney; cervix;
 KW liver; microvascular endothelial cell; glucose; FFA;
 KW skeletal muscle cell; adipocyte cell; pericyte cell;
 KW inner ear utricular supporting cell; T-lymphocyte cell;
 KW endothelial cell tube formation; bone disorder; cartilage disorder;
 KW sports injury; proteoglycan; articular cartilage defect; osteoarthritis;
 KW rheumatoid arthritis; haemoglobin-associated disorder thalassaemia;
 KW immune system cell infiltration.
 XX

CC various bone and/or cartilage disorders such as sports injuries and
CC arthritis. PRO polypeptides which stimulate the release of proteoglycans
CC from cartilage are useful for treating sports-related joint problems, PRO
CC articular cartilage defects, osteoarthritis and rheumatoid arthritis. PRO
CC polypeptides are also useful for treating various mammalian haemoglobin-
CC associated disorders such as various thalassaemias and conditions which
CC may benefit from enhanced local immune system cell infiltration. This
CC sequence represents a human PRO polypeptide of the invention. Note: The
CC sequence data for this patent is also available in electronic format from
CC USPTO at seqdata.uspto.gov/sequence.html.
XX
SQ Sequence 513 AA;

Query Match 99.6%; Score 2752; DB 6; Length 513;
Best Local Similarity 99.8%; Pred. No. 4.1e-261;
Matches 512; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 MKRLLLCLFFITFSAPPLVMTNEENMQLAQAYLNQFYSLIEGHNHVSQKNSLID 60
Db 1 MKRLLLCLFFITFSAPPLVMTNEENMQLAQAYLNQFYSLIEGHNHVSQKNSLID 60
QY 61 DKIREMAFFGLTVTGKLSNLTLEIMKTPRCGVPDVGQGYTLPGWRKYNLTIRIINYP 120
Db 61 DKIREMAFFGLTVTGKLSNLTLEIMKTPRCGVPDVGQGYTLPGWRKYNLTIRIINYP 120
QY 121 DMARAADVEAIOEGLEVSKVTPLETKISKGIADIMIAFRTRVHGRCPRYEDGGLVIG 180
Db 121 DMARAADVEAIOEGLEVSKVTPLETKISKGIADIMIAFRTRVHGRCPRYEDGGLVIG 180
QY 181 HAPFPGPLGGTHDEDENWTKDAGFNFLVAAHEFGHALGSHSNDQTALMFPNYS 240
Db 181 HAPFPGPLGGTHDEDENWTKDAGFNFLVAAHEFGHALGSHSNDQTALMFPNYS 240
QY 241 LDPRKYPISQDDINGIQSIYGLPKVPAPKKEPTIPHACDPDLTDAITTFRRVNFVFKG 300
Db 241 LDPRKYPISQDDINGIQSIYGLPKVPAPKKEPTIPHACDPDLTDAITTFRRVNFVFKG 300
QY 301 RHLWRIYDITDVEFELIASFWPSLPADLOAYENPRDKILVFKDENFMWIRGYAVLPDY 360
Db 301 RHLWRIYDITDVEFELIASFWPSLPADLOAYENPRDKILVFKDENFMWIRGYAVLPDY 360
QY 361 PKSIHTLGPGRVKKIDAAVCCKTKTYFFVGICWREDEMTQTMKGFQPVVVKHFFG 420
Db 361 PKSIHTLGPGRVKKIDAAVCCKTKTYFFVGICWREDEMTQTMKGFQPVVVKHFFG 420
QY 421 ISIRVDAAPQYKGFYFSSRGSKQFENIKTKNITRIMTNTWFOCKEKPQSSFGEDINKE 480
Db 421 ISIRVDAAPQYKGFYFSSRGSKQFENIKTKNITRIMTNTWFOCKEKPQSSFGEDINKE 480
QY 481 KAHSGGKILYHKSLIFIFGIVHLLKNTSIYQ 513
Db 481 KAHSGGKILYHKSLIFIFGIVHLLKNTSIYQ 513

RESULT 14
ADA18792
ID ADA18792 standard; protein; 513 AA.
XX
AC ADA18792;
DT
DT 20-NOV-2003 (first entry)
XX
DE Human PRO polypeptide #96.
XX
KW Human; PRO; secreted polypeptide; transmembrane polypeptide;
KW tumour necrosis factor-alpha; TNF-alpha; blood; chondrocyte cell; lung;
KW colon; breast; prostate; rectum; cervix; liver; tumour; cancer;
KW glucose uptake; FFA; adipocyte cell; pericyte cell; proteoglycan;
KW cartilage; inner ear utricular supporting cell; cytokine; A-peptide;
KW factor VIIA; endothelial cell.
XX
OS Homo sapiens.
XX

PN US2003054517-A1.
XX 20-MAR-2003.
XX 08-MAY-2002; 2002US-00141755.
XX 31-MAR-1997; 97WO-US005230.
PR 12-JUN-1998; 98WO-US012456.
PR 14-JUL-1998; 98WO-US014552.
PR 28-AUG-1998; 98WO-US017888.
PR 10-SEP-1998; 98WO-US018824.
PR 14-SEP-1998; 98WO-US019093.
PR 14-SEP-1998; 98WO-US019094.
PR 14-SEP-1998; 98WO-US019177.
PR 16-SEP-1998; 98WO-US019330.
PR 17-SEP-1998; 98WO-US019437.
PR 07-OCT-1998; 98WO-US021141.
PR 29-OCT-1998; 98WO-US022991.
PR 29-OCT-1998; 98WO-US022992.
PR 29-OCT-1998; 98WO-US024855.
PR 01-DEC-1998; 98WO-US025108.
PR 05-JAN-1999; 98WO-US000106.
PR 08-MAR-1999; 99WO-US005028.
PR 10-MAR-1999; 99WO-US005190.
PR 20-APR-1999; 99WO-US008615.
PR 14-MAY-1999; 99WO-US010733.
PR 02-JUN-1999; 99WO-US012252.
PR 01-SEP-1999; 99WO-US020111.
PR 08-SEP-1999; 99WO-US020594.
PR 13-SEP-1999; 99WO-US020944.
PR 15-SEP-1999; 99WO-US021090.
PR 15-SEP-1999; 99WO-US021547.
PR 05-OCT-1999; 99WO-US023089.
PR 29-NOV-1999; 99WO-US028214.
PR 30-NOV-1999; 99WO-US028313.
PR 30-NOV-1999; 99WO-US028409.
PR 01-DEC-1999; 99WO-US028301.
PR 01-DEC-1999; 99WO-US028634.
PR 02-DEC-1999; 99WO-US028551.
PR 02-DEC-1999; 99WO-US028564.
PR 02-DEC-1999; 99WO-US028565.
PR 16-DEC-1999; 99WO-US030095.
PR 20-DEC-1999; 99WO-US030911.
PR 20-DEC-1999; 99WO-US030999.
PR 22-DEC-1999; 99WO-US030720.
PR 30-DEC-1999; 99WO-US031243.
PR 30-DEC-1999; 99WO-US031274.
PR 05-JAN-2000; 2000WO-US000219.
PR 06-JAN-2000; 2000WO-US000277.
PR 06-JAN-2000; 2000WO-US000376.
PR 11-FEB-2000; 2000WO-US003565.
PR 18-FEB-2000; 2000WO-US004341.
PR 18-FEB-2000; 2000WO-US004342.
PR 22-FEB-2000; 2000WO-US004414.
PR 24-FEB-2000; 2000WO-US004914.
PR 24-FEB-2000; 2000WO-US005004.
PR 01-MAR-2000; 2000WO-US005601.
PR 02-MAR-2000; 2000WO-US005746.
PR 02-MAR-2000; 2000WO-US005841.
PR 10-MAR-2000; 2000WO-US006319.
PR 15-MAR-2000; 2000WO-US006884.
PR 20-MAR-2000; 2000WO-US007377.
PR 21-MAR-2000; 2000WO-US007532.
PR 30-MAR-2000; 2000WO-US008439.
PR 17-MAY-2000; 2000WO-US013705.
PR 22-MAY-2000; 2000WO-US014042.
PR 30-MAY-2000; 2000WO-US014941.
PR 02-JUN-2000; 2000WO-US015264.
PR 28-JUL-2000; 2000WO-US020710.
PR 11-AUG-2000; 2000WO-US022031.
PR 23-AUG-2000; 2000WO-US023522.
PR 24-AUG-2000; 2000WO-US023328.
PR 08-NOV-2000; 2000WO-US030952.

PR 10-NOV-2000; 2000WO-US030873.
PR 01-DEC-2000; 2000WO-US032678.
PR 20-DEC-2000; 2000US-00747259.
PR 20-DEC-2000; 2000WO-US034956.
PR 28-FEB-2001; 2001US-00796498.
PR 28-FEB-2001; 2001WO-US006520.
PR 01-MAR-2001; 2001WO-US006666.
PR 09-MAR-2001; 2001US-00802706.
PR 14-MAR-2001; 2001US-00808689.
PR 22-MAR-2001; 2001US-00816744.
PR 05-APR-2001; 2001US-00828366.
PR 10-MAY-2001; 2001US-00854208.
PR 10-MAY-2001; 2001US-00860216.
PR 18-MAY-2001; 2001US-00866028.
PR 25-MAY-2001; 2001US-00866034.
PR 25-MAY-2001; 2001US-00866034.
PR 01-JUN-2001; 2001WO-US017092.
PR 01-JUN-2001; 2001US-00872035.
PR 05-JUN-2001; 2001WO-US017800.
PR 05-JUN-2001; 2001US-00874503.
PR 14-JUN-2001; 2001US-00882636.
PR 19-JUN-2001; 2001US-00886342.
PR 20-JUN-2001; 2001WO-US019692.
PR 21-JUN-2001; 2001US-00887879.
PR 22-JUN-2001; 2001WO-US020116.
PR 29-JUN-2001; 2001WO-US021066.
PR 09-JUL-2001; 2001WO-US021735.
PR 18-JUL-2001; 2001US-00908827.
PR 06-AUG-2001; 2001US-00924419.
PR 09-AUG-2001; 2001US-00927796.
PR 16-AUG-2001; 2001US-00931836.
PR 19-DEC-2001; 2001US-00028072.

(GETH) GENENTECH INC.

PI Baker KP, Beresini M, Deforge L, Desnoyers L, Filvaroff E, Gao W;
PI Gerritsen ME, Goddard A, Godowski PJ, Gurney AL, Sherwood S;
PI Smith V, Stewart TA, Tumas D, Watanabe CK, Wood WI, Zhang Z;
XX WPI; 2003-521854/49.
DR N-PSDB; ADA18791.

XX New PRO nucleic acid, useful for preparing a composition for treating
PT e.g., tumors.

XX Claim 12; Fig 192; 660pp; English.

CC The invention relates to isolated human PRO polypeptides (secreted and
CC transmembrane polypeptides) and the polynucleotides encoding them. The
CC invention also relates to an antibody which specifically binds to a PRO
CC polypeptide, a method for stimulating the release of tumour necrosis
CC factor-alpha (TNF-alpha) from human blood, a method for stimulating the
CC proliferation or differentiation of chondrocyte cells and a method for
CC detecting the presence of a tumour in a mammal (e.g. lung, colon, breast,
CC prostate, rectal, cervical and liver tumours). The polynucleotides are
CC useful in molecular biology, including uses as hybridisation probes, in
CC chromosome and gene mapping, in generating antisense RNA and DNA and in
CC gene therapy. The polynucleotides may also be used in preparing PRO
CC polypeptides by recombinant techniques and in generating either
CC transgenic animals or knock-out animals which are useful in the
CC development and screening of therapeutically useful reagents. The PRO
CC polypeptides or antibodies are used in preparing a medicament for
CC treating a condition responsive to the polypeptides or antibodies, such
CC as tumours, for modulating the uptake of glucose or FFA by adipocyte
CC cells, for stimulating the proliferation of or gene expression in
CC pericyte cells, for stimulating the release of proteoglycans from
CC cartilage, for stimulating the proliferation of inner ear utricular
CC supporting cells, for stimulating the release of cytokines from PBMC
CC cells, for inhibiting the binding of A-peptide to factor VIIA, for
CC inhibiting the differentiation of adipocyte cells and for stimulating the
CC proliferation of endothelial cells. This sequence represents a human PRO
CC polypeptide of the invention. Note: The sequence data for this patent is
CC also available in electronic format from USPTO at

CC seqdata.uspto.gov/sequence.html.
XX Sequence 513 AA;
SQ

Query Match 99.6%; Score 2752; DB 6; Length 513;
Best Local Similarity 99.8%; Pred. No. 4.1e-261;
Matches 512; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 MKRLLLCLFFITFSSAPPLVRMTENENMQLAQAYLNQFYSLBIEGHLVQSKNRSLID 60
Db 1 MKRLLLCLFFITFSSAPPLVRMTENENMQLAQAYLNQFYSLBIEGHLVQSKNRSLID 60
Qy 61 DKIREMAFFGLTVTGKLDNLTLEIMKTPRCGPDVGVGYTLPGWKYNLYRIINVT 120
Db 61 DKIREMAFFGLTVTGKLDNLTLEIMKTPRCGPDVGVGYTLPGWKYNLYRIINVT 120
Qy 121 DMARAAVDEAIOEGLEVMSKVTPFKTKISKGIAIDIMAFRTVRVHGRCPRYFDGVLG 180
Db 121 DMARAAVDEAIOEGLEVMSKVTPFKTKISKGIAIDIMAFRTVRVHGRCPRYFDGVLG 180
Qy 181 HAPPGGLGDDTHFDEDEENWTKDGAGFNLFVAAHEFGHALGSHSNDQTALMFPNYS 240
Db 181 HAPPGGLGDDTHFDEDEENWTKDGAGFNLFVAAHEFGHALGSHSNDQTALMFPNYS 240
Qy 241 LDPKPYLSQDDINGIQSIYGGLPKVPAPKEPTIPHACDPDLTTFDAITTFREVMFPG 300
Db 241 LDPKPYLSQDDINGIQSIYGGLPKVPAPKEPTIPHACDPDLTTFDAITTFREVMFPG 300
Qy 301 RHLWRIYDITDVEFELIASFWPSLPADLQAAAYENPRDKILVFKDENFMWIRGAVILPDY 360
Db 301 RHLWRIYDITDVEFELIASFWPSLPADLQAAAYENPRDKILVFKDENFMWIRGAVILPDY 360
Qy 361 PKSHTLGFPGRVKKIDAAVCDKTRTKTYFVGICWRFDEMOTQMDKGPQVRVHFP 420
Db 361 PKSHTLGFPGRVKKIDAAVCDKTRTKTYFVGICWRFDEMOTQMDKGPQVRVHFP 420
Qy 421 ISIRVDAAFQYKGFPPFSGSKOFENYIKTKNITRMTNTWTFCKEKNSSFGFDINKE 480
Db 421 ISIRVDAAFQYKGFPPFSGSKOFENYIKTKNITRMTNTWTFCKEKNSSFGFDINKE 480
Qy 481 KAHSGGKILYHKSLSLFIFGIHVLLKNTSIYQ 513
Db 481 KAHSGGKILYHKSLSLFIFGIHVLLKNTSIYQ 513

RESULT 15

ADA61415
ID ADA61415 standard; protein; 513 AA.

XX AC ADA61415;

DT 20-NOV-2003 (first entry)

XX Homo sapiens.

XX Human; secreted and transmembrane protein; PRO;
KW Tumour necrosis factor alpha release; TNF-alpha release;
KW glucose uptake modulator; FFA uptake modulator;
KW cell proliferation stimulator; cell differentiation stimulator;
KW cell differentiation inhibitor; cytokine release stimulator; tumour;
KW lung tumour; colon tumour; breast tumour; prostate tumour; rectal tumour;
KW cervical tumour; liver tumour; chromosome mapping; gene mapping;
KW gene therapy; chromosome identification; chromosome marker.

XX Novel.

OS human.

OS secreted.

OS and.

OS transmembrane.

OS protein.

OS PRO5992.

XX US2003049816-A1.

XX 13-MAR-2003.
 XX 15-APR-2002; 2002US-00123262.
 XX 31-MAR-1997; 97WO-US005230.
 PR 12-JUN-1998; 98WO-US012456.
 PR 14-JUL-1998; 98WO-US014552.
 PR 28-AUG-1998; 98WO-US017888.
 PR 10-SEP-1998; 98WO-US018824.
 PR 14-SEP-1998; 98WO-US019093.
 PR 14-SEP-1998; 98WO-US019177.
 PR 16-SEP-1998; 98WO-US019330.
 PR 17-SEP-1998; 98WO-US019437.
 PR 07-OCT-1998; 98WO-US021141.
 PR 29-OCT-1998; 98WO-US022991.
 PR 29-OCT-1998; 98WO-US022992.
 PR 20-NOV-1998; 98WO-US024855.
 PR 01-DEC-1998; 98WO-US025108.
 PR 05-JAN-1999; 98WO-US000106.
 PR 08-MAR-1999; 98WO-US005028.
 PR 10-MAR-1999; 98WO-US005190.
 PR 20-APR-1999; 98WO-US008615.
 PR 14-MAY-1999; 98WO-US010733.
 PR 02-JUN-1999; 98WO-US012252.
 PR 01-SEP-1999; 98WO-US020111.
 PR 08-SEP-1999; 98WO-US020594.
 PR 13-SEP-1999; 98WO-US020944.
 PR 15-SEP-1999; 98WO-US021090.
 PR 15-SEP-1999; 98WO-US021547.
 PR 05-OCT-1999; 98WO-US023089.
 PR 29-NOV-1999; 98WO-US028214.
 PR 30-NOV-1999; 98WO-US028313.
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 PR 05-JAN-2000; 2000WO-US000219.
 PR 06-JAN-2000; 2000WO-US000277.
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 PR 11-FEB-2000; 2000WO-US003565.
 PR 18-FEB-2000; 2000WO-US004341.
 PR 18-FEB-2000; 2000WO-US004342.
 PR 22-FEB-2000; 2000WO-US004414.
 PR 24-FEB-2000; 2000WO-US004914.
 PR 24-FEB-2000; 2000WO-US005004.
 PR 01-MAR-2000; 2000WO-US005601.
 PR 02-MAR-2000; 2000WO-US005745.
 PR 02-MAR-2000; 2000WO-US005841.
 PR 10-MAR-2000; 2000WO-US006319.
 PR 15-MAR-2000; 2000WO-US006884.
 PR 20-MAR-2000; 2000WO-US007377.
 PR 21-MAR-2000; 2000WO-US007532.
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 PR 17-MAY-2000; 2000WO-US013705.
 PR 22-MAY-2000; 2000WO-US014042.
 PR 30-MAY-2000; 2000WO-US014941.
 PR 02-JUN-2000; 2000WO-US015264.
 PR 28-JUL-2000; 2000WO-US020710.
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 PR 23-AUG-2000; 2000WO-US023522.
 PR 24-AUG-2000; 2000WO-US023328.
 PR 08-NOV-2000; 2000WO-US030952.
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 PR 01-DEC-2000; 2000WO-US032678.
 PR 20-DEC-2000; 2000US-00747259.
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 PR 28-FEB-2001; 2001WO-US006520.
 PR 01-MAR-2001; 2001WO-US006666.
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 PR 06-AUG-2001; 2001US-00924419.
 PR 09-AUG-2001; 2001US-00927796.
 PR 16-AUG-2001; 2001US-00931836.
 PR 19-DEC-2001; 2001US-00028072.
 XX (GETH) GENENTECH INC.
 XX Baker KP, Beresini M, Deforge L, Desnoyers L, Filvaroff E, Gao W;
 PI Gerritsen ME, Goddard A, Godowski PJ, Gurney AL, Sherwood S;
 PI Smith V, Stewart TA, Tumas D, Watanabe CK, Wood WT, Zhang Z;
 XX WPI: 2003-695892/66.
 DR N-PSDB; ADA61414.
 XX
 PT New PRO nucleic acid and encode polypeptides, are useful for
 PT manufacturing a medicament for diagnosing or treating cancer.
 PS Claim 12; Fig 192; 660pp; English.
 XX
 CC The invention describes 305 nucleic acids encoding PRO (secreted and
 CC transmembrane) polypeptides (I). (I) is useful for stimulating the
 CC release of TNF-alpha from human blood, for modulating the uptake of
 CC glucose or FFA by skeletal muscle cells or adipocyte cells, for
 CC stimulating the proliferation or differentiation of chondrocyte cells,
 CC for stimulating the proliferation of or gene expression in pericyte
 CC cells, for stimulating the release of proteoglycans from cartilage, for
 CC stimulating the proliferation of inner ear utricular supporting cells,
 CC for stimulating the proliferation of T-lymphocyte cells, for stimulating
 CC the release of a cytokine from PMMC cells, for inhibiting the binding of
 CC A-peptide to factor VIIA, for inhibiting the differentiation of adipocyte
 CC cells, for stimulating proliferation of endothelial cells, for detecting
 CC the presence of tumour in a mammal. The tumour is lung, colon, breast,
 CC prostate, rectal, cervical or liver tumour. The oligonucleotide probes
 CC are useful for isolating genomic and cDNA nucleotide sequences or
 CC antisense probes. (I) is also useful as therapeutic agent. PRO is useful
 CC in assays to identify other proteins or molecules involved in binding
 CC interaction. A polynucleotide (II) encoding (I) is useful in chromosome
 CC and gene mapping, in generation of antisense RNA and DNA, in the
 CC preparation of PRO polypeptide, for generating transgenic animals or
 CC knockout animals which in turn are useful in the development and
 CC screening of therapeutically useful reagents, in gene therapy, for
 CC chromosome identification, as chromosome marker, and for generating
 CC probes. An anti-(I)-antibody is useful in diagnostic assays for PRO, e.g.
 CC detecting its expression in specific cells, tissues or serum, and for
 CC affinity purification of PRO from recombinant cell culture or natural
 CC sources. (I) and (II) are useful for tissue typing. This is the amino

CC acid sequence of a novel human secreted and transmembrane PRO
CC polypeptide.

XX
SQ Sequence 513 AA;

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Best Local Similarity 99.8%; Pred. No. 4.1e-261;
Matches 512; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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Search completed: November 15, 2004, 20:59:19
Job time : 92 secs


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RESULT 2
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; Sequence 192, Application US/10140002
; Patent No. 6725730
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Beresini, Maureen
; APPLICANT: DeForge, Laura
; APPLICANT: Desnoyers, Luc
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Sherwood, Steven
; APPLICANT: Smith, Victoria
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Watanabe, Colin K
; APPLICANT: Wood, William
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; TITLE OF INVENTION: ACIDS ENCODING THE SAME
; FILE REFERENCE: P3330R1C59
; CURRENT APPLICATION NUMBER: US/10/140,002
; CURRENT FILING DATE: 2002-05-06
; Prior Application removed - See Palm or File Wrapper
; NUMBER OF SEQ ID NOS: 550
; SEQ ID NO 192
; LENGTH: 513
; TYPE: PRT
; ORGANISM: Homo Sapien
US-10-140-002-192

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Score: 2752.00 Matches: 512
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Best Local Similarity: 99.81% Mismatches: 1
Query Match: 93.92% Indels: 0
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US-10-729-807-28 (1-1627) x US-10-140-002-192 (1-513)
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RESULT 3
 US-08-704-711A-20
 ; Sequence 20, Application US/08704711A
 ; Patent No. 6114159
 ; GENERAL INFORMATION:
 ; APPLICANT: WILL, Horst
 ; APPLICANT: HINZMANN, Bernd
 ; TITLE OF INVENTION: DNA SEQUENCES FOR MATRIX
 ; TITLE OF INVENTION: METALLOPROTEASES, THEIR PRODUCTION AND USE
 ; NUMBER OF SEQUENCES: 22
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSES: Foley & Lardner
 ; STREET: 3000 K Street, N.W., Suite 500
 ; CITY: Washington
 ; STATE: D.C.
 ; COUNTRY: USA
 ; ZIP: 20007-5109
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: PatentIn Release #1.0, Version #1.30
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/704,711A
 ; FILING DATE: 20-NOV-1996
 ; CLASSIFICATION: 435
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: WO PCT/DE95/00357
 ; FILING DATE: 17-MAR-1995
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: DE 4438838.1
 ; FILING DATE: 21-OCT-1994
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: DE 4409663.1
 ; FILING DATE: 17-MAR-1994
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: GRANADOS, Patricia D.
 ; REGISTRATION NUMBER: 33,683
 ; REFERENCE/DOCKET NUMBER: 26083/124
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: (202)672-5300
 ; TELEFAX: (202)672-5399

:	TELEX:	904136			
:	:	INFORMATION FOR SEQ ID NO: 20:			
:	:	SEQUENCE CHARACTERISTICS:			
:	:	LENGTH: 477 amino acids			
:	:	TYPE: amino acid			
:	:	STRANDEDNESS: single			
:	:	TOPOLOGY: linear			
<hr/>					
US-08-704-711A-20					
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Alignment Scores:					
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Score:	1254.00	Matches:	247		
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US-10-729-807-28 (1-1627) x US-08-704-711A-20 (1-477)					
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Db	41	TyrTyrAspLeuGluLysAspValLysGlnPheValArgGlyLeuAspSerGlyProVal	60		
QY	201	GATCACAAAATTCGGGAATCGAACATTTTTTGATTGACAGTCACTCGAAAACTGGAC	260		
Db	61	VallLysLysIleArgGluMetGlnLysPheLeuGlyLeuGluValThrGlyLysLeuAsp	80		
QY	261	TCAAACACCCCTTGAGATCATGAAGACACCGAGTGTGGGGTGCCTGATGTGGGCCAGTAT	320		
Db	81	SerAspThrLeuGluValMetArgLysProArgCysGlyValProAspValGlyHisPhe	100		
QY	321	GGCTACACCCCTCCCTGGG-----TGGAGAAATACAACCTCACCTACAGATAATA	371		
Db	101	--ArgThrPheProGlyIleProLysTrpArgLysThrHisLeuThrTyrArgIleVal	119		
QY	372	AACATATATCCCGATATGACGACGCTGCTGGATGAGCGCTATCCAAGAAGTTTAGAA	431		
Db	120	AsnTyrThrProAspLeuProLysAspAlaValAspSerAlaValGlnLysAlaLeuLys	139		
QY	432	GTGTGGAGCAAGTCACTCCACTAAATTCACCAAGATTTCAAAGGGATTCGACAGATC	491		
Db	140	ValTrpGluGluValThrProLeuThrPheSerArgLeuTyrGlyGluAlaAspIle	159		
QY	492	ATGATTGCTTTTAGGACTCGAGTCCATGGCTCGTCTCGCTAT---TTTCATGTGCC	548		
Db	160	MetIleSerPheAlaValArgGluHisGly-----AspPheTyrPropheAspGlyPro	177		
QY	549	TTGGGAGTCTTGGCGATGCGCTTTCCTCTGTGTCGGGTCTGGGTGGTGCACACTCATTTT	608		
Db	178	GlyAsnValLeuAlaHisAlaTyrAlaProGlyProGlyIleAsnGlyAspAlaHisPhe	197		
QY	609	GATCAGGATGAAAATCGACCAAGGATGAGCAGGATTCACCTGTTTCTTCTGGCTGCT	668		
Db	198	AspAspGluGlnTrpThrLysAspThrThrGlyThrAsnLeuPheLeuValAlaLa	217		
QY	669	CATGAATTTGGTCATGCACTGGGGTCTCTCACTCOAATGATCAACACGCTTGATGTTTC	728		
Db	218	HisGluIleGlyHisSerLeuGlyLeuPheHisSerAlaAsnThrGluAlaLeuMetTyr	237		
QY	729	CCAAATTATGTCCTCCCTG--GATCCGAAAATACCCACTTTTCTCAGATCATATCAAT	785		
Db	238	ProLeuTyrHisSerLeuThrAspLeuThrArgPheArgLeuSerGlnAspAspIleAsn	257		
QY	786	GGAATCCAGTCCATATGGA-----GGTCTGCTCAAGGTACCTGCT	827		

942 TATTATGATACAGGAGTGTGAGTTGAATTAATTCCTTCATCTCGCCATCTCTGCCA 1001
 : : : : :
 Db SerLeuArgLysLeuGluProGluLeuHisLeuSerPheThrProSerLeuPro 337
 : : : : :
 Qy 1002 GCTGATCTGCAAGCTGATACAGAG--AACCCAGAGATAAGATTCTGGTTTAAAGAT 1058
 : : : : :
 Db SerGlyValAspAlaIatyrGluValThrSerLysAspLeuValPheIlePheLysGly 357
 : : : : :
 Qy 1059 GAAACATCTTCGATGATCAGAGGATATGCTGTCTGCCAGATTATCCAAATCCATCAT 1118
 : : : : :
 Db AsnGlnPheTrpAlaIleArgGlyAsnGluValArgAlaGlyTyrProArgGlyIleHis 377
 : : : : :
 Qy 1119 ACATTAGCTTTCCAGACAGCTGTGAAGAAATAGATCAGCCGCTCTCTGTATAGACACACA 1178
 : : : : :
 Db ThrLeuGlyPheProThrValArgLysIleAspAlaIleSerAspLysGluLys 397
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 Qy 1179 AGAAACCTACTCTTTGTGGGCATTTGGTGTGGAGGTTTGATGAATGACCCAAACC 1238
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 Db AsnLysThrTyrPhePheValGluAspLysTyrTrpArgPheAspGluLysArgAsnSer 417
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 Qy 1239 ATGGACAAAGATTCGCGAGAGAGTGGTAAACACTTTCTCGGAATCAGTATCCGTGTT 1298
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 Db MetGluProGlyPheProLysGlnIleAlaGluAspPheProGlyIleAspSerLysIle 437
 : : : : :
 Qy 1299 GATGCTGCTTCCAGTACAAAGATTTCTTTTTCAGCCGTGATCAAGCAATTTGAA 1358
 : : : : :
 Db AspAlaValPheGluGluPheGlyPhePheTyrPhePheThrGlySerSerGlnLeuGlu 457
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 Db PheAspProAsnAlaLysValThrHisThrLeuLysSerAsnSerTrpLeuAsnCys 477

RESULT 5

US-09-521-220-20
 : Sequence 20, Application US/09521220
 : Patent No. 6399348
 : GENERAL INFORMATION:
 : APPLICANT: WILLS, Horst
 : HINZMANN, Bernd
 : TITLE OF INVENTION: DNA SEQUENCES FOR MATRIX
 : METALLOPROTEASES, THEIR PRODUCTION AND USE
 : NUMBER OF SEQUENCES: 22
 : CORRESPONDENCE ADDRESSES:
 : ADDRESSEE: Foley & Lardner
 : STREET: 3000 K Street, N.W., Suite 500
 : CITY: Washington
 : STATE: D.C.
 : COUNTRY: USA
 : ZIP: 20007-5109
 : COMPUTER READABLE FORM:
 : MEDIUM TYPE: Floppy disk
 : COMPUTER: IBM PC compatible
 : OPERATING SYSTEM: PC-DOS/MS-DOS
 : SOFTWARE: Patent In Release #1.0, Version #1.30
 : CURRENT APPLICATION DATA:
 : APPLICATION NUMBER: US/09/521,220
 : FILING DATE: 08-Mar-2000
 : CLASSIFICATION: <Unknown>
 : 21-OCT-1994
 : 17-MAR-1994
 : PRIOR APPLICATION DATA:
 : APPLICATION NUMBER: 08/704,711
 : FILING DATE: <Unknown>
 : APPLICATION NUMBER: DE 4438838.1
 : FILING DATE: 21-OCT-1994
 : APPLICATION NUMBER: DE 4409663.1
 : FILING DATE: 17-MAR-1994
 : ATTORNEY/AGENT INFORMATION:
 : NAME: GRANADOS, Patricia D.
 : REGISTRATION NUMBER: 33,683
 : REFERENCE/POCKET NUMBER: 26083/124
 : TELECOMMUNICATION INFORMATION:

TELEPHONE: (202)672-5300
 TELEFAX: (202)672-5399
 TELEX: 904136
 : INFORMATION FOR SEQ ID NO: 20:
 : SEQUENCE CHARACTERISTICS:
 : LENGTH: 477 amino acids
 : TYPE: amino acid
 : STRANDEDNESS: single
 : TOPOLOGY: linear
 : SEQUENCE DESCRIPTION: SEQ ID NO: 20:
 : US-09-521-220-20

Alignment Scores:
 Pred. No.: 4,49e-133 Length: 477
 Score: 1254.00 Matches: 247
 Percent Similarity: 66.04% Conservative: 70
 Best Local Similarity: 51.46% Mismatches: 145
 Query Match: 42.80% Indels: 18
 DB: 3 Gaps: 9

US-10-729-807-28 (1-1627) x US-09-521-220-20 (1-477)

Qy 24 ATGAGCGCTTCTGCTTCTGTGTGTTCTTCTTATAACATTTCTTCTGATTCCTT 83
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 Db 1 MetLysSerLeuProIleLeuLeuLeuCysValAlaValCysSerAlaTyrProLeu 20
 : : : : :
 Qy 84 GTCGGATGACGGAAATGAAGAA--AATATGCAACTGGCTCAGGCATATCTCAACAG 140
 : : : : :
 Db 21 AspGlyAlaAlaArgGlyGluAspThrSerMetAsnLeuValGlnLysTyrLeuGluAsn 40
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 Qy 141 TTCTACTCTCTTGAATAGAAAGGAATCATCTTTTCAAAAGCAAGATAGAGTCTCAT 200
 : : : : :
 Db 41 TyrTyrAspLeuGluLysAspValLysGlnPheValArgLysAspSerGlyProVal 60
 : : : : :
 Qy 201 GATGACAAATTCGGGAAATTCGAAGCATTTTGGATTGACAGTACTGGAACCTGGAC 260
 : : : : :
 Db 61 ValLysLysIleArgGluMetGlnLysPheLeuGlyLeuGluValThrGlyLysLeuAsp 80
 : : : : :
 Qy 261 TCAAACACCTTGAGATCATGACACACCCAGGTGTGGGTGCTGTATGTGGGCAGTAT 320
 : : : : :
 Db 81 SerAspThrLeuGluValMetArgLysProArgCysGlyValProAspValGlyHisPhe 100
 : : : : :
 Qy 321 GGCTACACCTCTCCCTGGG-----TGGAGAAATATACACCTCCTACAGAAATA 371
 : : : : :
 Db 101 ---ArgThrPheProGlyIleProLysTyrArgLysThrHisLeuThrTyrArgIleVal 119
 : : : : :
 Qy 372 AACTATCTCGGATATGCGACAGCTGTGTGATGAGGTATCCAGAGGTTTGA 431
 : : : : :
 Db 120 AsnTyrThrProAspLeuProLysAspAlaValAspSerAlaValGluLysAlaLeuLys 139
 : : : : :
 Qy 432 GTGTGGAGCAAAAGTCACTCCACTAAAATTCCACCAAGATTTCAAAGGGGATTCAGACATC 491
 : : : : :
 Db 140 ValTrpGluGluValThrProLeuThrPheSerArgLeuTyrGluGlyGluAlaAspIle 159
 : : : : :
 Qy 492 ATGATTGCTTTAGGACTCCAGTCCATGGTGGGTGCTCTCGCTAT---TTTGATGGTCCC 548
 : : : : :
 Db 160 MetIleSerPheAlaValArgGluHisGly-----AspPheTyrProPheAspGlyPro 177
 : : : : :
 Qy 549 TTGGAGTGTCTGGCCATGCTTTCTCTCGGTCTGGGTCTGGGTGAGCACATTTT 608
 : : : : :
 Db 178 GlyAsnValLeuAlaHisAlaTyrAlaProGlyIleAsnGlyAspAlaHisPhe 197
 : : : : :
 Qy 609 GATGAGATGAAAACTGGACCAAGGATGGACAGGATTTCAACTTGTCTTGTGGCTGCT 668
 : : : : :
 Db 198 AspAspAspGluGlnTrpThrLysAspThrThrGlyThrAsnLeuPheLeuValAlaAla 217
 : : : : :
 Qy 669 CATGAATTTGTGTATGATCGCTGGGCTCTCTCACTCCATGATCAACAGCCCTTGTGTTTC 728
 : : : : :
 Db 218 HisGluIleGlyHisSerLeuGlyLeuPheHisSerAlaAsnThrGluAlaLeuMetTyr 237
 : : : : :
 Qy 729 CCAATATTATGCTCCCTG---GATCCCCAGAAATACCCACTTCTCAGATGATCATCAAT 785
 : : : : :
 Db 238 ProLeuTyrHisSerLeuThrAspArgPheArgLeuSerGlnAspAspIleAsn 257

QY	150	CTTGAAATAGAAAGGAATCATCTTTCAACCAAGAAATAGGAGTCTCATAGATGCATAA	209
Db	44	LeuGluLysAspValLysGlnPhe---ArgArgLysAspSerAsnLeuLeuValLysLys	62
QY	210	ATTCCGGAAATGCAAGCAATTTTTTCGATTGACAGTCACTGGAAAACTGGCACTCAACACC	269
pb	63	IleGlnGluWetGlnLysPheLeuGlyLeuGluValThrGlyLysLeuAspThrAspThr	82

270	CTTGAGATCATGACGACACCCAGGTGCTGGGTGGCTGATGTGGCGCCAGTATGCTGCTAC---	326
83	LeuGluValMetArgIysProArgCysGlyValProAspValGlyHisSerSerPhe	102
327	---ACCCCTCCCTGGGTGGAGAAAATACAACTCACCTACAGAAATATAAATATACTCCG	383
103	ProGlyMetProIysTirpArgIysThrHisLeuThrTyArgIleValAsnThrPro	122
384	GATATGGCAGCAGCTGCTGTGGATGAGGCTATCCAAAGAGTTTGAAGTGTGGAGCAA	443
123	AspLeuProArgAspAlaValAspSerAlaIleGluLysAlaLeuLysValTrpGluGlu	142
444	GTCACTCCACTAAATTCACCAAGATTCCAAAGGGATTGCAGACATCATGATGCCTTT	503
143	ValThrProLeuThrPheSerArgLeuTyGluGlyGluAlaAspIleMetIleSerPhe	162
504	AGGACTCGAGTCATCGTGGTGTCTCGCTATTTTGGATGGTCCCTTGGGAGTGTCTGCG	563
163	AlaValLysGluHisGlyAspPhe---TyrSerPheAspGlyProGlyHisSerLeuAla	181
564	CATGCTCTTCTCCTCGTCCGGTCTGGGTGGTGCACATCATTTTCATGAGGATGAAC	623
182	HisAlaTyProProGlyProGlyLeuTyGlyAspIleHisPheAspAspGluLys	201
624	TGGACCAAGATGGAGCAGGATTCAACTGTGTTCTTGTGGTCTCATGAATGTGTCAT	683
202	TrpThrGluAspAlaSerGlyThrAsnLeuPheLeuAlaHisGluLeuGlyHis	221
684	GCATGGGGCTCTCACTCCAATGATCAACAGCCTTGATGTTCCAAATATGTCCTCC	743
222	SerLeuGlyLeuPheHisSerAlaAsnThrGluAlaLeuMetTyrProLeuTyAsnSer	241
744	CTG---GATCCCGAGAAAATACCCCACTTCTCAGGATGATATCAATGGAATCCAGTCCATC	800
242	PheThrGluLeuAlaGlnPheArgLeuSerGlnAspAspValAsnGlyIleGlnSerLeu	261
801	TATGGAGGCTGCTGCTAAGTACCTGCTTAAGCCAAAGAACCCCACT-----	845
262	TyrGlyProProAlaSerThrGluGluProLeuValProThrLysSerValProSer	281
846	-----ATACCCCATGCTGTGACCTGACTTGACTTTTCAGCTATCAACAATTC	896
282	GlySerGluMetProAlaLysCysAspProAlaLeuSerPheAspAlaIleSerThrLeu	301
897	CGCAGAGAAGTAATGTTCTTTAAAGGCAGGCACCTATGGAGGATCTATTATGATATCAGC	956
302	ArgGlyGluTyLeuPhePheLysAspArgTyPheTrpArgArgSerHisTrpAsnPro	321
957	GATGTTGAGTTTGAATTAATGCTTCATCTGCGCATCTCTGCCAGCTGATCTGCAAGCT	1016
322	GluProGluPheHisLeuIleSerAlaPheTrpProSerLeuProSerTyLeuAspAla	341
1017	GCATACGAG---AACCCGACAGATAAGATCTCGTGTGTTTAAAGATGAAACTTCTCGATG	1073
342	AlaTyGluValAsnSerArgAspThrValPheIlePheLysGlyAsnGluPheTrpAla	361
1074	ATCAGAGGATATGCTGCTCTGCCAGATTATCCCAAAATCCATCCATAGTGTTCCTCA	1133
362	IleArgGlyAsnGluValGlnAlaGlyTyProArgGlyIleHisThrLeuGlyPhePro	381
1134	GGAGCTGTGAAGAAAATAGATGCGCGCTCTGTGATAGACCCACAGAAAACCTACTTC	1193
382	ProThrIleArgLysIleAspAlaAlaValSerAspLysGluLysLysThrTyPhe	401
1194	TTTGTGGGCATTTGGTGTGAGGTTTTCATGAATGATCCCAACCATGACCAAGGATTC	1253
402	PheAlaAlaAspLysTyTrpArgPheAspGluAsnSerGlnSerMetGluGlnGlyPhe	421
1254	CGCAGACAGGTTGTAACACACTTCTTCGGAATCAGTATCCGCTGTGTGATGCTGCTTC	1313
422	ProArgLeuIleAlaAspAspPheProGlyValGluProLysValAspAlaValLeuGln	441
1314	TACAAAGGATTTCTCTTTTTCAGCCGTGGATCAAGCAATTTGAATACAACTTAAGACA	1373


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Db      382 ProThrIleArgLysIleAspAlaAlaValSerAspLysGluLysLysThrTyrPhe 401
QY      1194 TTTGTGGCATTGGTCTGGAGGTTTGTATGAATGACCCAAACCATGGACAAAGGATTC 1253
Db      402 PheAlaAlaAspLysTyrTrpArgPheAspGluAsnSerGlnSerMetGluGlnGlyPhe 421
QY      1254 CCGCAGAGAGTGTAACACACTTCTTCGGGAATCAGTATCCGTGTGATGCTGCTTCCAG 1313
Db      422 ProArgLeuIleAlaAspAspPheProGlyValGluProLysValAspAlaValLeuGln 441
QY      1314 TACAAGGATCTCTTTTTCAGCCGGGATCAAGCAATTTGAATCAACATTAAGACA 1373
Db      442 AlaPheGlyPhePheTyrPhePheSerGlySerGlnGlnPheGluPheAspProAsnAla 461
QY      1374 AAGAATATTACCCGAATCATGAGAACTAATACTTGGTTTCAATGC 1418
Db      462 ArgMetValThrHisIleLeuLysSerAsnSerTrpLeuHisCys 476

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RESULT 11

US-09-391-104-22

; Sequence 22, Application US/09391104

; Patent No. 639371

; GENERAL INFORMATION:

; APPLICANT: Abbott Laboratories

; APPLICANT: Falduto, Michael T.

; APPLICANT: Magnuson, Scott R.

; APPLICANT: Morgan, Douglas W.

; TITLE OF INVENTION: HUMAN MATRIX METALLOPROTEASE GENE,

; TITLE OF INVENTION: PROTEINS ENCODED THEREFROM AND METHODS

; TITLE OF INVENTION: OF USING SAME

; FILE REFERENCE: 6073.US.P1

; CURRENT APPLICATION NUMBER: US/09/391,104

; CURRENT FILING DATE: 1999-09-07

; PRIOR APPLICATION NUMBER: US 08/814,394

; PRIOR FILING DATE: 1997-03-11

; NUMBER OF SEQ ID NOS: 35

; SOFTWARE: FastSeq for Windows Version 3.0

; SEQ ID NO 22

; LENGTH: 476

; TYPE: PRT

; ORGANISM: Homo sapiens

US-09-391-104-22

Alignment Scores:

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Pred. No.:      8,4e-131      Length:      476
Score:          1234.00      Matches:      244
Percent Similarity: 67.58%      Conservative: 77
Best Local Similarity: 51.37%      Mismatches: 136
Query Match:      42.12%      Indels:      18
DB:               3          Gaps:       8

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US-10-729-807-28 (1-1627) x US-09-391-104-22 (1-476)

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QY      33 CTTCGTCTCGTGTCTCTTTTATAACATTTCTCTGCAATTCCTTAGTCCGGATG 92
Db      7 LeuValLeuLeuCysLeu-----ProValCysSerAlaTyrProLeuSerGlyAla 23
QY      93 ACGGAATATGAAGAA---AATATGCAACTGCTCAGGCATATCTCAACACGATCTTCTCT 149
Db      24 AlaLysGluGluAspSerAsnLysAspLeuAlaGlnGlnTyrLeuGluLysTyrTyrAsn 43
QY      150 CTTGAATATGAAGGAATCATCTTCTCAAGCAGAGATAGGATCTCATAGATGACAAA 209
Db      44 LeuGluLysAspValLysGlnPhe---ArgArgLysAspSerAsnLeuIleValLysLys 62
QY      210 ATTCCGGAATATGAAGCAATTTTTCGATTGACAGTGTGCTGGAATAACTGCACTCAACACC 269
Db      63 IleGlnGlyMetGlnLysPheLeuGlyLeuGluValThrGlyLysLeuAspThrAspThr 82
QY      270 CTTGAGATCATGAAGACACCCAGGTGTGGGGTGTGCTGATGGGGCAGCATATGGGTAC--- 326
Db      83 LeuGluValMetArgLysProArgCysGlyValProAspValGlyHisPheSerSerPhe 102

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QY      327 ---ACCTCCCTGGGTGGAGAAATACACCTCACCTACAGAAATAATAAACTATACTCCG 383
Db      103 ProGlyMetProLysTrpArgLysThrHisLeuThrTyrArgIleValAsnTyrThrPro 122
QY      384 GATATGGCAGCAGCTCTGTGGATGAGGCTATCAAGAAGGTTTAGAAGTGTGGAGCAAA 443
Db      123 AspLeuProArgAspAlaValAspSerAlaIleGluLysAlaLeuLysValTrpGluGlu 142
QY      444 GTCATCCCACTAAATTCACCAAGATTCAAGGGGATTCAGACATCATCATGATTCCTTT 503
Db      143 ValThrProLeuThrPheSerArgLeuTyrGluGlyGluAlaAspIleMetIleSerPhe 162
QY      504 AGGACTCGAGTCATCGTGGTCTCTCGCTATTTCGATCGTCCCTGGGAGTGTCTGGC 563
Db      163 AlaValLysGluHisGlyAspPhe---TyrSerPheAspGlyProGlyHisSerLeuAla 181
QY      564 CATGCCCTTCTCTCTCGTCCGGTCTGGGTGGTGCACACTCATTTTGTAGAGGATGAAC 623
Db      182 HisAlaTyrProProGlyProGlyLeuTyrGlyAspIleHisPheAspAspAspGluLys 201
QY      624 TGGACCAAGATGGACGAGGATTCACACTTCTTCTGTGGCTGCTCATGATTTGGTCAT 683
Db      202 TrpThrGluAspAlaSerGlyThrAsnLeuPheLeuValAlaAlaHisGluLeuGlyHis 221
QY      684 GCATCGGGCTCTCTCACTCCAATGATCAACAGCCTTGATGTTCCTCAAAATTTATGTCTCC 743
Db      222 SerLeuGlyLeuPheHisSerAlaAsnThrGluAlaLeuMetTyrProLeuTyrAsnSer 241
QY      744 CTG---GATCCCAAGAAATACCCACTTCTCAGATGATATCAATGAATCAATCCAGTCCATC 800
Db      242 PheThrGluLeuAlaGlnPheArgLeuSerGlnAspAspValAsnGlyIleGlnSerLeu 261
QY      801 TATGGAGCTCTGCTAAGTACCTGCTAAGCCAAAGCAAGCAACCCACT-----845
Db      262 TyrGlyProProAlaSerThrGluGluProLeuValProThrLysSerValProSer 281
QY      846 -----ATACCCCATGCTGTGACCCCTGACTTTTGACCTTTTGACGCTATCACAACTTTC 896
Db      282 GlySerGluMetProAlaLysCysAspProAlaLeuSerPheAspAlaIleSerThrLeu 301
QY      897 CGCAGAGAAGTAATGTCTTTAAAGCAGGACCTATGAGGAGTCTATTATGATATACAG 956
Db      302 ArgGlyGluTyrLeuPheLysAspArgTyrPheTrpArgArgSerHisTrpAsnPro 321
QY      957 GATGTTGAGTTGAATTAATTTGCTTCTGTCATCTGGCCATCTCTGCCAGTGTCTGCAAGCT 1016
Db      322 GluProGluPheHisLeuIleSerAlaPheTrpProSerLeuProSerTyrLeuAspAla 341
QY      1017 GCATACGAG---AACCCCGACAGATAAGATTTCTGTTTAAAGATGAAACCTTCTGGATG 1073
Db      342 AlaTyrGluValAsnSerArgAspThrValPheIlePheLysGlyAsnGluPheTrpAla 361
QY      1074 ATCAGAGATATGCTGCTTCCAGATATTCCTCAATTCCTCCATATCCATACATAGTTTCCA 1133
Db      362 IleArgGlyAsnGluValGlnAlaGlyTyrProArgGlyIleHisThrLeuGlyPhePro 381
QY      1134 GGACGTGTGAAGAAATAGATGACGACGCTCTGTGATAGACCAACAAAGAAAACCTACTTC 1193
Db      382 ProThrIleArgLysIleAspAlaValSerAspLysGluLysLysThrTyrPhe 401
QY      1194 TTTGTGGCATTGGTGTGGAGTTTGAATATGAAATGACCCCAACCATGGCAAGGATTC 1253
Db      402 PheAlaAlaAspLysTyrTrpArgPheAspGluAsnSerGlnSerMetGluGlnGlyPhe 421
QY      1254 CCGCAGAGAGTGTAAACACATCTTCTGATCATGATCCGTGTGTGATGCTGCTTCCAG 1313
Db      422 ProArgLeuIleAlaAspAspPheProGlyValGluProLysValAspAlaValLeuGln 441
QY      1314 TACAAGGATCTCTTCTTTTTCAGCCGGTCAAGCAATTTGAATCAACATTAAGACA 1373
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; SOFTWARE: PatentIn Ver. 2.0

DOE ID NO. 4

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:      LENGTH: 467

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LENGTH: 10
TYPE: PRT

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; TYPE: PRI
; ORGANTSM: Homo sapiens

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; ORGANISM: H
ITS-09-179-002-4

Alignment Scores:

Pred. No.:	1.63e-122	Length:	467
Score:	1161.00	Matches:	228
Percent Similarity:	63.35%	Conservative:	71
Best Local Similarity:	48.31%	Mismatches:	157
Query Match:	39.62%	Indels:	16
DB:	1	Gaps:	8

US-10-729-807-28 (1-1627) x US-09-178-002-4 (1-467)

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Qy	84	GTCCGGATGACGGAAAATGAAGAAAATATGCAATGGCTCAGGCATATCTCAACAGTTC	143
Db	23	-----ValSerSerLysGluLysAsnThrLysThrValGlnAspTyrLeuGluLysPhe	40
Qy	144	TACTCTCTTGAATATAGAGGGAATCATCTGTTCAAAGCAAGAATPAGGAGTCTCATAGAT	203
Db	41	TyrGlnLeuProSerAsnGlnTyrGlnSerThrArgLysAsnGlyThrAsnValIleVal	60
Qy	204	GACAAATTCGGAAAATGCACAGCATTTTTCGATGTACAGTGCAGTGGAAAATCGACTCA	263
Db	61	GluLysLeuLysGluMetGlnArgPhePheGlyLeuAsnValThrGlyLysProAsnGlu	80
Qy	264	AACACCTTGTAGATCATGAACACACCCAGGTGTGGGTGCCTGATGTGGCGCAGTATGCG	323
Db	81	GluThrLeuAspMetMetLysLysProArgCysGlyValProAspSerGly-----Gly	98
Qy	324	TACACCCCTC-----CCTGGGTGGAAAATAACAACCTCACCTACAGAATAATA	371
Db	99	PheMetLeuThrProGlyAsnProLysTrpGluArgThrAsnLeuThrTyrArgIleArg	118
Qy	372	AACATATCTCCGGATATGGCAGGAGCTCTGTGGATGAGGCTATCCAGAAGGTTTGA	431
Db	119	AsnTyrThrProGlnLeuSerGlnAlaGluValGluArgAlaIleLeuAspAlaPheGlu	138
Qy	432	GTGTGGAGCAAGTCACCTCCACTAAAATTCACCAAGATTTCAAAGGGGATTCACACATC	491
Db	139	LeuTrpSerValAlaSerProLeuIlePheThrArgIleSerGlnGlyGluAlaAspIle	158
Qy	492	ATGATGTCCTTTAGACATCGAGTCATCGT---CGGTGTCCTCGCTATTTTGATGGTCC	548
Db	159	AsnIleAlaPheTyrGlnArgAspHisGlyAspAsnSerPro-----PheAspGlyPro	176
Qy	549	TTGGAGTGTCTGGCATGCTCTTCTCCTGGTCGGGTCTGGGTGTGCACACTCATTTT	608
Db	177	AsnGlyIleLeuAlaHisAlaPheGlnProGlyGlnGlyIleGlyGlyAspAlaHisPhe	196
Qy	609	GATGAGGATGAAAACTGACCAAGGATGGAGCAGGATTCACCTGTCTTCTTGCTGCTGT	668
Db	197	AspAlaGluGluThrTrpThrAsnThrSerAlaAsnTyrAsnLeuPheLeuValAlaAla	216
Qy	669	CATGAAATTTGGTCATGCACTGGGGCTCTCTCACTCGAATGATCAACAGCCCTTGATTC	728
Db	217	HisGluPheGlyHisSerSerLeuGlyLeuAlaHisSerSerAspProGlyAlaLeuMetTyr	236
Qy	729	CCAAATATATGTCCTCGATCCCAAGAAAATACCCACTTTCTCAGATGATATCAATGGA	788
Db	237	ProAsnTyrAlaPheArgGluThrSerAsnTyrSerLeuProGlnAspAspIleAspGly	256
Qy	789	ATCCAGTCCATCTATFGAGGTCTGCCTAAGTACTGCTGAAGCCAAAGAAACCCACTATA	848
Db	257	IleGlnAlaIleTyr---GlyLeuSerSerAsnProIleGlnProThrGlyProSerThr	275

US-10-729-807-28 (1-1627) x US-09-391-104-24 (1-467)

QY	24	ATGAAGCCCTTCTGCTCTGTCTGTGGTTTGTTATTATAACATTTTCTTCGTGCATTTCTCCCTTTA	83
Db	4	LeuLysThrLeuProPheLeuLeuLeuHisValGlnIleSerLysAlaPhePro---	22
QY	84	GTCGGGATGACGGAAATGAACAATAATGCAACTGGCTCAGGCATATCTCAACAGTTC	143
Db	23	-----ValSerSerLysGluLysAsnThrLysThrValGlnAspTyLeuGlyLysPhe	40
QY	144	TACTCTCTTAATAGAAGGGAATCATCTTGTTCAAAGCAAGATAGGAGTCTCATAGAT	203
Db	41	TyrGlnLeuProSerAsnGlnTyrGlnSerThrArgLysAsnGlyThrAsnValIleVal	60
QY	204	GACAAAATTCGGAAAATCGACAGCATTTTTTGGAATTGACAGTAGCTGGAATACTGACATCA	263
Db	61	GluLysLeuLysGluMetGlnArgPheGlyLeuAsnValThrGlyLysProAsnGlu	80
QY	264	AACACCCTTGAGATCATCAAGACACCCAGGTGTGGGTGCCCTGATGTGGCCAGTATGCG	323
Db	81	GluThrLeuAspMetMetLysLysProArgCysGlyValProAspSerGly-----Gly	98
QY	324	TACACCCTC-----CCTGGGTGGGAAAAATACAACCTCACCTACAGATAATA	371
Db	99	PheMetLeuThrProGlyLysProLysTrpGluArgThrAsnLeuThyTyrArgIleArg	118
QY	372	AACATATCTCCGGATATGGCAGCAGCTGCTGTGGATGAGGCTATCCAAGAGGTTTGA	431
Db	119	AsnTyrThrProGlnLeuSerGluAlaGluValGluArgAlaIleLysAspAlaPheGlu	138
QY	432	GTGTGGAGCAAGTCACTCCCACTAAATTCACCAAGATTTCAAGGGGATTCGACATC	491
Db	139	LeuTrpSerValAlaSerProLeuIlePheThrArgIleSergInglyGluAlaAspIle	158
QY	492	ATGATTCGCTTTTAGGACTCGAGTCCATGGT---CGGTGCTCCGTATTTTGATGGTCCC	548
Db	159	AsnIleAlaPheTyrGlnArgAspHisGlyAspAsnSerPro-----PheAspGlyPro	176
QY	549	TTGGGATGCTTGGCCATGCTTTTCCTCGTTCGGTCCGGTCTGGGTGGTGACACTCATTTT	608
Db	177	AsnGlyIleLeuAlaHisAlaPheGlnProglyGlnglyIleGlyGlyAspAlaHisPhe	196
QY	609	GATCAGGATGAACACTGGACCAAGATGGAGCAGGATCAACTTGTTCCTGTGGCTGCT	668
Db	197	AspAlaGluGluThrItpThrAsnThrSerAlaAsnTyrAsnLeuPheLeuValAlaAla	216
QY	669	CATCAATTTGGTCATGCACTGGGCTCTCTCACTCCAATGATCAACACAGCCCTCATGPTC	728
Db	217	HisGluPheGlyHisSerLeuGlyLeuAlaHisSerSerAspProGlyAlaLeuMetTyr	236
QY	729	CGAAATATGCTCCCTGGATCCCGAAAAATACCCTTTCTCAGGATGATATCAATGGA	788
Db	237	ProAsnTyrAlaPheArgGluThrSerAsnTyrSerLeuProGlnAspAspIleAspGly	256
QY	789	ATCCAGTCCATCTATGGAGCTCGCCTAAGGTACTCTAAGCCAAAGAACCCACTATA	848
Db	257	IleGlnAlaIleTyr--GlyLeuSerSerAsnProIleGlnProThrGlyProSerThr	275
QY	849	CCCCATGCTGTCAACCTGACTTGACTTTTGACGCTATCAACTTTCCCGCAGAGAAGTA	908
Db	276	ProLysProCysaspProSerLeuThrPheAspAlaIleThrThrLeuArgGlyGluIle	295
QY	909	ATGTTCTTTAAAGCAGGCACCTATGAGGATCTTATATGATATCACGGATGTTGAGTTT	968
Db	296	LeuPhePheLysAspArgTyrPheTrpArgArgHisProGlnLeuGlnArgValGluMet	315
QY	969	GAATTAACTTCATTCGGCCATCTCTGCGCAGCTGATCTGCAAGCTGCATCAGAGAAC	1028
Db	316	AsnPheIleSerLeuPheTrpProSerLeuProThrGlyIleGlnAlaIleTyrGluAsp	335
QY	1029	---CCACAGATAAAGATTCTGTGTTTTTAAAGATCAAACTTCTGGATGATCAGAGGATAT	1085
Db	336	PheAspArgAsnLeullePheLeuPheLysGlyAsnGlnTyrTrpAlaLeuSergIlyTyr	355

RESULT 15

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US-08-448-489-13
; Sequence 13, Application US/08448489
; Patent No. 6184022
; GENERAL INFORMATION:
; APPLICANT: SEIKI, Motoharu
; APPLICANT: SATO, Hiroshi
; APPLICANT: SHINAGAWA, Akira
; TITLE OF INVENTION: NOVEL METALLOPROTEINASE AND ENCODING DNA THEREFOR
; FILE REFERENCE: 55-290P
; CURRENT APPLICATION NUMBER: US/08/448,489
; CURRENT FILING DATE: 1995-06-07
; NUMBER OF SEQ ID NOS: 19
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 13
; LENGTH: 468
; TYPE: PRT
; ORGANISM: Unknown
; FEATURE:
; OTHER INFORMATION: X = UNKNOWN
; FEATURE:
; OTHER INFORMATION: Description of Unknown Organism: Known Member of
; OTHER INFORMATION: Matrix Metalloproteinase Family
US-08-448-489-13

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Alignment Scores:		
Pred. No.:	1.63e-122	Length:
Score:	1161.00	Matches:
Percent Similarity:	63.3%	Conservative:
Best Local Similarity:	48.31%	Mismatches:
Query Match:	39.62%	Indels:
DB:	3	Gaps:
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		71
		228
		468

US-10-729-807-28 (1-1627) x US-08-448-489-13 (1-468)

24	ATGAAGCGCTTCTGCTCTCTGTTCTTTATACATTTTCTTCTGCATTTCCTTA	83
QY		
4	LeuLysThrLeuProPheLeuLeuLeuLeuHisValGlnIleSerLysAlaPhePro---	22
Db		
84	GTCCGGATGACGGAAATGANGAAATATGCAACTGCTCAGGCATATCTCAACCAAGTTC	143
QY		
23	-----ValSerSerLysGluLysAsnThrLysThrValGlnAspTyrLeuGluLysPhe	40
Db		
144	TACTCTCTGAATAGAAGGGAATCATCTTGTTCAAAGCAAGAAATAGGAGTCTCATAGAT	203
QY		
41	TyrGlnLeuProSerAsnGlnTyrGlnSerThrArgLysAsnGlyThrAsnValIleVal	60
Db		
204	GACAAATTCGGGAATGCAAGCATTTTTTTGGATTGACAGTACTGGAAAACCTGGACTCA	263
QY		

Db	61	GlulysLeuLysGluMetGlnArgPhePheGlyLeuAsnValThrGlyLysProAsnGlu	80
Qy	264	AAACCCCTCGAGATCATGAAGACACCCAGGTGTGGGTGCCTGATGTGGCCAGTATGCG	323
Db	81	GluthrLeuAspMetLysLysProArgCysGlyValProAspSerGly	98
Qy	324	TACACCTC-----CTGGGTGGAGAAATACAACCTCACCTACAGATAATA	371
Db	99	PheMetLeuThrProGlyAsnProLysTrpGluArgThrAsnLeuThrTyrArgIleArg	118
Qy	372	AACTATACTCCGATATGGCAGCAGCTGCTGTGGATGAGCTATCCAAGAAGTTTAGAA	431
Db	119	AsnTyrThrProGlnLeuSerGluAlaGluValGluArgAlaIleLysAspAlaPheGlu	138
Qy	432	GTGTGGAGCAAAAGTCATCCACTAAATTCACCAAGATTCAAGGGGATTCGACACATC	491
Db	139	LeuTrpSerValAlaAspProLeuIlePheThrArgIleSerGlnGlyLeuAlaAspIle	158
Qy	492	ATGATTCCCTTTAGACTCGAGTCCATGGT---CGGTGCTCCTCGCTATTGTATGTCCTC	548
Db	159	AsnIleAlaPheTyrGlnArgAspHisGlyAspAsnSerPro-----PheAspGlyPro	176
Qy	549	TTGGAGTGTCTTGCCATGCTTCCTTCCTGGTCCGGTCTGGGTGGTGCACATCAATTT	608
Db	177	AsnGlyIleLeuAlaHisAlaPheGlnProGlyGlnGlyIleGlyGlyAspAlaHisPhe	196
Qy	609	GATGAGGATGAAACTCGGACCAAGGATGGAGCAGGATTCACTGTGTTCTTGTGGCTGCT	668
Db	197	AspAlaGluGluThrTrpThrAsnThrSerAlaAsnTyrAsnLeuPheLeuValAlaAla	216
Qy	669	CATGAATTTGTGTCATGCACTGGGCTCTCTCACTCCAATCATCAACAGCCTTGATGTTT	728
Db	217	HisGluPheGlyHisSerLeuGlyLeuAlaHisSerSerAspProGlyAlaLeuMetTyr	236
Qy	729	CCAAATATTGTCTCCCTGGATCCCGCAAAATACCCACTTTCTCAGGATGATATCAATGGA	788
Db	237	ProAsnTyrAlaPheArgGluThrSerAsnTyrSerLeuProGlnAspAspIleAspGly	256
Qy	789	ATCCAGTCCATCTATGGAGGTCTGCTAAGTACTCTCTAAGCCCAAGAACCCACTATA	848
Db	257	IleGlnAlaIleTyr---GlyLeuSerSerAsnProIleGlnProThrGlyProSerThr	275
Qy	849	CCCCATGCTGTGACCTGACTTGACTTTTGACGCTATCAACTTTCCGACAGAGAATA	908
Db	276	ProLysProCysAspProSerLeuThrPheAspAlaIleThrLeuArgGlyGluIle	295
Qy	909	ATGTTCTTTAAAGGCAGCACCTATGGAGGATCTATTATGATATFCAGGATGTGAGTTT	968
Db	296	LeuPhePheLysAspArgTyrPheTrpArgArgHisProGlnLeuGlnArgValGluMet	315
Qy	969	GAATTAATGTCTCATCTGCGCATCTCTGCCAGCTGATCGAAGCTGCATACGAGAAC	1028
Db	316	AsnPheIleSerLeuPheTrpProSerLeuProThrGlyIleGlnAlaIleTyrGluAsp	335
Qy	1029	---CCCACAGATAAGATCTCGTTTAAAGATGAAACTTCTCGATGATCAGAGGATAT	1085
Db	336	PheAspArgAspLeuIlePheLeuPheLysGlyAsnGlnTyrTrpAlaLeuSerGlyTyr	355
Qy	1086	GCTGTCTGCCAGATTATCCCAAAATCCATCCATATTAGGTTTTTCCAGCAGCGTGAAG	1145
Db	356	AspIleLeuGlnGlyTyrProLysAspIleSerAsnTyrGlyPheProSerSerValGln	375
Qy	1146	AAAAATAGATGACCGCTGTGTGATGAACACACAGAAAACCTACTCTTTGTGGGCATT	1205
Db	376	AlaIleAspAlaAlaValPheTyrArgSer-----LysThrTyrPhePheValAsnAsp	393
Qy	1206	TGGTGTGGAGGTTTGAATGAAATGATGCCAAACCATGGACAAAGATTCCCCAGCAGAGT	1265
Db	394	GlnPheTrpArgTyrAspAsnGlnArgGlnPheMetGluProGlyTyrProLysSerIle	413
Qy	1266	GTAAAAACATTTCTCTGGAATCAGTATCCGTGTGTGATGTGTTCCAGTACAAGAGTTC	1325

QY 372 AACTATATCCGGATATGGACGAGCTGCTGTGGATGAGGCTATCCAAGACGTTTGA 431

GenCore version 5.1.6
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OM nucleic - protein search, using frame_plus_n2p model

Run on: November 15, 2004, 16:35:24 ; Search time 128 Seconds

(without alignments)

9119.571 Million cell updates/sec

Title: US-10-729-807-28

Perfect score: 2930

Sequence: 1 gcttcagctgaagaagaga.....aattcgtctcaaaatagaa 1627

Scoring table:

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-DB=A_Geneseq 23Sep04 -QFMT=fastan -SUFFIX=rag -MINMATCH=0.1 -LOOPEXT=0			
-LIST=45 -DOCALIGN=200 -THR SCORE=pct -THR MAX=100 -THR MIN=0 -ALIGN=15			
-MODE=LOCAL -OUTFMT=ptc -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=2000000000			
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-NO MAP -LARGEQUERY -NEG SCORES=0 -WAIT DSPBLOCK=100 -LONGLOG			
-DEV TIMEOUT=120 -WARN TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6			
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7			

Searched: 2002273 seqs, 358729299 residues

Total number of hits satisfying chosen parameters: 4004546

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Command line parameters:

-MODEL=frame+ n2p.model -DEV=xlh
-Q/-cgn2.1/USPTO spool/US10729807/runat 15112004.131150.14678/app query.fasta_1.1799
-DB=A_Geneseq 23Sep04 -QFMT=fastan -SUFFIX=rag -MINMATCH=0.1 -LOOPEXT=0
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-USER=US10729807 @CGN 1.1.127 @runat 15112004.131150.14678 -NCPU=6 -ICPU=3
-NO MAP -LARGEQUERY -NEG SCORES=0 -WAIT DSPBLOCK=100 -LONGLOG
-DEV TIMEOUT=120 -WARN TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database : A_Geneseq 23Sep04:*

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Geneseq1980s:								
Geneseq1990s:								
Geneseq2000s:								
Geneseq2001s:								
Geneseq2002s:								
Geneseq2003as:								
Geneseq2003bs:								
Geneseq2004s:								

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	2763	94.3	513	3	AAY90293 Human pep
2	2763	94.3	513	5	AAY90293 Human mat
3	2752	93.9	513	4	AAY12267 Human PRO
4	2752	93.9	513	4	AAY12267 Human TAN
5	2752	93.9	513	6	ABO17711 Novel hum
6	2752	93.9	513	6	ABO17711 Novel hum
7	2752	93.9	513	6	ABU80965 Human PRO
8	2752	93.9	513	6	ABU66665 Human PRO
9	2752	93.9	513	6	ABO32578 Secreted
10	2752	93.9	513	6	ABU59746 Novel sec
					ABO24936 Human sec

11	2752	93.9	513	6	ABU66941	Human sec
12	2752	93.9	513	6	ADA45711	Novel hum
13	2752	93.9	513	6	ADA76142	Human PRO
14	2752	93.9	513	6	ADA18792	Human PRO
15	2752	93.9	513	6	ADA61415	Homo sapi
16	2752	93.9	513	6	ADB19200	Novel hum
17	2752	93.9	513	6	ADB27741	Human PRO
18	2752	93.9	513	6	ADA86220	Novel hum
19	2752	93.9	513	6	ADB15784	Human PRO
20	2752	93.9	513	6	ADA47570	Human PRO
21	2752	93.9	513	6	ADA67365	Human PRO
22	2752	93.9	513	6	ADB30372	Human PRO
23	2752	93.9	513	6	ADA85668	Novel hum
24	2752	93.9	513	6	ADA96880	Human PRO
25	2752	93.9	513	6	ADA79184	Human PRO
26	2752	93.9	513	6	ADA87323	Novel hum
27	2752	93.9	513	6	ADB16525	Human PRO
28	2752	93.9	513	6	ADA91617	Novel hum
29	2752	93.9	513	6	ADB14680	Human PRO
30	2752	93.9	513	6	ADB18641	Novel hum
31	2752	93.9	513	6	ADA93856	Human PRO
32	2752	93.9	513	6	ADB19752	Novel hum
33	2752	93.9	513	6	ADB13064	Human PRO
34	2752	93.9	513	6	ABO43244	Novel hum
35	2752	93.9	513	6	ADA74318	Human PRO
36	2752	93.9	513	6	ADB24551	Human PRO
37	2752	93.9	513	6	ADA82075	Human PRO
38	2752	93.9	513	6	ADA75038	Human PRO
39	2752	93.9	513	6	ADA85116	Novel hum
40	2752	93.9	513	6	ADA84564	Novel hum
41	2752	93.9	513	6	ADB29820	Human PRO
42	2752	93.9	513	6	ADA80348	Human PRO
43	2752	93.9	513	6	ADA75590	Human PRO
44	2752	93.9	513	6	ADA46815	Human PRO
45	2752	93.9	513	6	ADB25111	Human PRO

ALIGNMENTS

RESULT 1

AAY90293

ID AAY90293 standard; protein; 513 AA.

XX

AC AAY90293;

XX

DT 24-OCT-2000 (first entry)

XX

DE Human peptidase, HPEP-10 protein sequence.

XX

KW Human; peptidase; cell proliferative disorder; arteriosclerosis;
KW psoriasis; myelofibrosis; cancer; autoimmune disorder; Crohn's disease;
KW inflammatory disorder; AIDS; anaemia; allergy; asthma; atherosclerosis;
KW Grave's disease; multiple sclerosis; scleroderma; infection; diabetes;
KW metabolic disorder; Addison's disease; cystic fibrosis; diagnosis;
KW glycogen storage disease; obesity; therapy; HPEP-10.

XX

OS Homo sapiens.

XX

PN WO200042201-A2.

XX

PD 20-JUL-2000.

XX

PF 11-JAN-2000; 2000WO-US000641.

XX

PR 11-JAN-1999; 99US-0172247P.

PR

PR 03-MAY-1999; 99US-0132253P.

XX

PR 27-MAY-1999; 99US-0136653P.

XX

PA (INCY-) INCYTE PHARM INC.

XX

PI Bandman O, Hillman JL, Tang YT, Azimzai Y, Baughn MR, Lal P;

XX

PI Yue H, Lu DAM;

WPI: 2000-482832/42.
N-PSDB; AAA37666.

An isolated polypeptide for diagnosis, prevention and treatment of cell proliferative, autoimmune/ inflammatory and metabolic disorders comprises a sequence encoding a human peptidase.

Claim 2; Page 100-101; 131pp; English.

This sequence represents a human peptidase, designated HPEP-10. The invention relates to 18 human peptidases designated HPEP-1 to HPEP-18, respectively. The peptidases can be used for treating a disease or condition associated with decreased expression or over expression of functional human peptidases. The diseases that can be diagnosed, prevented and treated include cell proliferative disorders (such as arteriosclerosis, psoriasis, myelofibrosis, and cancers), autoimmune/inflammatory disorders (such as AIDS, anaemia, allergies, Crohn's disease, asthma, atherosclerosis, Grave's disease, multiple sclerosis, and scleroderma), infections, and metabolic disorders (such as Addison's disease, diabetes, cystic fibrosis, glycogen storage diseases and obesity)

Alignment Scores:		
Pred. NO.:	4,13e-286	Length: 513
Score:	2763.00	Matches: 513
Percent Similarity:	100.00%	Conservative: 0
Best Local Similarity:	100.00%	Mismatches: 0
Query Match:	94.30%	Indels: 0
DB:	3	Gaps: 0

US-10-729-807-28 (1-1627) X AAY90293 (1-513)

QY	24	ATGAAGCGCCTTCTGCTTCTGTGTGTTTCTTTATAACATTTTCTTCGCAATTCCTCCCTTA	83
Db	1	MetLysArgLeuLeuLeuLeuLeuLeuLeuPhePheIleThrPheSerSerAlaPheProLeu	20
QY	84	GTCCGGATGACGGAAATGAAGAAATATGCAACTGGCTCAGGCATATCTCAACAGTTC	143
Db	21	ValArgMetThrGluAsnGluGluAsnMetGlnLeuAlaGlnAlaItyrLeuAsnGlnPhe	40
QY	144	TACTCTCTTGAATACGAAGGAATCATCTTGTTCAAAGCAAGAATAGGAGTCTCATAGAT	203
Db	41	TyrSerLeuGluIleGluGlyAsnHisLeuValGlnSerLysAsnArgSerLeuIleasp	60
QY	204	GACAAAATTCGGGAAATGCAAGCATTTTGTGATTCACAGTGCAGTGGAAAACTGCATCA	263
Db	61	AspLysIleArgGluMetGlnAlaPhePheGlyLeuThrValThrGlyLysLeuAspSer	80
QY	264	AACACCTTCGAGATCATGAAGACACCCAGGTGTGGGTGCCTGATCTGGCCAGATGAC	323
Db	81	AsnThrLeuGluIleMetLysThrProArgCysGlyValProaspValGlyGlnItyrGly	100
QY	324	TACACCTCCCTCGGTGGAGAAAATACAACCTCACCTACAGATAATAACTATATCTCCG	383
Db	101	TyrThrLeuProGlyItyrAlaGlyTyrAsnLeuThrTyrArgIleIleAsnItyrThrPro	120
QY	384	GATATGCGCAGCGTCTGTGGATAGGCTTATCCAAGAGCTTTAGAAGTGTGGACAA	443
Db	121	AspMetAlaArgAlaAlaValAspGluAlaIleGlnGluGlyLeuGluValTrpSerLys	140
QY	444	GTCACTCCACTAAAATTCACCAAGATTTCAAAGGGGATTCGACACATCATGATGGCTTT	503
Db	141	ValThrProLeuLysPheThrLysIleSerLysGlyIleAlaaspIleMetIleAlaPhe	160
QY	504	AGGACTCGAGTCATGTCGGTGTCTCGCTATTTTTGATGGTCCCTTGGGAGTGTCTGGC	563
Db	161	ArgThrArgValHisGlyArgCysProArgTyrPheAspGlyProLeuGlyValLeuGly	180
QY	564	CATGCCCTTCCTCGTCCGGGTCTGGTGGTCACACTCATTTTGATGAGGATGAAAAC	623
Db	181	HisAlaPheProGlyProGlyLeuGlyGlyAspThrHisPheAspGlyAspGluasn	200

RESULT. 2

ASB01.2	
AAE14392	
ID	AAE14392 standard; protein; 513 AA.
XX	
AC	AAE14392;
XX	
DT	16-OCT-2002 (first entry)
XX	


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Db      381  CysAspLysThrThrArgLysThrTyrPhePheValGlyIleTrpCysTrpArgPheAsp 400
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Db      401  GluMetThrGlnThrMetAspLysGlyPheProGlnArgValValLysHisPheProGly 420
QY      1284  ATCAGTATCCGTTGATGCTGCTTTCCAGTCAAAAGGATCTCTTTTCAGCCGTGGA 1343
Db      421  IleSerIleArgValAspAlaAlaPheGlnTyrLysGlyPhePhePheSerArgGly 440
QY      1344  TCAAGCAATTTGAATACATTAACATTAACAAAGATATTATCCCGAATCATGAGAACTAAT 1403
Db      441  SerLysGlnPheGluTyrAsnIleLysThrLysAsnIleThrArgIleMetArgThrAsn 460
QY      1404  ACTTGGTTTCAATGCAAAAGAACCAAAAGAACTCTCATTTGGTTTGTATCAACAGGAA 1463
Db      461  ThrTrpPheGlnCysLysGluProLysAsnSerSerPheGlyPheAspIleAsnLysGlu 480
QY      1464  AAAGCAATTCAGAGGCATTAAGATATTGTATCATAGAGTTTAAGCTTGTATTTT 1523
Db      481  LysAlaHisSerGlyGlyIleLysIleLeuTyrHisLysSerLeuSerLeuPheIlePhe 500
QY      1524  GGTATTCCTTCAATTCGCTGAAGAACACATCTCTATTATCAAA 1562
Db      501  GlyIleValHisLeuLeuLysAsnThrSerIleTyrGln 513

RESULT 3
AAU12267
ID  AAU12267 standard; protein; 513 AA.
XX
AC  AAU12267;
XX
DT  24-OCT-2001 (first entry)
XX
DE  Human PRO5992 polypeptide sequence.
XX
KW  Human secretory and transmembrane; PRO; mammalian; cancer; lung; breast;
KW  prostate; cervical; tumour necrosis factor-alpha; TNF-alpha; cartilage;
KW  ear; proliferation; glucose; free fatty acid; skeletal muscle; adipocyte;
KW  A-peptide; factor VIIA; gene therapy.
XX
OS  Homo sapiens.
XX
PN  WO200140466-A2.
XX
PD  07-JUN-2001.
XX
PF  01-DEC-2000; 2000WO-US032678.
XX
PR  01-DEC-1999; 99WO-US028301.
PR  01-DEC-1999; 99WO-US028634.
PR  02-DEC-1999; 99WO-US028551.
PR  02-DEC-1999; 99WO-US028564.
PR  02-DEC-1999; 99WO-US028565.
PR  09-DEC-1999; 99US-0170262P.
PR  16-DEC-1999; 99WO-US030095.
PR  20-DEC-1999; 99WO-US030911.
PR  20-DEC-1999; 99WO-US030999.
PR  30-DEC-1999; 99WO-US031243.
PR  30-DEC-1999; 99WO-US031274.
PR  05-JAN-2000; 2000WO-US000219.
PR  06-JAN-2000; 2000WO-US000277.
PR  11-FEB-2000; 2000WO-US000376.
PR  18-FEB-2000; 2000WO-US004341.
PR  24-FEB-2000; 2000WO-US004342.
PR  28-FEB-2000; 2000WO-US004414.
PR  24-FEB-2000; 2000WO-US004914.
PR  24-FEB-2000; 2000WO-US005004.
PR  01-MAR-2000; 2000WO-US005601.
PR  02-MAR-2000; 2000WO-US005841.
PR  03-MAR-2000; 2000US-0187202P.
PR  10-MAR-2000; 2000WO-US006319.

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PR  15-MAR-2000; 2000WO-US006884.
PR  20-MAR-2000; 2000WO-US007377.
PR  21-MAR-2000; 2000WO-US007532.
PR  30-MAR-2000; 2000WO-US008439.
PR  17-MAY-2000; 2000WO-US013705.
PR  22-MAY-2000; 2000WO-US014042.
PR  30-MAY-2000; 2000WO-US014941.
PR  02-JUN-2000; 2000WO-US015264.
PR  05-JUN-2000; 2000US-0209832P.
PR  28-JUL-2000; 2000WO-US020710.
PR  11-AUG-2000; 2000WO-US022031.
PR  23-AUG-2000; 2000WO-US023522.
PR  24-AUG-2000; 2000WO-US023328.
PR  08-NOV-2000; 2000WO-US030952.
PR  10-NOV-2000; 2000WO-US030873.
XX
PA  (GETH ) GENENTECH INC.
XX
PI  Baker KP, Beresini M, Deforge L, Desnoyers L, Filvaroff E, Gao W;
PI  Gerritsen ME, Goddard A, Godowski PJ, Gurney AL, Sherwood S;
PI  Smith V, Stewart TA, Tumas D, Watanabe CK, Wood WI, Zhang Z;
XX
DR  WPI; 2001-408281/43.
XX  N-PSDB; AAS21339.
XX
PT  Isolated , secretory and transmembrane PRO polypeptide used to detect
PT  other PRO polypeptides, link bioactive molecules to cells expressing PRO
PT  polypeptides, and detect the presence of mammalian tumors e.g. lung,
PT  breast, prostate, cervical.
XX
PS  Claim 12; Fig 192; 813pp; English.
XX
CC  AAU12172-AAU12446 represent novel human secretory and transmembrane PRO
CC  polypeptides. The PRO polypeptides are useful to detect other PRO
CC  polypeptides, to link bioactive molecules to cells expressing PRO
CC  polypeptides, to modulate biological activities of cells expressing PRO
CC  polypeptides, and to detect the presence of mammalian lung, colon,
CC  breast, prostate, rectal, cervical or liver tumours by comparing PRO
CC  polypeptide expression in a cell sample to that in a control sample. Some
CC  of the 275 sequences are also useful to stimulate the release of tumour
CC  necrosis factor-alpha (TNF-alpha) from human blood, the proliferation or
CC  differentiation of chondrocytes, the proliferation or gene expression in
CC  pericyte cells, the release of proteoglycans from cartilage, the
CC  proliferation of inner ear utricular supporting cells or of T-
CC  lymphocytes, the release of a cytokine from peripheral blood monocytes
CC  (PBMCs), or the proliferation of endothelial cells. Some of the PRO
CC  polypeptides may modulate glucose or free fatty acid uptake by skeletal
CC  muscle cells or by adipocytes; or inhibit binding of A-peptide to factor
CC  VIIA. The PRO polypeptides can be used in assays to identify molecules
CC  involved in binding interactions. The polynucleotides encoding PRO
CC  polypeptides can be used to generate probes, antisense RNA/DNA,
CC  transgenic or knock out animals and can be used in gene therapy
XX
SQ  Sequence 513 AA;
XX
XX
Alignment Scores:
Pred. No.: 6,23e-285 Length: 513
Score: 2752.00 Matches: 512
Percent Similarity: 99.81% Conservative: 0
Best Local Similarity: 99.81% Mismatches: 1
Query Match: 93.92% Indels: 0
DB: 4 Gaps: 0
XX
US-10-729-807-28 (1-1627) x AAU12267 (1-513)
QY 24 ATGAGCGCCTTCTGCTTCTGTTGTTGTTTATTAACATTTCTTCTGATTTCCCTTA 83
Db 1 MetLysArgLeuLeuLeuPheLeuPheLeuPheLeuPheLeuPheLeuPheLeuPheLeu 20
QY 84 GTCCGATGACGGAATCAAGAAAATATGCAACTGGCTGGCATATCTCAACAGTTC 143
Db 21 ValArgMetThrGluAsnGluGluAsnMetGlnLeuAlaGlnAlaTyrLeuAsnGlnPhe 40

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QY	144	TACTCTCTTGAATAGAGGAATCATCTTGTTCAGAGCAAGAAATAGGAGTCTCATAGAT	203	Db	401	GlutMetThrGlnThrMetAspLysGlyPheProGlnArgValLysHisPheProGly	420
Db	41	TyrSerLeuGluIleGluGlyAsnHisLeuValGlnSerLysAsnArgSerLeuIleAsp	60	QY	1284	ATCAGTATCCGTGTTGATGCTGTTTCCAGTACAAAGGATTCTCTTTTTCAGCCGTGGA	1343
QY	204	GACAAATTCGGGAATGCAAGCATTTTGTGGATTCACAGTACTGGAATACTGGACTCA	263	Db	421	IleSerIleArgValAspAlaPheGlnTyrLysGlyPhePhePheSerArgGly	440
Db	61	AspLysIleArgGluMetGlnAlaPhePheGlyLeuThrValThrGlyLysLeuAspSer	80	QY	1344	TCAAACAATTTGATATACAACTTAAGACAAAGAATATTACCCGAATCATGAGAATTAAT	1403
QY	264	AACACCTTTGAGATCATGAAGACACCCAGGTGGGTGCTCATGTGGCCAGTAGTGC	323	Db	441	SerLysGlnPheGluTyrAsnIleLysThrLysAsnIleThrArgIleMetArgThrAsn	460
Db	81	AsnThrLeuGluIleMetLysThrProArgCysGlyValProAspValGlyGlnTyrGly	100	QY	1404	ACTTGTCTTCAATGCAGAAAGACCAAGAACTCTCATTTGGTTTTCATATCAACAGGAA	1463
QY	324	TACACCTCCCTGGGTGGAGAAATACAACTCACCTACAGATAATAAATATATCTCG	383	Db	461	ThrTrpPheGlnCysLysGluProLysAsnSerSerPheGlyPheAspIleAsnLysGlu	480
Db	101	TyrThrLeuProGlyTrpArgLysTyrAsnLeuThrTyrArgIleIleAsnTyrThrPro	120	QY	1464	AAAGCACATTCAGGAGGCATAAAGATATTGTATCATTAAGAGTTTAAGCTTGTATTATTT	1523
QY	384	GATATGGCAGGAGCTCTGTGATGAGGTATCCAAAGAGTTTGAAGTGTGGAGCAAA	443	Db	481	LysAlaHisSerGlyGlyIleLysIleLeuTyrHisLysSerLeuSerLeuPheIlePhe	500
Db	121	AspMetAlaArgAlaAlaValAspGluAlaIleGlnGluGlyLeuGluValTrpSerLys	140	QY	1524	GGTATTGTTCATTTGCTGTAAGAAACATCTTCTATTATCAAA	1562
QY	444	GTCACTCCACTAAATTCACCAAGATTTCAGAGGATTCAGACATCATGATTCCTTT	503	Db	501	GlyIleValHisLeuLeuLysAsnThrSerIleTyrGln	513
Db	141	ValThrProLeuLysPheThrLysIleSerLysGlyIleAlaAspIleMetIleAlaPhe	160	RESULT 4			
QY	504	AGGACTCGAGTCCATGTCGTCTCTCGCTATTTTGTGTCCTTGGAGTGGCTTGGC	563	ID	AAU00469		
Db	161	ArgThrArgValHisGlyArgCysProArgTyrPheAspGlyProLeuGlyValLeuGly	180	XX	AAU00469 standard; protein; 513 AA.		
QY	564	CATGCTTTCCTCTGCTCGGTCTGGGTGTGGTGTGACACTCATTTTGTGATGAGATGAAAC	623	AC	AAU00469;		
Db	181	HisAlaPheProGlyProGlyLeuGlyGlyAspThrHisPheAspGluAspGluAsn	200	DT	04-JUL-2001 (first entry)		
QY	624	TGGACCAAGATGGAGCAGATTCAACTGTTTCTGTGCTGCTCATGAATTTGGTCT	683	DE	Human TANGO 210 protein.		
Db	201	TrpThrLysAspGlyAlaGlyPheAsnLeuPheLeuValAlaAlaHisGluPheGlyHis	220	XX	Human; TANGO 210; clone jthke034a06; TANGO 364; TANGO 366; INTERCEPT 394;		
QY	684	GCATGGGGCTCTCTCACTCCAATGATCAACAGCCTTGATCTTCCCAATATATCTCC	743	KW	INTERCEPT 400; TANGO 405; cellular process regulator; gene therapy;		
Db	221	AlaLeuGlyLeuSerHisSerAsnAspGlnThrAlaLeuMetPheProAsnTyrValSer	240	KW	MMP-8; matrix metalloproteinase-8; proteinase activity; bone marrow disorder;		
QY	744	CTGGATCCAGAAATACCTCTTCTCAGGATGATATCAATGGAATCCAGTCCATCTAT	803	XX	skin disorder; vascular hypertension; metastatic cancer.		
Db	241	LeuAspProArgLysTyrProLeuSerGlnAspAspIleAsnGlyIleGlnSerIleTyr	260	OS	Homo sapiens.		
QY	804	GGAGTCTGCTTAAGTACTCTAAGCCAAAGGACCCACTATACCCCATGCTCTGAC	863	XX	Key	Location/Qualifiers	
Db	261	GlyGlyLeuProLysValProLysProlLysGluProThrIleProHisAlaCysAsp	280	FT	Peptide	1..17	
QY	864	CCTGACTTGACTTTTGACGCTATCAAACTTTCCGAGAGAGTAAATGTTCTTTAAAGGC	923	FT	/label= Signal peptide	/note= "Specifically claimed"	
Db	281	ProAspLeuThrPheAspAlaIleThrThrPheArgArgGluValMetPhePheLysGly	300	FT	Protein	18..513	
QY	924	AGGCACCTATGAGGATCTATATGATATCAGGATGTGAGTTGAAATTAATGCTTCA	983	FT	/label= Mature TANGO 210 protein	/note= "Specifically claimed"	
Db	301	ArgHisLeuTrpArgIleTyrTyrAspIleThrAspValGluPheGluLeuIleAlaSer	320	FT	Domain	18..498	
QY	984	TTCTGGCCATCTCTGCCAGCTGATCTGCAAGCTGCATACGAGACCCAGAGATGAGTT	1043	FT	/note= "Optionally in alternative form #1 this domain is extracellular or in alternative form #2 this domain is intracellular. Specifically claimed"		
Db	321	PheTrpProSerLeuProAlaAspLeuGlnAlaIatyrGluAsnProArgAspLysIle	340	FT	Domain	489..506	
QY	1044	CTGTTTTTAAAGATGAAACTTCTGGATGATCAGAGATATGCTGTCTGCGAGATTAT	1103	FT	/label= Transmembrane domain	/note= "Specifically claimed"	
Db	341	LeuValPheLysAspGluAsnPheTrpMetIleArgGlyTyrAlaValLeuProAspTyr	360	FT	Domain	507..513	
QY	1104	CCCAATCCATCATAGATTAGTTTTCAGAGCTGTGAAGAAATAGATGCAGCCGTC	1163	FT	/note= "Optionally in alternative form #1 this domain is intracellular or in alternative form #2 this domain is extracellular. Specifically claimed"		
Db	361	ProLysSerIleHisThrLeuGlyPheProGlyArgValLysLysIleAspAlaAlaVal	380	XX	WO200118016-A1.		
QY	1164	TGTGATAGACACCAAGAAACCTACTCTTGTGGCATTTGCTGTGGAGTTTGTAT	1223	XX	15-MAR-2001.		
Db	381	CysAspLysThrThrArgLysThrThrPhePheValGlyIleTrpCysTrpArgPheAsp	400	XX	30-JUN-2000; 2000WO-US018174.		
QY	1224	GAAATGACCCCAACCATGGACAAAGGATTCCCGCAGAGAGTGGTAAACACATCTTCTCTGGA	1283	XX	10-SEP-1999; 99US-00393996.		
				XX	(MILL-) MILLENNIUM PHARM INC.		
				XX	Fraser CC, Sharp JD, Wrighton N, Myers PS, Goodearl ADJ;		
				XX	WPI; 2001-183280/18.		

AC ABO17711;
 XX
 DT
 XX 26-AUG-2003 (first entry)
 XX
 DE Novel human secreted and transmembrane protein PRO5992.
 XX
 KW Human; secreted and transmembrane protein; PRO; antiinflammatory;
 KW antiarteriosclerotic; cardiant; anti-infertility; anti-HIV; cytostatic;
 KW antidiabetic; gene therapy; tumour necrosis factor (TNF)-alpha release;
 KW TNF-alpha release; cell proliferation; cell differentiation;
 KW gene expression modulator; proteoglycan release; cytokine release;
 KW tumour; inflammatory disease; organ failure; atherosclerosis;
 KW cardiac injury; infertility; birth defect; premature aging; AIDS;
 KW acquired immunodeficiency syndrome; cancer; diabetic complication;
 KW chromosome mapping; gene mapping; pharmaceutical; diagnostic; biosensor;
 KW bioreactor; tissue typing.
 XX
 XX Homo sapiens.
 XX
 XX US2003032156-A1.
 PN
 PD 13-FEB-2003.
 XX
 XX 06-MAY-2002; 2002US-00140474.
 XX
 XX 31-MAR-1997; 97WO-US005230.
 PR 12-JUN-1998; 98WO-US012456.
 PR 14-JUL-1998; 98WO-US014552.
 PR 28-AUG-1998; 98WO-US017888.
 PR 10-SEP-1998; 98WO-US018824.
 PR 14-SEP-1998; 98WO-US019093.
 PR 14-SEP-1998; 98WO-US019094.
 PR 16-SEP-1998; 98WO-US019177.
 PR 16-SEP-1998; 98WO-US019330.
 PR 17-SEP-1998; 98WO-US019437.
 PR 07-OCT-1998; 98WO-US021141.
 PR 29-OCT-1998; 98WO-US022991.
 PR 29-OCT-1998; 98WO-US022992.
 PR 20-NOV-1998; 98WO-US024855.
 PR 01-DEC-1998; 98WO-US025108.
 PR 05-JAN-1999; 98WO-US000106.
 PR 08-MAR-1999; 98WO-US005028.
 PR 10-MAR-1999; 98WO-US005190.
 PR 20-APR-1999; 98WO-US008615.
 PR 14-MAY-1999; 98WO-US010733.
 PR 02-JUN-1999; 98WO-US012252.
 PR 01-SEP-1999; 98WO-US020111.
 PR 08-SEP-1999; 98WO-US020594.
 PR 13-SEP-1999; 98WO-US020944.
 PR 15-SEP-1999; 98WO-US021090.
 PR 15-SEP-1999; 98WO-US021547.
 PR 05-OCT-1999; 98WO-US023089.
 PR 29-NOV-1999; 98WO-US028214.
 PR 30-NOV-1999; 98WO-US028313.
 PR 30-NOV-1999; 98WO-US028409.
 PR 01-DEC-1999; 98WO-US028301.
 PR 01-DEC-1999; 98WO-US028634.
 PR 02-DEC-1999; 98WO-US028551.
 PR 02-DEC-1999; 98WO-US028564.
 PR 02-DEC-1999; 98WO-US028565.
 PR 16-DEC-1999; 98WO-US030095.
 PR 20-DEC-1999; 98WO-US030911.
 PR 20-DEC-1999; 98WO-US030999.
 PR 22-DEC-1999; 98WO-US030720.
 PR 30-DEC-1999; 98WO-US031243.
 PR 30-DEC-1999; 98WO-US031274.
 PR 05-JAN-2000; 2000WO-US000219.
 PR 06-JAN-2000; 2000WO-US000277.
 PR 06-JAN-2000; 2000WO-US000376.
 PR 11-FEB-2000; 2000WO-US003565.
 PR 18-FEB-2000; 2000WO-US004341.
 PR 18-FEB-2000; 2000WO-US004342.
 PR 22-FEB-2000; 2000WO-US004414.

PR 24-FEB-2000; 2000WO-US004914.
 PR 24-FEB-2000; 2000WO-US005004.
 PR 01-MAR-2000; 2000WO-US005601.
 PR 02-MAR-2000; 2000WO-US005746.
 PR 10-MAR-2000; 2000WO-US005841.
 PR 10-MAR-2000; 2000WO-US006319.
 PR 15-MAR-2000; 2000WO-US006884.
 PR 20-MAR-2000; 2000WO-US007377.
 PR 21-MAR-2000; 2000WO-US007532.
 PR 30-MAR-2000; 2000WO-US008439.
 PR 17-MAY-2000; 2000WO-US013705.
 PR 22-MAY-2000; 2000WO-US014042.
 PR 30-MAY-2000; 2000WO-US014941.
 PR 02-JUN-2000; 2000WO-US015264.
 PR 28-JUL-2000; 2000WO-US020710.
 PR 11-AUG-2000; 2000WO-US022031.
 PR 23-AUG-2000; 2000WO-US023522.
 PR 24-AUG-2000; 2000WO-US023328.
 PR 08-NOV-2000; 2000WO-US030952.
 PR 10-NOV-2000; 2000WO-US030873.
 PR 01-DEC-2000; 2000WO-US032678.
 PR 20-DEC-2000; 2000US-00747259.
 PR 20-DEC-2000; 2000WO-US034956.
 PR 28-FEB-2001; 2001US-00796498.
 PR 28-FEB-2001; 2001WO-US006520.
 PR 01-MAR-2001; 2001WO-US006666.
 PR 09-MAR-2001; 2001US-00802706.
 PR 14-MAR-2001; 2001US-00808689.
 PR 22-MAR-2001; 2001US-00816744.
 PR 05-APR-2001; 2001US-00828366.
 PR 10-MAY-2001; 2001US-00854208.
 PR 10-MAY-2001; 2001US-00854280.
 PR 18-MAY-2001; 2001US-00860216.
 PR 25-MAY-2001; 2001US-00866038.
 PR 25-MAY-2001; 2001WO-US017092.
 PR 01-JUN-2001; 2001US-00872035.
 PR 01-JUN-2001; 2001WO-US017800.
 PR 05-JUN-2001; 2001US-00874503.
 PR 14-JUN-2001; 2001US-00882636.
 PR 19-JUN-2001; 2001US-00886342.
 PR 20-JUN-2001; 2001WO-US019692.
 PR 21-JUN-2001; 2001US-00887879.
 PR 22-JUN-2001; 2001WO-US020116.
 PR 29-JUN-2001; 2001WO-US021066.
 PR 09-JUL-2001; 2001WO-US021735.
 PR 18-JUL-2001; 2001US-00908827.
 PR 06-AUG-2001; 2001US-00924419.
 PR 09-AUG-2001; 2001US-00927796.
 PR 16-AUG-2001; 2001US-00931836.
 PR 19-DEC-2001; 2001US-00028072.
 XX
 PA (GETH) GENENTECH INC.
 XX
 XX Baker KP, Beresini M, Deforge L, Desnoyers L, Filvaroff E, Gao W;
 PI Gerisken ME, Goddard A, Godowski PJ, Gurney AL, Sherwood S;
 PI Smith V, Stewart TA, Tumas D, Watanabe CK, Wood WI, Zhang Z;
 XX
 DR WPI; 2003-341980/32.
 DR N-PSDB; ACD23948.
 XX
 PT New secreted and transmembrane PRO nucleic acids, for treating
 PT inflammation, organ failure, atherosclerosis, cardiac injury,
 PT infertility, birth defects, premature aging, acquired immunodeficiency
 PT syndrome (AIDS), or cancer.
 XX
 PS Claim 12; Fig 192; 660pp; English.
 XX
 CC The invention describes an isolated nucleic acid (I) comprising, or which
 CC has 80 % sequence identity to, or the full-length coding sequence of, one
 CC of 275 nucleotide sequences, and which encodes a corresponding
 CC polypeptide selected from 275 amino acid sequences, where all sequences
 CC are given in the specification. The polypeptide encoded by (I) is used to

CC detect PRO polypeptides, link a bioactive molecule to a cell expressing a
CC PRO polypeptide, modulate a biological activity of a cell, stimulate the
CC release of tumour necrosis factor (TNF)-alpha from human blood, modulate
CC the uptake of glucose or free fatty acid by cells, stimulate or inhibit
CC the proliferation or differentiation of cells or gene expression,
CC stimulate the release of proteoglycans, stimulate the release of cytokine
CC from peripheral blood mononuclear cells, inhibit the binding of A-peptide
CC to factor VIIA, or detect the presence of tumour in a mammal. The nucleic
CC acid and polypeptide encoded by it, are useful for treating inflammatory
CC diseases, organ failure, atherosclerosis, cardiac injury, infertility,
CC birth defects, premature aging, acquired immunodeficiency syndrome
CC (AIDS), cancer, or diabetic complications. The nucleic acid is useful as
CC hybridisation probes, in chromosome and gene mapping, and in generating
CC antisense RNA or DNA. The polypeptides are useful as pharmaceuticals,
CC diagnostics, biosensors or bioreactors. Both are useful in tissue typing.
CC This is the amino acid sequence of a novel human secreted and
CC transmembrane PRO polypeptide
XX
SQ Sequence 513 AA;

Alignment Scores:
Pred. No.: 6,23e-285 Length: 513
Score: 2752.00 Matches: 512
Percent Similarity: 99.81% Conservative: 0
Best Local Similarity: 99.81% Mismatches: 1
Query Match: 93.92% Indels: 0
DB: 6 Gaps: 0

US-10-729-807-28 (1-1627) x AB017711 (1-513)

QY	24	ATGAAGCGCTCTGCTCTGCTGCTGCTTTTACATTTCTTCTGCTGCTTCCCTTA	83
DB	1	MetLysArgLeuLeuLeuLeuPheLeuPhePheLeuPheSerAlaPheProLeu	20
QY	84	GTCGGATGACGGAATGAAGAAATATGCACTGGCTCAGGCATATCTCAACAGTTC	143
DB	21	ValArgMetThrGluAsnGluGluAsnMetGlnLeuAlaGlnAlaTyrLeuAsnGlnPhe	40
QY	144	TACTCTCTGAAATAGAGGAATCATCTGTGTTCAAGCAAGATAGAGTCTCATAGAT	203
DB	41	TyrSerLeuGluLeuGluGlyAsnHisLeuValGlnSerLysAsnArgSerLeuLeuAsp	60
QY	204	GACAAATTCGGGAATGCAAGCATTTTGGATTGACAGTCACTGGAAACCTGACTCA	263
DB	61	AspLysileArgGluMetGlnAlaPhePheGlyLeuThrValThrGlyLysLeuAspSer	80
QY	264	AACACCTCTGAGATCATGAACACACCCAGGTGTGGGTGCTGATGTGGCCAGTATGCC	323
DB	81	AsnThrLeuGluLeuMetLysThrProArgCysGlyValProAspValGlyGlnTyrGly	100
QY	324	TACACCTCTGCTGGTGAGAAATATACACCTCCTACAGATTAATAACTATCTCCG	383
DB	101	TyrThrLeuProGlyTyrArgLysTyrAsnLeuThrTyrArgLysLeuAsnTyrThrPro	120
QY	384	GATATGCAAGCATGCTGTGATGAGCTATCAAGAAAGTTTAGAGTGTGAGCAAA	443
DB	121	AspMetAlaArgAlaAlaValAspGluAlaGlnGlnGluGlyLeuGluValTrpSerLys	140
QY	444	GTCACTCCACATAAATTCACCAAGATTTCAAGGGGATTCAGACATCATGATTCCTTT	503
DB	141	ValThrProLeuLysPheThrLysileSerLysGlyLeuAlaAspMetLeuAlaPhe	160
QY	504	AGGATGAGTCCATGTCGGTGCTGCTGCTATTTGATGTCCTGGGAGTCTGGC	563
DB	161	ArgThrArgValHisGlyArgCysProArgTyrPheAspGlyProLeuGlyValLeuGly	180
QY	564	CATGCTTTCTCTGCTGGTCCGGTCTGCTGGTGCTGACACTCATTTTGTAGGAGTGAAC	623
DB	181	HisAlaPheProProGlyProGlyLeuGlyGlyAspThrHisPheAspGluAspGluAsn	200
QY	624	TGGACCAAGATGAGGAGGATTCACATTTGCTTCTGCTGCTCATGAATTTGCTCAT	683
DB	201	TrpThrLysAspGlyAlaGlyPheAsnLeuPheLeuValAlaAlaHisGluPheGlyHis	220

QY	684	GCACCTGGGCTCTCTCACCTCAATGATCAACAGCCTTGATGTTTCCCAATATGCTCC	743
DB	221	AlaLeuGlyLeuSerHisSerAsnAspGlnThrAlaLeuMetPheProAsnTyrValSer	240
QY	744	CTGGATCCCAAGAAATACCCACTTTCTCAGGATGATATCAATGGAATCCAGTCCATCTAT	803
DB	241	LeuAspProArgLysTyrProLeuSerGlnAspAspIleAsnGlyIleGlnSerIleTyr	260
QY	804	GGAGGTCTGCTTAAGTACTGCTAAGCAACCAAGAACCCACTATACCCATGCTGTCAC	863
DB	261	GlyGlyLeuProLysValProAlaLysProLysGluProThrProThrProHisAlaCysAsp	280
QY	864	CCTGACTCTGCTTTTGCAGCTATCAAACTTTCCGACAGAGAAGTATGTTCTTTAAAGGC	923
DB	281	ProAspLeuThrPheAspAlaIleThrThrPheArgArgGluValMetPhePheLysGly	300
QY	924	AGGCACCTATGGAGGATCTATTATGATATACACGATGTTGAGTTGAATTAATGCTTCA	983
DB	301	ArgHisLeuTrpArgIleTyrTyrAspIleThrAspValGluPheGluLeuIleAlaSer	320
QY	984	TTCTGGCCATCTCTGCGCAGCTGATCTGCAAGCTGCATACGAGAACCCAGAGATAAGATT	1043
DB	321	PheTrpProSerLeuProAlaAspLeuGlnAlaAlaTyrGluAsnProArgAspLysIle	340
QY	1044	CTGGTTTAAAGATGAAAACTTCTGGATGATCAGAGGATATGCTGTTTCCAGATTAT	1103
DB	341	LeuValPheLysAspGluAsnPheTrpMetIleArgGlyTyrAlaValLeuProAspTyr	360
QY	1104	CCCAATCCATCCATCATATTAGTGTTCAGGACGTTGGAAGAAATAGATGACGCCGTC	1163
DB	361	ProLysSerIleHisThrLeuGlyPheProGlyArgValLysLysIleAspAlaAlaVal	380
QY	1164	TGTGATAGACCAACAGAAACCTCTCTTGTGGCATTTGCTCTCGAGGTTTGAT	1223
DB	381	CysAspLysThrThrArgLysThrTyrPhePheValGlyIleThrCysTrpArgPheAsp	400
QY	1224	GAATGACCCAAACCCATGGCAAGGATTCGCCAGAGAGTGGTAAACACTTTCTCTGGA	1283
DB	401	GluMetThrGlnThrMetAspLysGlyPheProGlnArgValValLysHisPheProGly	420
QY	1284	ATCAGTATCCGTGTGATGCTGCTTCCAGTACAAAGGATTTCTTTTTCAGCCGTGGA	1343
DB	421	IleSerIleArgValAspAlaAlaPheGlnTyrLysGlyPhePhePheSerArgGly	440
QY	1344	TCAAAGCAATTTGAATACACATTAACACAAAGATATTACCCGAATCATGAGAACTAAT	1403
DB	441	SerLysGlnPheGluTyrAsnIleLysThrLysAsnIleThrArgIleMetArgThrAsn	460
QY	1404	ACTTGGTTTCAATGCAAGAACCAAGAACTCTCTCATTTGTTTGTATATCAACAGGAA	1463
DB	461	ThrTrpPheGlnCysLysGluProLysAsnSerSerPheGlyPheAspIleAsnLysGlu	480
QY	1464	AAAGCAATTCAGAGGAGCATTAAGATATTGTATCATAGAGTTTAAAGTGTGTTATTTT	1523
DB	481	LysAlaHisSerGlyGlyIleLysIleLeuTyrHisLysSerLeuSerLeuPheIlePhe	500
QY	1524	GGTATTCTCATTTGCTGAAACACACTTCTATTATCAA 1562	
DB	501	GlyIleValHisLeuLeuLysAsnThrSerIleIleTyrGln 513	

RESULT 6

ABU80965
ID ABU80965 standard; protein; 513 AA.
XX ABU80965;
AC
DT 23-JUN-2003 (first entry)
XX
DX Human PRO polypeptide #96.
XX Human; PRO polypeptide; secreted and transmembrane protein;
KW anti-PRO antibody; diagnostic assay; gene expression; diabetes;

bone disorder; cartilage disorder; rheumatoid arthritis; obesity;
 KW sports injury; osteoarthritis; hyper-insulinaemia; hypo-insulinaemia;
 KW hearing loss; coagulation disorder; stroke; heart attack; cardiac;
 KW antidiabetic; anorectic; vulnerable; antiarthritic; osteopathic;
 KW antirheumatic; auditory; cerebroprotective; angiogenic.

XX Homo sapiens.

XX US2003004311-A1.

PN 02-JAN-2003.

PD 19-DEC-2001; 2001US-00028072.

XX 18-JUN-1997; 97US-0049911P.

XX 26-AUG-1997; 97US-0056974P.

XX 17-SEP-1997; 97US-0059113P.

XX 17-SEP-1997; 97US-0059115P.

XX 17-SEP-1997; 97US-0059117P.

XX 17-SEP-1997; 97US-0059122P.

XX 17-SEP-1997; 97US-0059184P.

XX 18-SEP-1997; 97US-0059263P.

XX 19-SEP-1997; 97US-0059352P.

XX 19-SEP-1997; 97US-0059588P.

XX 24-SEP-1997; 97US-0059836P.

XX 17-OCT-1997; 97US-0062250P.

XX 17-OCT-1997; 97US-0062285P.

XX 17-OCT-1997; 97US-0062287P.

XX 17-OCT-1997; 97US-0063755P.

XX 24-OCT-1997; 97US-0062814P.

XX 24-OCT-1997; 97US-0062816P.

XX 24-OCT-1997; 97US-0063045P.

XX 24-OCT-1997; 97US-0063082P.

XX 24-OCT-1997; 97US-0063127P.

XX 27-OCT-1997; 97US-0063327P.

XX 27-OCT-1997; 97US-0063329P.

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XX 28-OCT-1997; 97US-0063561P.

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XX 29-OCT-1997; 97US-0063733P.

XX 29-OCT-1997; 97US-0063735P.

XX 29-OCT-1997; 97US-0063738P.

XX 03-NOV-1997; 97US-0064248P.

XX 07-NOV-1997; 97US-0064809P.

XX 12-NOV-1997; 97US-0065186P.

XX 17-NOV-1997; 97US-0065846P.

XX 21-NOV-1997; 97US-0066364P.

XX 24-NOV-1997; 97US-0066453P.

XX 24-NOV-1997; 97US-0066511P.

XX 24-NOV-1997; 97US-0066770P.

XX 11-DEC-1997; 97US-0069212P.

XX 11-DEC-1997; 97US-0069278P.

XX 11-DEC-1997; 97US-0069334P.

XX 16-DEC-1997; 97US-0069694P.

XX 23-JAN-1998; 98US-0072320P.

XX 04-FEB-1998; 98US-0073612P.

XX 09-FEB-1998; 98US-0074086P.

XX 09-FEB-1998; 98US-0074092P.

XX 12-MAR-1998; 98US-0077791P.

XX 20-MAR-1998; 98US-0078910P.

XX 25-MAR-1998; 98US-0079294P.

XX 27-MAR-1998; 98US-0079663P.

XX 27-MAR-1998; 98US-0079728P.

XX 31-MAR-1998; 98US-0080165P.

XX 12-JUN-1998; 98WO-US012456.

XX 14-JUL-1998; 98WO-US014552.

XX 28-AUG-1998; 98WO-US017888.

XX 10-SEP-1998; 98WO-US018824.

XX 14-SEP-1998; 98WO-US019033.

XX 14-SEP-1998; 98WO-US019094.

XX 14-SEP-1998; 98WO-US019177.

XX 16-SEP-1998; 98WO-US019330.

XX 17-SEP-1998; 98WO-US019437.

PR 07-OCT-1998; 98WO-US021141.
 PR 29-OCT-1998; 98WO-US022991.
 PR 29-OCT-1998; 98WO-US022992.
 PR 20-NOV-1998; 98WO-US024855.
 PR 01-DEC-1998; 98WO-US025108.
 PR 05-JAN-1999; 99WO-US000106.
 PR 08-MAR-1999; 99WO-US005028.
 PR 10-MAR-1999; 99WO-US005190.
 PR 20-APR-1999; 99WO-US008615.
 PR 14-MAY-1999; 99WO-US010733.
 PR 02-JUN-1999; 99WO-US012252.
 PR 01-SEP-1999; 99WO-US020111.
 PR 08-SEP-1999; 99WO-US020594.
 PR 13-SEP-1999; 99WO-US020944.
 PR 15-SEP-1999; 99WO-US021090.
 PR 15-SEP-1999; 99WO-US021547.
 PR 05-OCT-1999; 99WO-US023089.
 PR 29-NOV-1999; 99WO-US028214.
 PR 30-NOV-1999; 99WO-US028313.
 PR 30-NOV-1999; 99WO-US028409.
 PR 01-DEC-1999; 99WO-US028301.
 PR 01-DEC-1999; 99WO-US028634.
 PR 02-DEC-1999; 99WO-US028551.
 PR 02-DEC-1999; 99WO-US028564.
 PR 16-DEC-1999; 99WO-US030095.
 PR 20-DEC-1999; 99WO-US030911.
 PR 20-DEC-1999; 99WO-US030999.
 PR 30-DEC-1999; 99WO-US031243.
 PR 30-DEC-1999; 99WO-US031274.
 PR 05-JAN-2000; 2000WO-US000219.
 PR 06-JAN-2000; 2000WO-US000277.
 PR 06-JAN-2000; 2000WO-US000376.
 PR 11-FEB-2000; 2000WO-US003565.
 PR 18-FEB-2000; 2000WO-US004341.
 PR 18-FEB-2000; 2000WO-US004342.
 PR 22-FEB-2000; 2000WO-US004414.
 PR 24-FEB-2000; 2000WO-US004914.
 PR 24-FEB-2000; 2000WO-US005004.
 PR 01-MAR-2000; 2000WO-US005601.
 PR 02-MAR-2000; 2000WO-US005746.

(GETH) GENENTECH INC.

Baker KP, Beresini M, DeForge L, Desnoyers L, Filvaroff E, Gao W;
 Gerritsen ME, Goddard A, Godowski PJ, Gurney AL, Sherwood S;
 PI Smith V, Stewart TA, Tumas D, Watanabe CK, Wood WI, Zhang Z;

XX WPI; 2003-352836/33.

XX N-PSDB; ACA67089.

New isolated PRO polypeptide useful for treating diabetes, rheumatoid
 arthritis, sports injuries, obesity, hearing loss in mammals, stroke, or
 heart attack.

XX Claim 12; Fig 192; 643pp; English.

The present invention relates to the isolation of novel human PRO
 polypeptides, and the polynucleotide sequences encoding them. The PRO
 polypeptides are secreted and transmembrane proteins. The PRO
 polypeptides and polynucleotides are useful for preparing a medicament
 useful in the treatment of diabetes, bone and/or cartilage disorders
 (e.g. rheumatoid arthritis, sports injuries, osteoarthritis), obesity,
 hyper- or hypo-insulinaemia, hearing loss, and coagulation disorders
 (e.g. stroke, heart attack). Anti-PRO antibodies are useful in diagnostic
 assays for PRO, by detecting its expression in specific cells, tissues or
 serum, and for affinity purification of PRO from recombinant cell culture
 or natural sources. AB08070-AB081144 represent the human PRO
 polypeptides of the invention. Note: The sequence data for this patent
 was obtained in electronic format directly from the USPTO web site at
 seqdata.uspto.gov/psipsDIDEntry.html

XX Sequence 513 AA;

QY	24	ATGAAGCCCTCTCTGCTTCTCTGTTGTTCTTTAATACATTTTCTCTGCAATTCCTCCCTTA	83
Db	1	MetLysArgLeuLeuLeuPheLeuPheHeIleThrPheSerSerAlaPheProLeu	20
QY	84	GTCCGGATGACGGAAAAATGCAAGAAATATGCAACTGGCTCAGGCTATATCTCAACAGTTC	143
Db	21	ValArgMetThrGluAsnGluGluAsnMetGlnLeuAlaGlnAlaTyrLeuAsnGlnPhe	40
QY	144	TACTCTCTTGAAAAATAGAAGGAATCATCTTGTTCAAAGCAAGATAGGAGTCTCATAGAT	203
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QY	204	GACAAAAATTCGGGAAATCCAGCACTTTTGTGATTGCAGTGCACCTGAGGAAAACTGACATCA	263
Db	61	AspLysIleArgGluMetGlnAlaPheGlyLeuThrValThrGlyLysLeuAspSer	80
QY	264	AACACCTTGAGATCATGAAGACACCCAGGTGTGGGTGCCCTGATGTGGCCAGATATGCG	323
Db	81	AsnThrLeuGluIleMetLysThrProArgCysGlyValProAspValGlyGlnTyrGly	100
QY	324	TACACCTCTCCCTGGGTGGAGAAAAATACAACTCACCTACAGATTAATAACTATACTCCG	383
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QY	384	GATATGGCACGAGCTGCTGTGATCAGGCTATCCAAAGAGGTTTAGAAGTGGGAGCAAA	443
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QY	444	GTCACTCCCACTAAAAATTCACCAAGAGTTTCAAAGGGGATTGCAGACATCATGATGCCCTT	503
Db	141	ValThrProLeuLysPheThrLysIleSerLysGlyIleAlaAspIleMetIleAlaPhe	160
QY	504	AGGACTCGAGTCCATGTCGGTGTCTCGCTATTTTGTGTCCTCCCTGGGAGTGTCTGGC	563
Db	161	ArgThrArgValHisGlyArgCysProArgTyrPheAspGlyProLeuGlyValLeuGly	180
QY	564	CATGCTTTCTCTCTGTCGGGTCTGGGTGTGTGACACTCATTTGATCAGCATGAAAC	623
Db	181	HisAlaPheProGlyProGlyLeuGlyGlyAspThrHisPheAspGluAspGluAsn	200
QY	624	TGGACCAAGATGGAGCAGGATCAACTGTTTCTTGCGTCTCATGAATTTGGTCAAT	683
Db	201	TrpThrLysAspGlyAlaGlyPheAsnLeuPheLeuValAlaAlaHisGluPheGlyHis	220
QY	684	GCACTGGGGCTCTCTCACTCCATGATCAAAAGCCTTCATGCTTCCCAATATATCTCC	743
Db	221	AlaLeuGlyLeuSerHisSerAsnAspGlnThrAlaLeuMetPheProAsnTyrValSer	240
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QY	804	GGAGTCTGCCTAAGGTACCTGCTAAGCAAAGGAACCCACTATATCCCATGCTGTGAC	863
Db	261	GlyGlyLeuProLysValProAlaLysProLysGluProThrIleProHisAlaCysAsp	280
QY	864	CCTGACTTCACCTTTTGACGCTATCAACCTTTCCGACAGAGAGTAAATGTTCTTTAAGGC	923
Db	281	ProAspLeuThrPheAspAlaIleThrThrPheArgArgGluValMetPhePheLysGly	300
QY	924	AGGCACCTATGGAGGATCTATTATGATATCACGGATGTTTCAGTTTCAAATTAATTCCTCA	983

PR 17-SEP-1998; 98WO-US019437.
 PR 07-OCT-1998; 98WO-US021141.
 PR 29-OCT-1998; 98WO-US022991.
 PR 29-OCT-1998; 98WO-US022992.
 PR 29-OCT-1998; 98WO-US024855.
 PR 01-DEC-1998; 98WO-US025108.
 PR 05-JAN-1999; 98WO-US000106.
 PR 08-MAR-1999; 98WO-US005028.
 PR 10-MAR-1999; 98WO-US005190.
 PR 10-MAR-1999; 98WO-US008615.
 PR 14-MAY-1999; 98WO-US010733.
 PR 02-JUN-1999; 98WO-US012252.
 PR 01-SEP-1999; 98WO-US020111.
 PR 08-SEP-1999; 98WO-US020594.
 PR 13-SEP-1999; 98WO-US020944.
 PR 15-SEP-1999; 98WO-US021090.
 PR 15-SEP-1999; 98WO-US021547.
 PR 05-OCT-1999; 98WO-US023089.
 PR 29-NOV-1999; 98WO-US028214.
 PR 30-NOV-1999; 98WO-US028313.
 PR 30-NOV-1999; 98WO-US028409.
 PR 01-DEC-1999; 98WO-US028301.
 PR 01-DEC-1999; 98WO-US028634.
 PR 02-DEC-1999; 98WO-US028551.
 PR 02-DEC-1999; 98WO-US028564.
 PR 02-DEC-1999; 98WO-US028565.
 PR 16-DEC-1999; 98WO-US030095.
 PR 20-DEC-1999; 98WO-US030911.
 PR 20-DEC-1999; 98WO-US030999.
 PR 22-DEC-1999; 98WO-US030720.
 PR 30-DEC-1999; 98WO-US031243.
 PR 30-DEC-1999; 98WO-US031274.
 PR 05-JAN-2000; 2000WO-US000219.
 PR 06-JAN-2000; 2000WO-US000277.
 PR 06-JAN-2000; 2000WO-US000376.
 PR 11-FEB-2000; 2000WO-US003565.
 PR 18-FEB-2000; 2000WO-US004341.
 PR 18-FEB-2000; 2000WO-US004342.
 PR 22-FEB-2000; 2000WO-US004414.
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 PR 24-FEB-2000; 2000WO-US005004.
 PR 01-MAR-2000; 2000WO-US005601.
 PR 02-MAR-2000; 2000WO-US005746.
 PR 02-MAR-2000; 2000WO-US005841.
 PR 10-MAR-2000; 2000WO-US006319.
 PR 15-MAR-2000; 2000WO-US006884.
 PR 20-MAR-2000; 2000WO-US007377.
 PR 21-MAR-2000; 2000WO-US007532.
 PR 30-MAR-2000; 2000WO-US008439.
 PR 17-MAY-2000; 2000WO-US013705.
 PR 22-MAY-2000; 2000WO-US014042.
 PR 30-MAY-2000; 2000WO-US014941.
 PR 02-JUN-2000; 2000WO-US015264.
 PR 28-JUL-2000; 2000WO-US020710.
 PR 11-AUG-2000; 2000WO-US022031.
 PR 23-AUG-2000; 2000WO-US023522.
 PR 24-AUG-2000; 2000WO-US023328.
 PR 08-NOV-2000; 2000WO-US030952.
 PR 10-NOV-2000; 2000WO-US030873.
 PR 01-DEC-2000; 2000WO-US032678.
 PR 20-DEC-2000; 2000WO-US00747259.
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 PR 28-FEB-2001; 2001US-00796498.
 PR 28-FEB-2001; 2001WO-US006520.
 PR 01-MAR-2001; 2001WO-US006666.
 PR 09-MAR-2001; 2001US-00802706.
 PR 14-MAR-2001; 2001US-00808689.
 PR 22-MAR-2001; 2001US-00816744.
 PR 05-APR-2001; 2001US-00828366.
 PR 10-MAY-2001; 2001US-00854208.
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 PR 25-MAY-2001; 2001US-00866034.
 PR 25-MAY-2001; 2001WO-US017092.
 PR 01-JUN-2001; 2001US-00872035.
 PR 01-JUN-2001; 2001WO-US017800.
 PR 05-JUN-2001; 2001US-00874503.
 PR 14-JUN-2001; 2001US-00882636.
 PR 19-JUN-2001; 2001US-00886342.
 PR 20-JUN-2001; 2001WO-US019692.
 PR 21-JUN-2001; 2001US-00887879.
 PR 22-JUN-2001; 2001WO-US020116.
 PR 29-JUN-2001; 2001WO-US021066.
 PR 09-JUL-2001; 2001WO-US021735.
 PR 18-JUL-2001; 2001US-00908827.
 PR 06-AUG-2001; 2001US-00924419.
 PR 09-AUG-2001; 2001US-00927796.
 PR 16-AUG-2001; 2001US-00931836.
 PR 19-DEC-2001; 2001US-00028072.
 XX (GETH) GENENTECH INC.
 XX Baker KP, Beresini M, Deforge L, Desnoyers L, Filvaroff E, Gao W;
 PI Gerritsen ME, Goddard A, Godowski PU, Gurney AL, Sherwood S;
 PI Smith V, Stewart TA, Tumas D, Watanabe CK, Wood WI, Zhang Z;
 XX WPI; 2003-332040/31.
 DR N-PSDB; ACA03698.
 XX
 PT New secreted and transmembrane PRO nucleic acids, useful for gene
 PT therapy, in chromosome and gene mapping, as chromosome markers, in tissue
 PT typing, and in chromosome identification.
 XX
 PS Claim 12; Fig 192; 660pp; English.
 XX
 CC The present invention relates to the isolation of novel human PRO
 CC polypeptides, and the polynucleotide sequences encoding them. The PRO
 CC polypeptides are secreted and transmembrane proteins. The PRO
 CC polypeptides are useful for detecting other PRO polypeptides, for linking
 CC bioactive molecules to cells expressing PRO polypeptides, for modulating
 CC biological activities of cells expressing PRO polypeptides, and for
 CC identifying agonists or antagonists. The PRO polypeptides are useful for
 CC for stimulating the release of tumour necrosis factor (TNF)-alpha from
 CC human blood, for stimulating the proliferation or differentiation of
 CC chondrocytes, and detecting the presence of tumours. The polynucleotide
 CC sequences encoding PRO polypeptides are useful as hybridisation probes,
 CC in chromosome and gene mapping, in the generation of antisense RNA and
 CC DNA, in the preparation of PRO polypeptides, for generating transgenic
 CC animals or knockout animals, for the genetic analysis of individuals with
 CC genetic disorders, and in gene therapy. ABU66570-ABU66844 represent the
 CC human PRO polypeptides of the invention. Note: The sequence data for this
 CC patent was obtained in electronic format directly from the USPTO web site
 CC at seqdata.uspto.gov/psipsIDEntry.html
 XX
 SQ Sequence 513 AA;
 Alignment Scores:
 Pred. No.: 6, 23e-285 Length: 513
 Score: 2752.00 Matches: 512
 Percent Similarity: 99.81% Conservative: 0
 Best Local Similarity: 99.81% Mismatches: 1
 Query Match: 93.92% Indels: 0
 DB: 6 Gaps: 0
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 QY 24 ATGAAGCGCTTCGCTTCTGTTGTTTATACATTTTCTGCAATTCCTCCCTTA 83
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 QY 84 GTCGGATACGGAAATGAAGAAATATGCAATGCTGCTAGGCAATCTCAACAGTTC 143
 Db 21 ValArgMetThrGluAsnGluGluAsnMetGlnLeuAlaGlnLeuAsnGlnPhe 40
 QY 144 TACTCTTGAATAGAAAGGAATCATCTTGTTCAAAGCAAGATAGGAGTCTCATAGAT 203

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Db      61  AspLysIleArgGluMetGlnAlaPhePheGlyLeuThrValThrGlyLysLeuAspSer 80
QY      264  AACACCTTGAGATCATGAAAGACACCCAGGTGTGGGTGCTGATGTGGCCAGTATGGC 323
Db      81  AsnThrLeuGluIleMetLysThrProArgCysGlyValProAspValGlyGlnTyrGly 100
QY      324  TACACCTCCCTCGTGGAGAAATCAACCTCACCTACAGATATATAACTATATCTCCG 383
Db      101  TyrThrLeuProGlyTyrArgLysTyrAsnLeuThrTyrArgIleIleAsnTyrThrPro 120
QY      384  GATATGGCAGAGCTGCTGTGGATGAGCTATCCAAAGAGTTTAGAAGTGTGGAGCAAA 443
Db      121  AspMetAlaArgAlaAlaValAspGluAlaIleGlnGluGlyLeuGluValTyrSerLys 140
QY      444  GTCACTCCACTAAATTCACAGATTTCAGAGGATTCAGACATCATGATTGCCCTT 503
Db      141  ValThrProLeuLysPheThrLysIleSerLysGlyIleAlaAspIleMetIleAlaPhe 160
QY      504  AGGACTCGAGTCATGTCGTGCTGCTGCTATTTTGTATGTCCTTGGAGTGTTCGGC 563
Db      161  ArgThrArgValHisGlyArgCysProArgTyrPheAspGlyProLeuGlyValLeuGly 180
QY      564  CATGCCCTTCTCCTGCTCCGGGTGCTGGGTGACACTCATTTTGTATGAGGATGAAAC 623
Db      181  HisAlaPheProProGlyProGlyLeuGlyGlyAspThrHisPheAspGluAspGluAsn 200
QY      624  TGGACCAAGATGGAGAGATCAACTGTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 683
Db      201  TrpThrLysAspGlyAlaGlyPheAsnLeuPheLeuValAlaHisGluPheGlyHis 220
QY      684  GCATCGGGCTCTCTCACTCAATGATCAACAGCCTTGATGTTTCCCAATTTATGCTCC 743
Db      221  AlaLeuGlyLeuSerHisSerAsnAspGlnThrAlaLeuMetPheProAsnTyrValSer 240
QY      744  CTGGATCCCAAGAAATACCACTTTCTCAGATGATTCATGGAATCCAGTCCATCTAT 803
Db      241  LeuAspProArgLysTyrProLeuSerGlnAspIleAsnGlyIleGlnSerIleTyr 260
QY      804  GGAGTCTGCTAGTACCTGCTAAGCAAGCAACCACTATACCCCATGCTGCTGAC 863
Db      261  GlyGlyLeuProLysValProAlaLysProLysGluProIlePheHisAlaCysAsp 280
QY      864  CCTGACTTGACTTTTGACGCTATCACAACTTTCCGACAGAGTAATGTTCTTTAAAGC 923
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QY      924  AGGCACCTATGAGGATCTATATGATATCAGGATGTTGAGTTGATTAATTTGCTTCA 983
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QY      984  TTCGCGCATCTCTGCGCAGCTGATCTGCAAGCTGCATACAGAGACCCAGAGATAAGATT 1043
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QY      1044  CTGGTTTTTAAAGATGAAACTCTGGATGATCAGAGATATGCTGCTCCAGATAT 1103
Db      341  LeuValPheLysAspGluAsnPheTrpMetIleArgGlyTyrAlaValLeuProAspTyr 360
QY      1104  CCCAAATCCATCATACATTAAGTTTCCAGGACGTGTGAGAAATAGATGACCGCTC 1163
Db      361  ProLysSerIleHisThrLeuGlyPheProGlyArgValLysLysIleAspAlaVal 380
QY      1164  TGTGATAGACACAAAGAAACCTACTTTTGTGGCATTTGCTGCTGGAGTTTCAT 1223
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421  IleSerIleArgValAspAlaAlaPheGlnTyrLysGlyPhePhePheSerArgGly 440
1344  TCAAGCAATTTGAATACAACTTAAGACAAAGATATTACCCGAATCATAGAACTAAT 1403
441  SerLysGlnPheGluTyrAsnIleLysThrLysAsnIleThrArgIleMetArgThrAsn 460
1404  ACTTGTTTCAATGCAAAAGAACCAAAAGACTCTCTCATTTGCTGTTTCATATCAACAGAA 1463
461  ThrTrpPheGlnCysLysGluProLysAsnSerSerPheGlyPheAspIleAsnLysGlu 480
1464  AAGACACATTCAGAGGCATARAAGATATTGTATCATAGAGTTTAAGCTTGTATTATTTT 1523
481  LysAlaHisSerGlyGlyIleLysIleLeuTyrHisSerLeuSerLeuPheIlePhe 500
1524  GGTATTGTTTCATTGCTGCAAAAACACTTCTATTATTCAA 1562
501  GlyIleValHisLeuLeuLysAsnThrSerIleTyrGln 513

RESULT 8
ABO32578
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XX  ABO32578;
XX  17-SEP-2003 (first entry)
DE  Secreted polypeptide-related protein #40.
XX  Human; TANGO; INTERCEPT; secreted polypeptide; immune disorder;
XX  hormonal disorder; proliferative disorder; cancer; thyroid disorder;
XX  diabetes; multiple sclerosis; lupus; neurological disorder; anaemia;
XX  Alzheimer's disease; Parkinson's disease; cardiovascular disorder;
XX  myocardial infarction; congestive heart disease; blood platelet disorder;
XX  thrombocytopenia; blood vessel; atherosclerosis; vasculitis.
XX  Homo sapiens.
XX  US2003022279-A1.
XX  30-JAN-2003.
XX  12-JAN-2001; 2001US-00759130.
XX  14-JUN-1999; 99US-00333159.
XX  29-JUN-1999; 99US-00342364.
XX  10-SEP-1999; 99US-00393996.
XX  19-OCT-1999; 99US-00420707.
XX  07-JAN-2000; 2000US-00479249.
XX  27-APR-2000; 2000US-00559497.
XX  24-MAY-2000; 2000US-00578063.
XX  16-JUN-2000; 2000US-00596194.
XX  23-JUN-2000; 2000US-00602871.
XX  30-JUN-2000; 2000US-00608452.
XX  (FRAS/) FRASER C C.
XX  (BARN/) BARNES T M.
XX  (SHAR/) SHARP J D.
XX  (KIRS/) KIRST S J.
XX  (MYER/) MYERS P S.
XX  (LEIB/) LEIBY K R.
XX  (HOLT/) HOLTZMAN D A.
XX  (MCCA/) MCCARTHY S A.
XX  (WRIG/) WRIGHTON N.
XX  (MACK/) MACKAY C R.
XX  (GOOD/) GOODEARL A D J.
XX  Fraser CC, Barnes TM, Sharp JD, Kirst SJ, Myers PS, Leiby KR;
XX  Holtzman DA, Mccarthy SA, Wrighton N, Mackay CR, Goodearl ADJ;

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DR [WPI: 2003-456290/43](#).
 DR [N-PSDB: ACD66739, ACD66740](#).
 XX
 PT New nucleic acid molecule encoding a secreted protein (e.g. TANGO 202,
 PT TANGO 210 or INTERCEPT 217), useful for diagnosing, preventing or
 PT treating disorders such as cancer, diabetes or atherosclerosis, and in
 PT forensic biology.
 XX
 PS Claim 9; Fig 15A-15D; 482pp; English.
 XX
 CC The invention relates to secreted polypeptide-related proteins and
 CC nucleic acids (TANGO and INTERCEPT proteins and nucleic acids). The
 CC nucleic acids, proteins and antibodies specific to the proteins are
 CC useful in screening assays, predictive medicine (e.g. diagnostic assays,
 CC prognostic assays, monitoring clinical trials and pharmacogenetics) and
 CC prophylactic and therapeutic methods. The sequences are used in
 CC diagnosing, preventing or treating proliferative disorders (e.g.
 CC cancers), hormonal disorders (e.g. diabetes or thyroid disorders), immune
 CC disorders (e.g. multiple sclerosis or lupus), neurological disorders
 CC (e.g. Alzheimer's disease or Parkinson's disease), cardiovascular
 CC disorders (e.g. myocardial infarction or congestive heart disease), blood
 CC platelet disorders (e.g. thrombocytopenia or anaemia) and disorders
 CC involving blood vessels (e.g. atherosclerosis or vasculitis). The nucleic
 CC acids may also be used in chromosome mapping, tissue typing and forensic
 CC biology, and as surrogate markers. This sequence represents a secreted
 CC polypeptide-related protein of the invention. Note: The sequence data for
 CC this patent was obtained in electronic format directly from USPTO at
 CC [segdata.uspto.gov/sequence.html](#)
 XX
 SQ Sequence 513 AA;

 Alignment Scores:
 Align. No.: 6,23e-285 Length: 513
 Pred. No.: 2752.00 Matches: 512
 Percent Similarity: 99.81% Conservative: 0
 Best Local Similarity: 99.81% Mismatches: 1
 Query Match: 93.92% Indels: 0
 DB: 6 Gaps: 0

 US-10-729-807-28 (1-1627) x ABO32578 (1-513)

 QY 24 ATGAAGCGCCTCTGCTTCTGTGTGTTGTTTATATAACATTTTCTTCTGCATTTCCTCTTA 83
 Db 1 MetLysArgLeuLeuLeuLeuPheLeuPhePheLeuThrPheSerSerAlaPheProLeu 20

 QY 84 GTCGGATGACGGAAATGAGAAATATGCAACTGGCTCAGGCATATCTCAACAGTTC 143
 Db 21 ValArgMetThrGluAsnGluGluAsnMetGlnLeuAlaGlnAlaTyrLeuAsnGlnPhe 40

 QY 144 TACTCTCTTGAATAGAGAGGAATCATCTGTGTTCAAAGCAGAAATAGGAGTCTCATAGAT 203
 Db 41 TyrSerLeuGluIleGluGluYAsnHisLeuValGlnSerLysAsnArgSerLeuIleAsp 60

 QY 204 GACAAAATTCGGAAATGCAAGCATTTTTTGGATTGACAGTGACTGGAAAACCTGGACTCA 263
 Db 61 AspLysIleArgGluMetGlnAlaPhePheGlyLeuThrValThrGlyLysLeuAspSer 80

 QY 264 AACACCCTTGATCATCAAGACACCCAGGTGTGGGTGCTGTGATGTGGCCAGATGAGC 323
 Db 81 AsnThrLeuGluIleMetLysThrProArgCysGlyValProAspValGlyGlnTyrGly 100

 QY 324 TACACCCCTCCCTGGGTGGAGAAATACAACTCACCCTACAGAAATAATAAATATACTACG 383
 Db 101 TyrThrLeuProGlyTyrArgLysTyrAsnLeuThrTyrArgIleIleAsnTyrThrPro 120

 QY 384 GATATGGCAGAGCTGCTGTGGATGAGGCTATCCCAAGAGGTTTAGAAGTGTGGAGCAA 443
 Db 121 AspMetAlaArgAlaAlaValAspGluAlaIleGlnGluGlyLeuGluValTrpSerLys 140

 QY 444 GTCACCTCACTAAATTCACCAAGATTTCAAAGGGATTCAGACATCATGATGCCTTT 503
 Db 141 ValThrProLeuLysPheThrLysIleSerLysGlyIleAlaAspIleMetIleAlaPhe 160

in modulating at least one biological activity of a cell expressing a PRO polypeptide. PRO1312 stimulates hypertrophy of neonatal heart and is thus useful for treating cardiac insufficiency disorders. PRO1154 and PRO1186 stimulate adrenal cortical capillary endothelial growth, and PRO536, PRO943, PRO828, PRO1068 or PRO535, PRO826, PRO819, PRO1126, PRO1360 and PRO1387 induce c-fos in endothelial cells, and are thus useful for treating conditions or disorders where angiogenesis would be beneficial, e.g. wound healing and antagonist of this polypeptide are useful for treating cancerous tumours. PRO812 inhibits vascular endothelial growth factor (VEGF) stimulated proliferation of endothelial cells and is thus useful for inhibiting endothelial cell growth in mammals which would be beneficial in inhibiting tumour growth. PRO826, PRO1068, PRO1184, PRO1346 and PRO1375 stimulate proliferation of stimulated T-lymphocytes and are therapeutically useful for enhancing immune response. PRO828, PRO826, PRO1068 or PRO1132 enhance survival of retinal neurons cells (PRO1132 is also enhances survival/proliferation of rod photoreceptor cells) and therefore are useful for treating retinal disorders of injuries, e.g. retinitis pigmentosa, AMD. PRO819, PRO813 and PRO1066 induce proliferation of mammalian kidney mesangial cells, and therefore are useful for treating kidney disorders associated with decreased mesangial cell function such as Berger disease or other nephropathies associated with dermatitis, herpeticiformis or Crohn's disease. PRO1310, PRO844, PRO1312, PRO1192 and PRO1387 induce the proliferation and/or redifferentiation of chondrocytes in culture and are thus useful for treating sports injuries, and arthritis. This is the amino acid sequence of a novel human PRO protein

SQ Sequence 513 AA;

Alignment Scores:

Pred. No.: 6.23e-285 Length: 513
Score: 2752.00 Matches: 512
Percent Similarity: 99.81% Conservative: 0
Best Local Similarity: 99.81% Mismatches: 1
Query Match: 93.92% Indels: 0
DB: 6 Gaps: 0

US-10-729-807-28 (1-1627) x ABUS9746 (1-513)

QY	24	ATGAAGCGCTCTGCTTCTGTGTTGTTGTTTATTAACATTTTCTCTCATTTCCCTTA	83
DB	1	MetLysArgLeuLeuLeuLeuPheLeuPhePheLeuThrPheSerSerAlaPheProLeu	20
QY	84	GTCCGGATCAGCGAAATCAAGAAATATGCACTGGCTCAGGCATATCTCAACCGTTC	143
DB	21	ValArgMetThrGluAsnGluGluAsnMetGlnLeuAlaGlnAlaTyrLeuAsnGlnPhe	40
QY	144	TACTCTTTGAATAGAGGGAATCATCTTGTTCAGCAAGAAATAGGAGTCTCTAGAT	203
DB	41	TyrSerLeuGluLeuGluGluGluAsnHisLeuValGlnSerLysAsnArgSerLeuLeuAsp	60
QY	204	GCAGAAATCGGGAATGCAAGCATTTTGTGATTGACAGTGCAGTGGAAAACTGGACTCA	263
DB	61	AspLysIleArgGluMetGlnAlaPhePheGlyLeuThrValThrGlyLysLeuAspSer	80
QY	264	AACACCTTTGACATCATGAAGACACCCAGTGTGGGTGCTGATGTGGCCAGTATGGC	323
DB	81	AsnThrLeuGluLeuMetLysThrProArgCysGlyValProAspValGlyGlnTyrGly	100
QY	324	TACACCTCTCCCTGGGTGGGAAATATACACCTCACCTACAGATAATAAATATATCTCCG	383
DB	101	TyrThrLeuProGlyTyrArgLysTyrAsnLeuThrTyrArgIleLeuAsnTyrThrPro	120
QY	384	GATATGGCAGCGTCTGCTGTGATGAGGTATTCAGAAAGGTTTACAGTGTGGAGCAA	443
DB	121	AspMetAlaArgAlaAlaValAspGluAlaIleGlnGluGlyLeuGluValTrpSerLys	140
QY	444	GTCACCTCCACTAAATTCACCAAGATTTCAAGGGGATTCAGACATCATGATTCGCTTT	503
DB	141	ValThrProLeuLysPheThrLysIleSerLysGlyIleAlaAspIleMetIleAlaPhe	160
QY	504	AGGACTCGAGTCCATGTCGGTGTCTCGCTATTTGATGTCCTTGGAGTCTTGCC	563

DB	161	ArgThrArgValHisGlyArgCysProArgTyrPheAspGlyProLeuGlyValLeuGly	180
QY	564	CATGCTTTCCTCTCTGGTCCGGTCTGGGTGGTGCACACTCAITTTTGTATGAGGTAAAC	623
DB	181	HisAlaPheProGlyProGlyLeuGlyGlyAspThrHisPheAspGluAspGluAsn	200
QY	624	TGGACCAAGATGAGCAGAGATTCACACTTGTGTTCTTGTGGCTCTCATGATTTGGTCAT	683
DB	201	TrpThrLysAspGlyAlaGlyPheAsnLeuPheLeuValAlaAlaHisGluPheGlyHis	220
QY	684	GCACTGGGGTCTCTCACTCCCAATGATCAACAGCTTGATGTTCCCAATTTATGCTCC	743
DB	221	AlaLeuGlyLeuSerHisSerAsnAspGlnThrAlaLeuMetPheProAsnTyrValSer	240
QY	744	CTGGATCCAGAAAAATACCACCTTTCTCAGGATGATATCAATGGAATCCAGTCCATCTAT	803
DB	241	LeuAspProArgLysTyrProLeuSerGlnAspAspIleAsnGlyIleGlnSerIleTyr	260
QY	804	GGAGTCTCCCTAAGGTACTCTGTAAGCCAAAGAACCCACTATATCCCATGCTGTGAC	863
DB	261	GlyGlyLeuProLysValProAlaLysProLysGluProThrIleProHisAlaCysAsp	280
QY	864	CCTGACTTCTGCTTTCAGCTATCAACTTTCCGAGAGAGTAACTATGTTCTTTAAGGC	923
DB	281	ProAspLeuThrPheAspAlaIleThrThrPheArgGluValMetPhePheLysGly	300
QY	924	AGSCACTATGAGGAGTCTATTATGATATCACGGATGTTGAGTTTGAATTAATTTGTTCA	983
DB	301	ArgHisLeuTrpArgIleTyrTyrAspIleThrAspValGluPheGluLeuIleAlaSer	320
QY	984	TTCTGGCCATCTCTGCCAGCTGATCTGCAAGCTGCATAGAGAACCCAGAGATAGATT	1043
DB	321	PheTrpProSerLeuProAlaAspLeuGlnAlaTyrGluAsnProArgAspLysIle	340
QY	1044	CTGGTTTTTAAAGATGAAAACTTCTGGATGATCAGAGGATATGCTCTTGTCCAGATTAT	1103
DB	341	LeuValPheLysAspGluAsnPheTrpMetIleArgGlyTyrAlaValLeuProAspTyr	360
QY	1104	CCCAATCCATCATACATTAGTGTTCAGGACCTGTGAGAAATAGATGACGCGTTC	1163
DB	361	ProLysSerIleHisThrLeuGlyPheProGlyArgValLysLysIleAspAlaVal	380
QY	1164	TGTGATAGACACACAAAGAACCTACTCTTTTGGGGCATTTGGTGTGGAGTTTGTAT	1223
DB	381	CysAspLysThrThrArgLysThrTyrPhePheValGlyIleTrpCysTrpArgPheAsp	400
QY	1224	GAAATGACCCAAACCATGACAAAGATTCCCGCAGAGAGTGTAAACACATTTCTCTGA	1283
DB	401	GluMetThrGlnThrMetAspLysGlyPheProGlnArgValValLysHisPheProGly	420
QY	1284	ATCAGTATCCGTGTTGATGCTCTTTCAGTACAAAGGATTCCTCTTTTCAGCCGTGA	1343
DB	421	IleSerIleArgValAspAlaAlaPheGlnTyrLysGlyPhePhePheSerArgGly	440
QY	1344	TCAAGACATTTGATACAACTTAAGCAAGATATTTACCGAATCATGAGAACTAAT	1403
DB	441	SerLysGlnPheGluTyrAsnIleLysThrLysAsnIleThrArgIleMetArgThrAsn	460
QY	1404	ACTTGTGTTTCAATGCAAGAACCAAGAACTCTCATTTGTTTGTATATCAACAGAA	1463
DB	461	ThrTrpPheGlnCysLysGluProLysAsnSerPheGlyPheAspIleAsnLysGlu	480
QY	1464	AAAGCACATTCAGGAGGCATAAAGATTTGTATCATATAAGAGTTTAAAGCTTGTATTTT	1523
DB	481	LysAlaHisSerGlyGlyIleLysIleLeuTyrHisLysSerLeuSerLeuPheIlePhe	500
QY	1524	CGTATTGTTTCAATTCCTGAAACCACTTCTATTTATCAA	1562
DB	501	GlyIleValHisLeuLeuLysAsnThrSerIleTyrGln	513

RESULT 10

ABO24936

ID ABO24936 standard; protein; 513 AA.

XX	ABO24936;	01-MAR-2000;	2000WO-US005601.	PR
AC		02-MAR-2000;	2000WO-US005746	PR
XX		02-MAR-2000;	2000WO-US005841.	PR
DT		10-MAR-2000;	2000WO-US006319.	PR
XX		15-MAR-2000;	2000WO-US006884.	PR
XX		20-MAR-2000;	2000WO-US007377.	PR
XX		21-MAR-2000;	2000WO-US007532.	PR
XX		30-MAR-2000;	2000WO-US008439.	PR
KW	Human, PRO; secreted protein; transmembrane protein; tumour; cytostatic;	17-MAY-2000;	2000WO-US013705.	PR
KW	gene therapy; tumour necrosis factor-alpha; TNF-alpha; blood;	22-MAY-2000;	2000WO-US014042.	PR
KW	proteoglycan; cartilage; cytokine; peripheral blood mononuclear cell;	30-MAY-2000;	2000WO-US014941.	PR
KW	PMBC; glucose uptake; FFA; skeletal muscle cell; adipocyte cell;	28-JUN-2000;	2000WO-US015264.	PR
KW	chondrocyte cell proliferation; chondrocyte cell differentiation;	28-JUL-2000;	2000WO-US020710.	PR
KW	pericyte cell; inner ear utricular supporting cell; T-lymphocyte cell;	11-AUG-2000;	2000WO-US022031.	PR
KW	endothelial cell; A-peptide; factor VIIA.	23-AUG-2000;	2000WO-US023522.	PR
XX		24-AUG-2000;	2000WO-US023328.	PR
OS	Homo sapiens.	08-NOV-2000;	2000WO-US030952.	PR
XX		10-NOV-2000;	2000WO-US030873.	PR
PN	US2003036179-A1.	01-DEC-2000;	2000WO-US032678.	PR
XX		20-DEC-2000;	2000US-00747259.	PR
PD		20-DEC-2000;	2000WO-US034956.	PR
XX		28-FEB-2001;	2001US-00796498.	PR
XX		28-FEB-2001;	2001WO-US006520.	PR
XX		01-MAR-2001;	2001WO-US006666.	PR
XX		09-MAR-2001;	2001US-00802706.	PR
XX		14-MAR-2001;	2001US-00808689.	PR
PR		22-MAR-2001;	2001US-00816744.	PR
PR		05-APR-2001;	2001US-00828366.	PR
PR		10-MAY-2001;	2001US-00854208.	PR
PR		18-MAY-2001;	2001US-00854280.	PR
PR		25-MAY-2001;	2001US-00860216.	PR
PR		25-MAY-2001;	2001US-00866028.	PR
PR		25-MAY-2001;	2001US-00866034.	PR
PR		25-MAY-2001;	2001WO-US017092.	PR
PR		01-JUN-2001;	2001US-00872035.	PR
PR		01-JUN-2001;	2001WO-US017800.	PR
PR		05-JUN-2001;	2001US-00874503.	PR
PR		14-JUN-2001;	2001US-00882636.	PR
PR		19-JUN-2001;	2001US-00886342.	PR
PR		20-JUN-2001;	2001WO-US019692.	PR
PR		21-JUN-2001;	2001US-00887879.	PR
PR		22-JUN-2001;	2001WO-US020116.	PR
PR		29-JUN-2001;	2001WO-US021066.	PR
PR		09-JUL-2001;	2001WO-US021735.	PR
PR		18-JUL-2001;	2001US-00908827.	PR
PR		06-AUG-2001;	2001US-00924419.	PR
PR		09-AUG-2001;	2001US-00927796.	PR
PR		16-AUG-2001;	2001US-00931836.	PR
PR		19-DEC-2001;	2001US-00028072.	PR
XX		(GETH) GENENTECH INC.		PA
XX		Baker KP, Beresini M, Deforge L, Desnoyers L, Filvaroff E, Gao W;		XX
PI	Gerritsen ME, Goddard A, Godowski PJ, Gurney AL, Sherwood S;			PI
PI	Smith V, Stewart TA, Tumas D, Watanabe CK, Wood WL, Zhang Z;			PI
XX		WPI; 2003-466355/44.		XX
DR	N-PSDB; ACD41890.			DR
XX		New isolated nucleic acid encoding a PRO polypeptide, e.g. PRO1114 or		XX
PT	PRO4978, useful in molecular biology, chromosome and gene mapping, in			PT
PT	generating antisense RNA and DNA, and in gene therapy.			PT
XX		Claim 12; Fig 192; 659pp; English.		XX
PS		The invention relates to an isolated nucleic acid comprising at least 80%		PS
XX		sequence identity to a PRO (secreted and transmembrane protein) cDNA		XX
CC		comprising a nucleic acid (a) encoding a PRO polypeptide, or its		CC
CC		extracellular domain (with or without its associated signal peptides),		CC
CC		which comprises any of the 275 120-850 residue amino acid sequences,		CC
CC		given in the specification; (b) comprising any of the 275 300-3500		CC
CC		nucleotide sequences, given in the specification; or (c) comprising the		CC
CC		full-length coding sequence of the nucleotide sequences given in the		CC

specification, or of the DNA deposited under any of the American Type Culture Collection (ATCC) Accession Numbers listed in the specification. Also included are a vector comprising the novel nucleic acid, a host cell comprising the vector, producing a PRO polypeptide, the isolated PRO polypeptides detailed above, a chimaeric molecule comprising the PRO polypeptide of fused to a heterologous amino acid sequence, an anti-PRO antibody, detecting a PRO polypeptide in a sample suspected of containing the PRO polypeptide, linking a bioactive molecule to a cell expressing a PRO polypeptide, modulating at least one biological activity of a cell expressing a PRO polypeptide, stimulating the release of tumour necrosis factor-alpha (TNF-alpha) from human blood, (or proteoglycans from cartilage or cytokine from peripheral blood mononuclear cells (PBMC)), modulating the uptake of glucose or FFA by skeletal muscle cells or adipocyte cells, stimulating the proliferation or differentiation of chondrocyte cells (or proliferation of or gene expression in pericyte cells), stimulating the proliferation of inner ear utricular supporting cells (or of T-lymphocyte cells, or of endothelial cells), inhibiting the binding of A-peptide to factor VIIA, or differentiation of adipocyte cells, detecting the presence of a tumour in a mammal and an oligonucleotide probe derived from any of the nucleotide sequences given in the specification. The polynucleotide is useful in molecular biology, including uses as hybridisation probes, in chromosome and gene mapping, in generating antisense RNA and DNA, and in gene therapy. The polynucleotide may also be used in preparing PRO polypeptides by recombinant techniques, and in generating either transgenic animals or knock-out animals which, in turn, are useful in the development and screening of therapeutically useful reagents. The PRO polypeptide or the antibody is used in preparing a medicament for treating a condition responsive to the polypeptide or antibody, such as tumours, and in various diagnostic assays. The present sequence represents a PRO polypeptide

SQ Sequence 513 AA;

Alignment Scores:

Pred. No.: 6,23e-285 Length: 513
Score: 2752.00 Matches: 512
Percent Similarity: 99.81% Conservative: 0
Best Local Similarity: 99.81% Mismatches: 1
Query Match: 93.92% Indels: 0
DB: 6 Gaps: 0

US-10-729-807-28 (1-1627) x ABO24936 (1-513)

24 ATGAAGCGCTCTCTCTGTTGTTGTTTATTAACATTTTCTCTGCAATTCCTCTTA 83
1 MetLysArgLeuLeuLeuLeuPheLeuPhePheLeuPheSerSerAlaPheProLeu 20
84 GTCCGGATGACGGAAAATGAAGAAATATGCAACTGGCTCAGGCATATCTCAACAGTTC 143
21 ValArgMetThrGluAsnGluGluAsnMetGlnLeuAlaGlnAlaTyrLeuAsnGlnPhe 40
144 TACTCTCTTGAATAGAGGAATCATCTTGTTCAGACAGAAATAGAGTCTATAGAT 203
41 TyrSerLeuGluIleGluGlyAsnHisLeuValGlnSerLysAsnArgSerLeuIleAsp 60
204 GACAAAATTCGGGAATGCAAGCATTTTGTGATTGACAGTGACTGGAAAATCTGACATCA 263
61 AspLysIleArgGluMetGlnAlaPhePheGlyLeuThrValThrGlyLysLeuAspSer 80
264 AACACCTTGATCATGAAGACACCCAGGTGTGGGTGCTGTGATGTGGGCCAGTATGGC 323
81 AsnThrLeuGluIleMetLysThrProArgCysGlyValProAspValGlyGlnTyrGly 100
324 TACACCTCCCTGGGTGAGAAAATACAACTCACCCTACAGATATAACTATACTCCG 383
101 TyrThrLeuProGlyTyrArgLysTyrAsnLeuThrTyrArgIleAsnTyrThrPro 120
384 GATATGGCAGCAGCTGCTGTGATCAGGCTATCCAAAGAGTTTAGAGTGTGGAGCAA 443
121 AspMetAlaArgAlaValAspGluAlaIleGlnGluGlyLeuGluValTyrSerLys 140
444 GTCACCTCCACTAAATTCACCAAGATTTCAAAGGGGATTGCAGACATCATGATGCTTT 503

141 ValThrProLeuLysPheThrLysIleSerLysGlyIleAlaAspIleMetIleAlaPhe 160
504 AGGACTCGAGTCCATGTCGGTGTCTCGCTATTTTGTGCTGCTCATCAATTTGCTCAT 563
161 ArgThrArgValHisGlyArgCysProArgTyrPheAspGlyProLeuGlyValLeuGly 180
564 CATGCTTTTCCCTCCGCTCGGCTCGGCTGAGCAGCTCATCTTTGATGAGGATGAAAC 623
181 HisAlaPheProProGlyProGlyLeuGlyGlyAspThrHisPheAspGluAsn 200
624 TGGACCAAGATGAGCAGCATTTCAACTTGTGCTGCTCATCAATTTGCTCAT 683
201 TrpThrLysAspGlyAlaGlyPheAsnLeuPheLeuValAlaHisGluPheGlyHis 220
684 GCATGGGCTCTCTCACTCAATGATCAACAGCCTTGATGTTCCCAATATGCTCTCC 743
221 AlaLeuGlyLeuSerHisSerAsnAspGlnThrAlaLeuMetPheProAsnTyrValSer 240
744 CTGGATCCCAAGAAATACCATTTTCTCAGGATGATATCAATGGATCCAGTCCATCTAT 803
241 LeuAspProArgLysTyrProLeuSerGlnAspAspIleAsnGlyIleGlnSerIleTyr 260
804 GGAGTCTGCTTAAGGTACTCTAAGCCAAAGGAACCCACTATATACCCCATCGCTGTGAC 863
261 GlyGlyLeuProLysValProAlaLysProLysGluProThrIleProHisAlaCysAsp 280
864 CTGACTTGACTTTTGGCTATCAACTTTCCGAGAGAAAGTAAATGTTCTTTAAAGC 923
281 ProAspLeuThrPheAspAlaIleThrThrPheArgArgGluValMetPhePheLysGly 300
924 AGGCACCTATGAGGATCTATTATGATATCAGGATGTTGAGTTTGAATTAATGCTTCA 983
301 ArgHisLeuTrpArgIleTyrTyrAspIleThrAspValGluPheGluLeuIleAsp 320
984 TTCTGCGCATCTCTCCAGCTGATCTGCAAGCTGCATACGAGAACCCAGAGATAAGATT 1043
321 PheTrpProSerLeuProAlaAspLeuGlnAlaTyrGluAsnProArgAspLysIle 340
1044 CTGGTTTTTAAAGATGAAAATCTCTGGATGATCAGAGGATATGCTGTCTGCGAGATTAT 1103
341 LeuValPheLysAspGluAsnPheTrpMetIleArgGlyTyrAlaValLeuProAspTyr 360
1104 CCCAATCCATCCATACATTAAGTTTCCAGACCTGTGAAGAAATAGATGACGCCGTC 1163
361 ProLysSerIleHisThrLeuGlyPheProGlyArgValLysLysIleAspAlaVal 380
1164 TGTGATAAGACCAAGAAAACCTACTTCTTGTGGGCATTTGGTGTGGAGGTTTGAT 1223
381 CysAspLysThrThrArgLysThrTyrPhePheValGlyIleTyrCysTrpArgPheAsp 400
1224 GAATGACCCCAACCATGGAACAAAGGATTCGCGCAGAGAGTGGTAAACACTTTCTCGA 1283
401 GluMetThrGlnThrMetAspLysGlyPheProGlnArgValValLysHisPheProGly 420
1284 ATCAGTACCGTGTGATGCTGCTTCCAGTACAAAGATTTCTTCTTTTTCAGCGGTGA 1343
421 IleSerIleArgValAspAlaPheGlnTyrLysGlyPhePhePhePheSerArgGly 440
1344 TCAAGCAATTTGAATACCAATTAAGCAAGAAATATTACCCGAATCATCAGAACTAAT 1403
441 SerLysGlnPheGluTyrAsnIleLysThrLysAsnIleThrArgIleMetCargThrAsn 460
1404 ACTTGGTTTCAATCAAGAACCAAGAACTCTCATTTGTTTGTATATCAACAGAA 1463
461 ThrTrpPheGlnCysLysGluProLysAsnSerSerPheGlyPheAspIleAsnLysGlu 480
1464 AAAGCATTTCCAGGAGCATTAAGATATTGATCATAGAGTTTAAAGTTTAACTTTATTTT 1523
481 LysAlaHisSerGlyGlyIleLysIleLeuTyrHisLysSerLeuSerLeuPheIlePhe 500
1524 GGTATTGTTTCAATTTGCTGAAAACACTTCTATTATCA 1562

comprises the full-length coding sequence of the DNA deposited under American Type Culture Collection (ATCC) accession number in a list given in the specification. Also included are vectors and host cells for producing PRO proteins, PRO fusion proteins, anti-PRO antibodies, PRO extracellular domains and mature sequences, methods of detecting PRO proteins, methods for stimulating the release of TNF-alpha (tumour necrosis factor alpha) from human blood, (and the proliferation of differentiation of chondrocyte cells, the proliferation of, or gene expression in pericyte cells, the release or proteoglycans from cartilage, proliferation of inner ear articular supporting cells, the proliferation of T-lymphocyte cells, the release of a cytokine from peripheral blood mononuclear cells (PBMC), or the proliferation of endothelial cells), a method for modulating the uptake of glucose or free fatty acid (FFA) by skeletal muscle cells, a method for inhibiting the binding of A-peptide to factor VIIa, or the differentiation of adipocyte cells, a method for detecting the presence of a tumour in a mammal and an oligonucleotide probe derived from any of the nucleotide sequences cited above. The nucleic acids and polypeptides are useful for treating inflammatory diseases, organ failure, atherosclerosis, cardiac injury, infertility, birth defects, premature aging, AIDS (acquired immunodeficiency syndrome), cancer, or diabetic complications. The nucleic acids are useful as hybridisation probes, in chromosome and gene mapping, and in generating antisense RNA or DNA. The polypeptides are useful as pharmaceuticals, diagnostics, biosensors or bioreactors. Both are useful in tissue typing. The present sequence represents a PRO protein of the invention

XX
SQ Sequence 513 AA;

Alignment Scores:

Pred. No.:	6,23e-285	Length:	513
Score:	2752.00	Matches:	512
Percent Similarity:	99.81%	Conservative:	0
Best Local Similarity:	99.81%	Mismatches:	1
Query Match:	93.92%	Indels:	0
DB:	6	Gaps:	0

US-10-729-807-28 (1-1627) x ABU66941 (1-513)

24	ATGAGAGCGCTTCTGCTCTCTGTTGTGTTCTTTATAACATTTCTTCTGCAATTTCCCTTA	83	
Db			
1	MetLysArgLeuLeuLeuLeuPheLeuPhePheIleThrPheSerSerAlaPheProLeu	20	
QY	84	GTCCGGATGACGGAAATCAAGAAATATGCAATGGCTCAGGCATATCTCAACCAAGTTC	143
Db			
21	ValArgMetThrGluAsnGluGluAsnMetGlnLeuAlaGlnAlaTyrLeuAsnGlnPhe	40	
QY	144	TACTCTCTTGAATAGAAGGAATCATCTTCTTCAAAGCAAGATAGGAGTCTCATAGAT	203
Db			
41	TyrSerLeuGluIleGluGlyAsnHisLeuValGlnSerLysAsnArgSerLeuIleAsp	60	
QY	204	GACAAATTCGGAAATCCAGACATTTTTCGATTGACAGTACTGGAATCGAACTCA	263
Db			
61	AspLysIleArgGluMetGlnAlaPhePheGlyLeuThrValThrGlyLysLeuAspSer	80	
QY	264	AACACCTTGAGATCATCAAGACACCCAGGTGGGTGCTGATGTGGCCAGTAGTGC	323
Db			
81	AsnThrLeuGluIleMetLysThrProArgCysGlyValProAspValGlyGlnTyrGly	100	
QY	324	TACACCTTCCCTGGGTGGAGAAAATACAACCTCACCTACAGAATAATAACTACTCCG	383
Db			
101	TyrThrLeuProGlyTyrArgLysTyrAsnLeuThrTyrArgIleIleAsnTyrThrPro	120	
QY	384	GATATGGCAGCAGCTGCTGCGATGAGCGCTATCCAAGAGGTTTAGAGTGTGCACAA	443
Db			
121	AspMetAlaArgAlaAlaValAspGluAlaIleGlnGluGlyLeuGluValTyrSerLys	140	
QY	444	GTCACTCCCAATAAAATCCACCAAGATTCAAAGGGGATTGCAGACATCATGATTGCTTT	503
Db			
141	ValThrProLeuLysPheThrLysIleSerLysGlyIleAlaAspIleMetIleAlaPhe	160	
QY	504	AGGACTCGAGTCCATGGTCGTGTCCTCGCTATTTTTGATGGTCCCTTGGAGTGTGCG	563

XX	ADA45711;	24-FEB-2000; 2000WO-US005004.	PR
AC		01-MAR-2000; 2000WO-US005601.	PR
DT		02-MAR-2000; 2000WO-US005746.	PR
XX		10-MAR-2000; 2000WO-US005841.	PR
XX		15-MAR-2000; 2000WO-US006319.	PR
DE	20-NOV-2003 (first entry)	16-MAR-2000; 2000WO-US006884.	PR
XX	Novel human secreted and transmembrane protein PRO5992.	21-MAR-2000; 2000WO-US007377.	PR
XX		21-MAR-2000; 2000WO-US007532.	PR
KW	Human; secreted and transmembrane protein; PRO;	30-MAR-2000; 2000WO-US008439.	PR
KW	Tumour necrosis factor alpha release; TNF-alpha release;	17-MAY-2000; 2000WO-US013705.	PR
KW	glucose uptake modulator; FFA uptake modulator;	22-MAY-2000; 2000WO-US014042.	PR
KW	cell proliferation stimulator; cell differentiation stimulator;	30-MAY-2000; 2000WO-US014941.	PR
KW	cell differentiation inhibitor; cytokine release stimulator; tumour;	02-JUN-2000; 2000WO-US015264.	PR
KW	lung tumour; colon tumour; breast tumour; prostate tumour; rectal tumour;	28-JUL-2000; 2000WO-US020710.	PR
KW	cervical tumour; liver tumour; chromosome mapping; gene mapping;	11-AUG-2000; 2000WO-US022031.	PR
KW	gene therapy; chromosome identification; chromosome marker.	23-AUG-2000; 2000WO-US023522.	PR
XX		24-AUG-2000; 2000WO-US023328.	PR
OS	Homo sapiens.	08-NOV-2000; 2000WO-US030952.	PR
XX		10-NOV-2000; 2000WO-US030873.	PR
XX	US2003022328-A1.	01-DEC-2000; 2000WO-US032678.	PR
XX		20-DEC-2000; 2000US-00747259.	PR
PD	30-JAN-2003.	20-DEC-2000; 2000WO-US034956.	PR
XX		28-FEB-2001; 2001US-00796498.	PR
PF	16-APR-2002; 2002US-00123904.	28-FEB-2001; 2001WO-US006520.	PR
XX		01-MAR-2001; 2001WO-US006666.	PR
PR	31-MAR-1997; 97WO-US005230.	09-MAR-2001; 2001US-00802706.	PR
PR	12-JUN-1998; 98WO-US012456.	14-MAR-2001; 2001US-00808689.	PR
PR	14-JUL-1998; 98WO-US014552.	22-MAR-2001; 2001US-00816744.	PR
PR	28-AUG-1998; 98WO-US017888.	05-APR-2001; 2001US-00828366.	PR
PR	10-SEP-1998; 98WO-US018824.	10-MAY-2001; 2001US-00854208.	PR
PR	14-SEP-1998; 98WO-US019093.	18-MAY-2001; 2001US-00854280.	PR
PR	14-SEP-1998; 98WO-US019094.	25-MAY-2001; 2001US-00860216.	PR
PR	14-SEP-1998; 98WO-US019177.	25-MAY-2001; 2001US-00866028.	PR
PR	16-SEP-1998; 98WO-US019330.	01-JUN-2001; 2001US-00872035.	PR
PR	17-SEP-1998; 98WO-US019437.	01-JUN-2001; 2001WO-US017800.	PR
PR	07-OCT-1998; 98WO-US021141.	05-JUN-2001; 2001US-00874503.	PR
PR	29-OCT-1998; 98WO-US022992.	14-JUN-2001; 2001US-00882636.	PR
PR	29-OCT-1998; 98WO-US022992.	19-JUN-2001; 2001US-00886342.	PR
PR	20-NOV-1998; 98WO-US024855.	20-JUN-2001; 2001WO-US019692.	PR
PR	01-DEC-1998; 98WO-US025108.	21-JUN-2001; 2001US-00887879.	PR
PR	05-JAN-1999; 99WO-US000106.	22-JUN-2001; 2001WO-US020116.	PR
PR	08-MAR-1999; 99WO-US005028.	29-JUN-2001; 2001WO-US021066.	PR
PR	10-MAR-1999; 99WO-US005190.	09-JUL-2001; 2001WO-US021735.	PR
PR	20-APR-1999; 99WO-US008615.	18-JUL-2001; 2001US-00908827.	PR
PR	14-MAY-1999; 99WO-US010733.	06-AUG-2001; 2001US-00924419.	PR
PR	02-JUN-1999; 99WO-US012252.	09-AUG-2001; 2001US-00927796.	PR
PR	01-SEP-1999; 99WO-US020111.	16-AUG-2001; 2001US-00931836.	PR
PR	08-SEP-1999; 99WO-US020594.	19-DEC-2001; 2001US-00028072.	XX
PR	13-SEP-1999; 99WO-US020944.	(GETH) GENENTECH INC.	PA
PR	15-SEP-1999; 99WO-US021090.	Baker KP, Beresini M, Deforge L, Desnoyers L, Filvaroff E, Gao W;	XX
PR	15-SEP-1999; 99WO-US021547.	Gerritsen ME, Goddard A, Godowski PJ, Gurney AL, Sherwood S;	PI
PR	05-OCT-1999; 99WO-US023089.	Smith V, Stewart TA, Tumas D, Watanabe CK, Wood WI, Zhang Z;	PI
PR	29-NOV-1999; 99WO-US028214.	WPI; 2003-584997/55.	XX
PR	30-NOV-1999; 99WO-US028313.	N-PSDB; ADA45710.	DR
PR	30-NOV-1999; 99WO-US028409.	Novel secreted and transmembrane polypeptide for modulating biological	XX
PR	01-DEC-1999; 99WO-US028301.	activity of cell expressing the polypeptide, identifying agonists or	PT
PR	01-DEC-1999; 99WO-US028301.	antagonists of polypeptide, and as molecular weight markers.	PT
PR	02-DEC-1999; 99WO-US028634.	Claim 12; Fig 192; 659pp; English.	XX
PR	02-DEC-1999; 99WO-US028551.	The invention describes 305 nucleic acids encoding PRO (secreted and	PS
PR	02-DEC-1999; 99WO-US028564.	transmembrane) polypeptides (I). (I) is useful for stimulating the	CC
PR	02-DEC-1999; 99WO-US028565.	release of TNF-alpha from human blood, for modulating the uptake of	CC
PR	16-DEC-1999; 99WO-US030095.	glucose or FFA by skeletal muscle cells or adipocyte cells, for	CC
PR	20-DEC-1999; 99WO-US030911.	stimulating the proliferation or differentiation of chondrocyte cells,	CC
PR	20-DEC-1999; 99WO-US030939.	for stimulating the proliferation of or gene expression in paricyte	CC
PR	22-DEC-1999; 99WO-US030720.	cells, for stimulating the release of proteoglycans from cartilage, for	CC
PR	30-DEC-1999; 99WO-US031243.		
PR	30-DEC-1999; 99WO-US031274.		
PR	05-JAN-2000; 2000WO-US000219.		
PR	06-JAN-2000; 2000WO-US000277.		
PR	06-JAN-2000; 2000WO-US000376.		
PR	11-FEB-2000; 2000WO-US000356.		
PR	18-FEB-2000; 2000WO-US004341.		
PR	18-FEB-2000; 2000WO-US004342.		
PR	22-FEB-2000; 2000WO-US004414.		
PR	24-FEB-2000; 2000WO-US004914.		

stimulating the proliferation of inner ear utricular supporting cells, for stimulating the proliferation of T-lymphocyte cells, for stimulating the release of a cytokine from BMC cells, for inhibiting the binding of A-peptide to factor VIIA, for inhibiting the differentiation of adipocyte cells, for stimulating proliferation of endothelial cells, for detecting the presence of tumour in a mammal. The tumour is lung, colon, breast, prostate, rectal, cervical or liver tumour. The oligonucleotide probes are useful for isolating genomic and cDNA nucleotide sequences or antisense probes. (I) is also useful as therapeutic agent. PRO is useful in assays to identify other proteins or molecules involved in binding interaction. A polynucleotide (II) encoding (I) is useful in chromosome and gene mapping, in generation of antisense RNA and DNA, in the preparation of PRO polypeptide, for generating transgenic animals or knockout animals which in turn are useful in the development and screening of therapeutically useful reagents, in gene therapy, for chromosome identification, as chromosome marker, and for generating probes. An anti-(I)-antibody is useful in diagnostic assays for PRO, e.g. detecting its expression in specific cells, tissues or serum, and for affinity purification of PRO from recombinant cell culture or natural sources. (I) and (II) are useful for tissue typing. This is the amino acid sequence of a novel human secreted and transmembrane PRO polypeptide.

SQ Sequence 513 AA;

Alignment Scores:

Pred. No.: 6-23e-285 Length: 513
Score: 2752.00 Matches: 512
Percent Similarity: 99.81% Conservative: 0
Best Local Similarity: 99.81% Mismatches: 1
Query Match: 93.92% Indels: 0
DB: Gaps: 0

US-10-729-807-28 (1-1627) x ADA45711 (1-513)

QY 24 ATGACGGCTCTGCTTCTGTGTTGTTCTTTTATACATTTTCTTCTGCAATTCCTTA 83
DB 1 MetLysArgLeuLeuLeuPheLeuPhePheIleThrPheSerSerAlaPheProLeu 20
QY 84 GTCCGGATGACGGAATGAGAAATATGCACTGCTGCTGAGCATATCTCAACGATTC 143
DB 21 ValArgMetThrGluAsnGluGluAsnMetGlnLeuAlaGlnAlaThrLeuAsnGlnPhe 40
QY 144 TACTCTCTTGAATGAGGGGAATCATCTTGTTCCTCAAGCAAGAAATAGGAGTCTCATAGAT 203
DB 41 TyrSerLeuGluIleGluGlyAsnHisLeuValGlnSerLysAsnArgSerLeuIleAsp 60
QY 204 GACAAATTCGGAAATGCAAGCATTTTGTGATTGACAGTCACTGGAATACTGCACTCA 263
DB 61 AspLysIleArgGluMetGlnAlaPhePheGlyLeuThrValThrGlyLysLeuAspSer 80
QY 264 AACACCTTGAGTATGAGACACCCAGGTGTGGGTGCTGATGTGGCCAGTATGGC 323
DB 81 AsnThrLeuGluIleMetLysThrProArgCysGlyValProAspValGlyGlnTyrGly 100
QY 324 TACACCTCCCTGGTGGGAGAAATACAACTCACCTACAGATTAATAAATATCTCCG 383
DB 101 TyrThrLeuProGlyTyrPheArgLysThrAsnLeuThrTyrArgIleAsnTyrThrPro 120
QY 384 GATATGGCAGCGTCTGTGATGAGGCTATCCCAAGAGGTTTGAAGTGTGGAGCAAA 443
DB 121 AspMetAlaArgAlaAlaValAspGluAlaGlnGluGlyLeuGluValTrpSerLys 140
QY 444 GTCATCTCACTAAATTCACAGATTTCAAGGGGATTCAGACATCATGATGCTTT 503
DB 141 ValThrProLeuLysPheThrLysIleSerLysGlyIleAlaAspIleMetIleAlaPhe 160
QY 504 AGGACTCCAGTCCATGTCGGTCTCTCGCTATTTTGTGTCCTTGGAGTGTGGC 563
DB 161 ArgThrArgValHisGlyArgCysProArgTyrPheAspGlyProLeuGlyValLeuGly 180
QY 564 CATGCTTTCCTCGTGGTCCGGTCTGGGTGTGACACTCATTTTGTGAGGATGAAAC 623

DB 181 HisAlaPheProGlyProGlyLeuGlyGlyAspThrHisPheAspGluAspGluAsn 200
QY 624 TGGACCAAGATGGAGCAGATTCAACTTCTTCTTGTGCTGCTCATGATTTGGTCAT 683
DB 201 TrpThrLysAspGlyAlaGlyPheAsnLeuPheValAlaHisGluPheGlyHis 220
QY 684 GCACTGGGCTCTCTCACTCAATGATCAACAGCCTTGATGTCCTCCAAATATGCTCC 743
DB 221 AlaLeuGlyLeuSerHisSerAsnAspGlnThrAlaLeuMetPheProAsnTyrValSer 240
QY 744 CTGGATCCCAAGAAATACCCACATTTCTCAGGATGATATCAATGAAATCCAGTCCATCTAT 803
DB 241 LeuAspProArgLysTyrProLeuSerGlnAspAspIleasnGlyIleGlnSerIleTyr 260
QY 804 GGAGTCTGCTAAGGTACTCTGCTAAGCCAAAGAAACCCACTATATCCCATGCTCTGTGAC 863
DB 261 GlyGlyLeuProLysValProAlaLysProLysGluProThrIleProHisAlaCysAsp 280
QY 864 CTTGACTTTCAGCTTTCAGCTATCACAATTTCCGAGAGAGTAATGTTCTTTAAGGC 923
DB 281 ProAspLeuThrPheAspAlaIleThrThrPheArgArgGluValMetPhePheLysGly 300
QY 924 AGGCACCTATGAGGATCTATTATGATATCAGCATGTTGAGTTTCAATTAATTTGCTTCA 983
DB 301 ArgHisLeuTrpArgIleTyrTyrAspIleThrAspValGluPheGluLeuIleAlaSer 320
QY 984 TTCTGCCCATCTCTGCCAGCTGATTCGAAGCTGCATACAGAACCCCGAGATAAGATT 1043
DB 321 PheTrpProSerLeuProAlaAspLeuGlnAlaAlaTyrGluAsnProArgAspLysIle 340
QY 1044 CTGGTTTTAAAGATGAAACTTCTGGATGATCAGAGGATATGCTCTCTGTCAGATTAT 1103
DB 341 LeuValPheLysAspGluAsnPheTrpMetIleArgGlyTyrAlaValLeuProAspTyr 360
QY 1104 CCCAAATCCATCATACATTAGTCTTCCAGACAGTGTCAAGAAATAGATGACGCGTC 1163
DB 361 ProLysSerIleHisThrLeuGlyPheProGlyArgValLysLysIleAspAlaVal 380
QY 1164 TGTGATAGACACCAAGAAAACCTTACTTCTTGTGGGATTTGGTGTGGAGTTTGAT 1223
DB 381 CysAspLysThrThrArgLysThrTyrPhePheValGlyIleTrpCysTrpArgPheAsp 400
QY 1224 GAAATGACCCCAACCATGACAAAGATTCGCCGAGAGAGTGTAAACACTTTCTCTGGA 1283
DB 401 GluMetThrGlnThrMetAspLysGlyPheProGlnArgValValLysHisPheProGly 420
QY 1284 ATCAGTATCCGTGTGATGCTCTTCCAGTACAAAGGATTTCTCTTTTTCAGCCGTGGA 1343
DB 421 IleSerIleArgValAspAlaAlaPheGlnTyrLysGlyPhePhePheSerArgGly 440
QY 1344 TCAAGCAATTTGAATACAACTTAAGCAAGATATTACCGAATATCCGAATCATGAGAACTAAT 1403
DB 441 SerLysGlnPheGluTyrAsnIleLysThrLysAsnIleThrArgIleMetArgThrAsn 460
QY 1404 ACTTGTTTCAATGCAAGAACCAAGACTCCTCATTTGGTTTGGATATCAACAGGAA 1463
DB 461 ThrTrpPheGlnCysLysGluProLysAsnSerSerPheGlyPheAspIleAsnLysGlu 480
QY 1464 AAAGCACATTCAGGAGGATAAAGATATTGTATCATAGAGTTTAAGCTTTGTTTATTTT 1523
DB 481 LysAlaHisSerGlyIleLysIleLeuTyrHisLysSerLeuSerLeuPheIlePhe 500
QY 1524 GGTATTGTTTCAATTCCTGAAACCACTTCTATTATCAAA 1562
DB 501 GlyIleValHisLeuLeuLysAsnThrSerIleTyrGln 513
RESULT 13
ADA76142
ID ADA76142 standard; protein; 513 AA.
XX
AC ADA76142;
XX
DT 20-NOV-2003 (first entry)

XX	Human PRO polypeptide #96.	PR	02-MAR-2000; 2000WO-US005746.
DE		PR	02-MAR-2000; 2000WO-US005841.
XX		PR	10-MAR-2000; 2000WO-US006319.
KW	Human; PRO; secreted polypeptide; transmembrane polypeptide;	PR	15-MAR-2000; 2000WO-US006884.
KW	tumour necrosis factor-alpha; TNF-alpha; chondrocyte cell; tumour;	PR	20-MAR-2000; 2000WO-US007377.
KW	cancer; adrenal; lung; colon; breast; prostate; rectum; kidney; cervix;	PR	21-MAR-2000; 2000WO-US007532.
KW	liver; microvascular endothelial cell; glucose; FFA;	PR	30-MAR-2000; 2000WO-US008439.
KW	skeletal muscle cell; adipocyte cell; pericyte cell;	PR	17-MAY-2000; 2000WO-US013705.
KW	inner ear utricular supporting cell; T-lymphocyte cell;	PR	22-MAY-2000; 2000WO-US014042.
KW	endothelial cell tube formation; bone disorder; cartilage disorder;	PR	30-MAY-2000; 2000WO-US014941.
KW	sports injury; proteoglycan; articular cartilage defect; osteoarthritis;	PR	02-JUN-2000; 2000WO-US015264.
KW	rheumatoid arthritis; haemoglobin-associated disorder thalassaemia;	PR	28-JUL-2000; 2000WO-US020710.
KW	immune system cell infiltration.	PR	11-AUG-2000; 2000WO-US022031.
XX		PR	23-AUG-2000; 2000WO-US023522.
OS	Homo sapiens.	PR	24-AUG-2000; 2000WO-US023328.
XX		PR	08-NOV-2000; 2000WO-US030952.
PN		PR	10-NOV-2000; 2000WO-US030873.
XX		PR	01-DEC-2000; 2000WO-US032678.
XX		PR	20-DEC-2000; 2000US-0074259.
PD		PR	20-DEC-2000; 2000WO-US034956.
XX		PR	28-FEB-2001; 2001US-00796498.
PF		PR	01-MAR-2001; 2001WO-US006520.
XX		PR	01-MAR-2001; 2001WO-US006666.
PR		PR	09-MAR-2001; 2001US-00802706.
PR		PR	14-MAR-2001; 2001US-00808689.
PR		PR	22-MAR-2001; 2001US-00816744.
PR		PR	05-APR-2001; 2001US-00828366.
PR		PR	10-MAY-2001; 2001US-00854208.
PR		PR	10-MAY-2001; 2001US-00854208.
PR		PR	18-MAY-2001; 2001US-00860216.
PR		PR	25-MAY-2001; 2001US-00866034.
PR		PR	25-MAY-2001; 2001US-00866028.
PR		PR	01-JUN-2001; 2001WO-US017092.
PR		PR	01-JUN-2001; 2001US-00872035.
PR		PR	01-JUN-2001; 2001WO-US017800.
PR		PR	05-JUN-2001; 2001US-00874503.
PR		PR	14-JUN-2001; 2001US-00882636.
PR		PR	19-JUN-2001; 2001US-00886342.
PR		PR	20-JUN-2001; 2001WO-US019692.
PR		PR	21-JUN-2001; 2001US-00887879.
PR		PR	22-JUN-2001; 2001WO-US020116.
PR		PR	29-JUN-2001; 2001WO-US021066.
PR		PR	09-JUL-2001; 2001WO-US021735.
PR		PR	18-JUL-2001; 2001US-00908827.
PR		PR	06-AUG-2001; 2001US-00924419.
PR		PR	09-AUG-2001; 2001US-00927796.
PR		PR	16-AUG-2001; 2001US-00931836.
PR		PR	19-DEC-2001; 2001US-00028072.
XX			(GETH) GENENTECH INC.
XX		PI	Baker KP, Beresini M, DeForge L, Desnoyers L, Filvaroff E, Gao W;
PI		PI	Gerritsen ME, Goddard A, Godowski PJ, Gurney AL, Sherwood S;
PI		PI	Smith V, Stewart TA, Tumas D, Watanabe CK, Wood WI, Zhang Z;
XX			WPI; 2003-687639/65.
DR			N-PSDB; ADA76141.
XX			New isolated nucleic acid encoding a secreted and transmembrane
PT			polypeptide, designated e.g. PRO114 or PRO4978, useful in chromosome and
PT			gene mapping, in generating antisense RNA and DNA, and in gene therapy.
XX			Claim 12; Fig 192; 659pp; English.
PS			The invention relates to isolated human PRO polypeptides (secreted and
XX			transmembrane polypeptides) and the polynucleotides encoding them. The
CC			invention also relates to an antibody which specifically binds to a PRO
CC			polypeptide, a method for stimulating the release of tumour necrosis
CC			factor-alpha (TNF-alpha) from human blood, a method for stimulating the
CC			proliferation or differentiation of chondrocyte cells and a method for
CC			detecting the presence of a tumour in a mammal (e.g. adrenal, lung,
CC			colon, breast, prostate, rectal, kidney, cervical and liver tumours). The
CC			polynucleotides are useful in molecular biology, including uses as

hybridisation probes, in chromosome and gene mapping, in generating antisense RNA and DNA and in gene therapy. The polynucleotides may also be used in preparing PRO polypeptides by recombinant techniques and in generating either transgenic animals or knock-out animals which are useful in the development and screening of therapeutically useful reagents. The PRO polypeptides or antibodies are used in preparing a medicament for treating a condition responsive to the polypeptides or antibodies, such as tumours, for stimulating and inhibiting proliferation of human microvascular endothelial cells, for modulating the uptake of glucose or FFA by skeletal muscle cells, for adipocyte cells, for stimulating differentiation of adipocyte cells, for modulating the uptake of the proliferation of or gene expression in pericyte cells, for stimulating cells, for inducing endometrial cell tube formation and for treating various bone and/or cartilage disorders such as sports injuries and arthritis. PRO polypeptides which stimulate the release of proteoglycans from cartilage are useful for treating sports-related joint problems, articular cartilage defects, osteoarthritis and rheumatoid arthritis. PRO polypeptides are also useful for treating various mammalian haemoglobin-associated disorders such as various thalassaemias and conditions which may benefit from enhanced local immune system cell infiltration. This sequence represents a human PRO polypeptide of the invention. Note: The sequence data for this patent is also available in electronic format from USPTO at seqdata.uspto.gov/sequence.html.

SQ Sequence 513 AA;

Alignment Scores:
 Pred. No.: 6,23e-285 Length: 513
 Score: 2752.00 Matches: 512
 Percent Similarity: 99.81% Conservative: 0
 Best Local Similarity: 99.81% Mismatches: 1
 Query Match: 93.92% Indels: 0
 DB: Gaps: 0

US-10-729-807-28 (1-1627) x ADA76142 (1-513)

QY	24	ATGAAGCGCTCTGCTTCTGTTGTTTCTTTTATACATTTTCTTCTGCTATTCCTTGA	83
Db	1	MetLysArgLeuLeuLeuPheLeuPhePheLeuPhePheLeuPhePheLeuPheProLeu	20
QY	84	GTCGCGATACGGAATGAGAAATATGCACTGGCTCAGGCATATCTCAACCAATTC	143
Db	21	ValArgMetThrGluAsnGluGluAsnMetGlnLeuAlaGlnAlaTyrLeuAsnGlnPhe	40
QY	144	TACTCTCTTGAATAGAGGGAATCATCTGTTTCAAGCAAGAATAGGAGTCTCATAGAT	203
Db	41	TyrSerLeuGluIleGluGlyAsnHisLeuValGlnSerLysAsnArgSerLeuIleAsp	60
QY	204	GACAAATTCGGGAATGCAAGCATTTTGTGGATTGACAGTGAAGTGAAGTGAAGTGA	263
Db	61	AspLysIleArgGluMetGlnAlaPhePheGlyLeuThrValThrGlyLysLeuAspSer	80
QY	264	AACACCTTGAGTCATGAGACACCCAGGTGTGGGTGCTGATGTGGGCGAGTATGGC	323
Db	81	AsnThrLeuGluIleMetLysThrProArgCysGlyValProAspValGlyGlnTyrGly	100
QY	324	TACACCTCTCCCTGGGTGGGAAATATACAACTTTCAGTGAAGTGAAGTGAAGTGAAG	383
Db	101	TyrThrLeuProGlyTyrArgLysThrAsnLeuThrTyrArgIleIleAsnTyrThrPro	120
QY	384	GATATGGACGAGCTGCTGTGGATGAGGCTATCCAGAGAGTGTAGAGTGGAGCAAA	443
Db	121	AspMetAlaArgAlaAlaValAspGluAlaIleGlnGluGlyLeuGluValTyrSerLys	140
QY	444	GTCACCTCCACTAAATTCACCAAGATTCACAGGGGATTCAGACATCATGATTCCTTC	503
Db	141	ValThrProLeuLysPheThrLysIleSerLysGlyIleAlaAspIleMetIleAlaPhe	160
QY	504	AGGACTCGAGTCATGCTGGGTGCTCTGCTATTTTGTATGTCCTTGGAGTGTGGC	563
Db	161	ArgThrArgValHisGlyArgCysProArgTyrPheAspGlyProLeuGlyValLeuGly	180

QY	564	CATGCTTCTCTCTGCTCGGCTCGGCTCGGCTCGGCTCGGCTCGGCTCGGCTCGGCTCGG	623
Db	181	HisAlaPheProProGlyProGlyLeuGlyGlyAspThrHisPheAspGluAspGluAsn	200
QY	624	TGACCAAGGATGGAGCAGGATTCAACTTGTTTCTTGCTGCTGCTGCTGCTGCTGCTGCTG	683
Db	201	TyrThrLysAspGlyAlaGlyPheAsnLeuPheLeuValAlaAlaHisGluPheGlyHis	220
QY	684	GCACTGGGCTCTCTCACTCAATGATCAACAGCCTTGATGTTCCCAAAATATATGCTTCC	743
Db	221	AlaLeuGlyLeuSerHisSerAsnAspGlnThrAlaLeuMetPheProAsnTyrValSer	240
QY	744	CTGATCCCAAGAAATACCCACTTCTCAGATGATATCAATGGAATCCAGTCCATCTAT	803
Db	241	LeuAspProArgLysTyrProLeuSerGlnAspIleAsnGlyIleGlnSerIleTyr	260
QY	804	GGAGGTCTGCTTAAGGTACCTGCTTAAGCCAAAGCAACCCACTATACCCCTGCTGNGAC	863
Db	261	GlyGlyLeuProLysValProAlaLysProLysGluProThrIleProHisAlaCysAsp	280
QY	864	CTGACTTGACTTTCAGCTATCACAACTTTCGACAGAGAGTAATGTTCTTTAAAGGC	923
Db	281	ProAspLeuThrPheAspAlaIleThrThrPheArgArgGluValMetPhePheLysGly	300
QY	924	AGGCACCTATGAGGATCTATATGATATCAACGATGTTGAGTTCGATTAATTCGTTCA	983
Db	301	ArgHisLeuThrArgIleTyrAspIleThrAspValGluPheGluLeuIleAlaSer	320
QY	984	TTCTGCCCATCTCTGCCAGCTGATCTGCAAGCTGCAATACAGAACCCACAGATAAGATT	1043
Db	321	PheTyrProSerLeuProAlaAspLeuGlnAlaAlaTyrGluAsnProArgAspLysIle	340
QY	1044	CTGGTTTTTAAGATGAAACTTCTGGATGATCAGAGGATATGCTGCTTCCAGATATAT	1103
Db	341	LeuValPheLysAspGluAsnPheTrpMetIleArgGlyTyrAlaValLeuProAspTyr	360
QY	1104	CCCAATTCATCCATACATAGTGTTCAGGACGTCGTGAGAAATAGATGAGCGGTC	1163
Db	361	ProLysSerIleHisThrLeuGlyPheProGlyArgValLysLysIleAspAlaVal	380
QY	1164	TGTGTAAGACACCAAGAAAAACCTACTTCTTGTGGGCTTGTGGTGGAGGTTTGTAT	1223
Db	381	CysAspLysThrThrArgLysThrTyrPhePheValGlyIleTyrCysIrrargPheAsp	400
QY	1224	GAAATGACCCAAACCATGGACAAAGATTCGCCGAGAGAGTGTAAACACATTTCTCTGA	1283
Db	401	GluMetThrGlnThrMetAspLysGlyPheProGlnArgValValLysHisPheProGly	420
QY	1284	ATCAGTATCCGTTGATGCTGCTTCCAGTACAAAGGATTCCTCTTTTTCAGCGTGA	1343
Db	421	IleSerIleArgValAspAlaAlaPheGlnTyrLysGlyPhePhePheSerArgGly	440
QY	1344	TCAAGCAATTTGAATACAACTTAAGACAAAGAAATATTACCCGAATCATGAGAATAAT	1403
Db	441	SerLysGlnPheGluTyrAsnIleLysThrLysAsnIleThrArgIleMetArgThrAsn	460
QY	1404	ACTTGGTTTCAATGCAAGAACCAAGAACTCTCATTTGGTTTGTATATCAACAAGAA	1463
Db	461	ThrTrpPheGlnCysLysGluProLysAsnSerSerPheGlyPheAspIleAsnLysGlu	480
QY	1464	AAAGCACATTCAGGAGGATTAAGATATTGTATCATAGAGTTTAAGCTTGTATTTTT	1523
Db	481	LysAlaHisSerGlyGlyIleLysIleLeuTyrHisLysSerLeuSerLeuPheIlePhe	500
QY	1524	GATATTGTTTCAATTTGCTGAAAAACACTTCTTATTTATCAA	1562
Db	501	GlyIleValHisLeuLeuLysAsnThrSerIleTyrGln	513

RESULT 14
 ADA18792
 ID ADA18792 standard; protein; 513 AA.
 XX
 AC ADA18792;

XX DT 20-NOV-2003 (first entry)
XX DE Human PRO polypeptide #96.
XX KW Human; PRO; secreted polypeptide; transmembrane polypeptide;
KW tumour necrosis factor-alpha; TNF-alpha; blood; chondrocyte cell; lung;
KW colon; breast; prostate; rectum; cervix; liver; tumour; cancer;
KW glucose uptake; FFA; adipocyte cell; pericyte cell; proteoglycan;
KW cartilage; inner ear utricular supporting cell; cytokine; A-peptide;
KW factor VIIA; endothelial cell.
XX OS Homo sapiens.
XX PN US2003054517-A1.
XX PD 20-MAR-2003.
XX PF 08-MAY-2002; 2002US-00141755.
XX PR 31-MAR-1997; 97WO-US005230.
PR 12-JUN-1998; 98WO-US012456.
PR 14-JUL-1998; 98WO-US014552.
PR 28-AUG-1998; 98WO-US017888.
PR 10-SEP-1998; 98WO-US018824.
PR 14-SEP-1998; 98WO-US019093.
PR 14-SEP-1998; 98WO-US019094.
PR 14-SEP-1998; 98WO-US019177.
PR 16-SEP-1998; 98WO-US019330.
PR 17-SEP-1998; 98WO-US019437.
PR 07-OCT-1998; 98WO-US021141.
PR 29-OCT-1998; 98WO-US022991.
PR 29-OCT-1998; 98WO-US022992.
PR 20-NOV-1998; 98WO-US024855.
PR 01-DEC-1998; 98WO-US025108.
PR 05-JAN-1999; 98WO-US000106.
PR 08-MAR-1999; 98WO-US005028.
PR 10-MAR-1999; 98WO-US005190.
PR 20-APR-1999; 98WO-US008615.
PR 14-MAY-1999; 98WO-US010733.
PR 02-JUN-1999; 98WO-US012252.
PR 01-SEP-1999; 98WO-US020111.
PR 08-SEP-1999; 98WO-US020594.
PR 13-SEP-1999; 98WO-US020944.
PR 15-SEP-1999; 98WO-US021090.
PR 15-SEP-1999; 98WO-US021547.
PR 05-OCT-1999; 98WO-US023089.
PR 29-NOV-1999; 98WO-US028214.
PR 30-NOV-1999; 98WO-US028313.
PR 30-NOV-1999; 98WO-US028409.
PR 01-DEC-1999; 98WO-US028301.
PR 01-DEC-1999; 98WO-US028634.
PR 02-DEC-1999; 98WO-US028551.
PR 02-DEC-1999; 98WO-US028564.
PR 02-DEC-1999; 98WO-US028565.
PR 16-DEC-1999; 98WO-US030095.
PR 20-DEC-1999; 98WO-US030911.
PR 20-DEC-1999; 98WO-US030999.
PR 22-DEC-1999; 98WO-US030720.
PR 30-DEC-1999; 98WO-US031243.
PR 30-DEC-1999; 98WO-US031274.
PR 05-JAN-2000; 2000WO-US000219.
PR 06-JAN-2000; 2000WO-US000277.
PR 06-JAN-2000; 2000WO-US000376.
PR 11-FEB-2000; 2000WO-US003565.
PR 18-FEB-2000; 2000WO-US004341.
PR 18-FEB-2000; 2000WO-US004342.
PR 22-FEB-2000; 2000WO-US004414.
PR 24-FEB-2000; 2000WO-US004914.
PR 24-FEB-2000; 2000WO-US005004.
PR 01-MAR-2000; 2000WO-US005601.
PR 02-MAR-2000; 2000WO-US005746.
PR 02-MAR-2000; 2000WO-US005841.
PR 10-MAR-2000; 2000WO-US006319.
PR 15-MAR-2000; 2000WO-US006884.
PR 20-MAR-2000; 2000WO-US007377.
PR 21-MAR-2000; 2000WO-US007532.
PR 30-MAR-2000; 2000WO-US008439.
PR 17-MAY-2000; 2000WO-US013705.
PR 22-MAY-2000; 2000WO-US014042.
PR 30-MAY-2000; 2000WO-US014941.
PR 02-JUN-2000; 2000WO-US015264.
PR 28-JUL-2000; 2000WO-US020710.
PR 11-AUG-2000; 2000WO-US022031.
PR 23-AUG-2000; 2000WO-US023522.
PR 24-AUG-2000; 2000WO-US023328.
PR 08-NOV-2000; 2000WO-US030952.
PR 10-NOV-2000; 2000WO-US030873.
PR 01-DEC-2000; 2000WO-US032878.
PR 20-DEC-2000; 2000US-00747259.
PR 20-DEC-2000; 2000WO-US034956.
PR 28-FEB-2001; 2001US-00796498.
PR 28-FEB-2001; 2001WO-US006520.
PR 01-MAR-2001; 2001WO-US006666.
PR 09-MAR-2001; 2001US-00802706.
PR 14-MAR-2001; 2001US-00808689.
PR 22-MAR-2001; 2001US-00816744.
PR 05-APR-2001; 2001US-00828366.
PR 10-MAY-2001; 2001US-00854208.
PR 10-MAY-2001; 2001US-00854280.
PR 18-MAY-2001; 2001US-00860216.
PR 25-MAY-2001; 2001US-00866028.
PR 25-MAY-2001; 2001US-00866034.
PR 25-MAY-2001; 2001WO-US017092.
PR 01-JUN-2001; 2001US-00872035.
PR 01-JUN-2001; 2001WO-US017800.
PR 05-JUN-2001; 2001US-00874503.
PR 14-JUN-2001; 2001US-00882636.
PR 19-JUN-2001; 2001US-00886342.
PR 20-JUN-2001; 2001WO-US019692.
PR 21-JUN-2001; 2001US-00887879.
PR 22-JUN-2001; 2001WO-US020116.
PR 29-JUN-2001; 2001WO-US021066.
PR 09-JUL-2001; 2001WO-US021735.
PR 18-JUL-2001; 2001US-00908827.
PR 06-AUG-2001; 2001US-00924419.
PR 16-AUG-2001; 2001US-00927796.
PR 19-DEC-2001; 2001US-00931836.
PR 19-DEC-2001; 2001US-00028072.
XX (GETH) GENENTECH INC.
XX Baker KP, Beresini M, Deforge L, Desnoyers L, Filvaroff E, Gao W;
PI Gerritsen ME, Goddard A, Godowski PJ, Gurney AL, Sherwood S;
PI Smith V, Stewart TA, Tumas D, Watanabe CK, Wood WI, Zhang Z;
XX WPI; 2003-521854/49.
XX N-PSDB; ADA18791.
XX New PRO nucleic acid, useful for preparing a composition for treating
XX e.g., tumors.
XX Claim 12; Fig 192; 660pp; English.
XX The invention relates to isolated human PRO polypeptides (secreted and
CC transmembrane polypeptides) and the polynucleotides encoding them. The
CC invention also relates to an antibody which specifically binds to a PRO
CC polypeptide, a method for stimulating the release of tumour necrosis
CC factor-alpha (TNF-alpha) from human blood, a method for stimulating the
CC proliferation or differentiation of chondrocyte cells and a method for
CC detecting the presence of a tumour in a mammal (e.g. lung, colon, breast,
CC prostate, rectal, cervical and liver tumours). The polynucleotides are
CC useful in molecular biology, including uses as hybridisation probes, in
CC chromosome and gene mapping, in generating antisense RNA and DNA and in
CC gene therapy. The polynucleotides may also be used in preparing PRO
CC polypeptides by recombinant techniques and in generating either

transgenic animals or knock-out animals which are useful in the development and screening of therapeutically useful reagents. The PRO polypeptides or antibodies are used in preparing a medicament for treating a condition responsive to the polypeptides or antibodies, such as tumours, for modulating the uptake of glucose or FFA by adipocyte cells, for stimulating the proliferation of or gene expression in pericyte cells, for stimulating the release of proteoglycans from cartilage, for stimulating the proliferation of inner ear utricular supporting cells, for stimulating the release of cytokines from PBMC cells, for inhibiting the binding of A-peptide to factor VIIA, for inhibiting the differentiation of adipocyte cells and for stimulating the proliferation of endothelial cells. This sequence represents a human PRO polypeptide of the invention. Note: The sequence data for this patent is also available in electronic format from USPTO at seqdata.uspto.gov/sequence.html.

XX Sequence 513 AA;

Alignment Scores:

Pred. No.: 6,23e-285 Length: 513
Score: 2752.00 Matches: 512
Percent Similarity: 99.81% Conservatives: 0
Best Local Similarity: 99.81% Mismatches: 1
Query Match: 93.92% Indels: 0
DB: Gaps: 0

US-10-729-807-28 (1-1627) x ADA18792 (1-513)

QY 24 ATGAAGGGCTTCGCTTCGCTGTTCTTTATTAACATTTCTCTGCAATTCCTTA 83
DB 1 MetLysArguLeuLeuLeuPheLeuPhePheLeuThrPheSerSerAlaPheProLeu 20
QY 84 GTCGGCATGACGGAATAAGAGAAATATGCACTGCTCAGGCATATCTCACCGATTC 143
DB 21 ValArgMetThrGluAsnGluGluAsnMetGlnLeuAlaGlnAlaTyrLeuAsnGlnPhe 40
QY 144 TACTCTTTCAATAGAGGGATATCTTTGTTCAAGCAAGAAATAGGAGTCTCATAGAT 203
DB 41 TyrSerLeuGluileGluGlyAsnHisLeuValGlnSerLysAsnArgSerLeuileAsp 60
QY 204 GACAAATTCGGGAATGCAAGCATTTTGTGATTCACAGTGCAGAACTGGACTCA 263
DB 61 AspLysIleArgGluMetGlnAlaPhePheGlyLeuThrValThrGlyLysLeuAspSer 80
QY 264 AACACCTTGAGATCATGAAGACACCGAGTGGGGTCCCTGATGTCGGCCAGATGCG 323
DB 81 AsnThrLeuGluileMetLysThrProArgCysGlyValProAspValGlyGlnTyrGly 100
QY 324 TACCCCTCCCTGGGTGGAGAAATACAACTCACCCTACAGATAATAAATATCTCCG 383
DB 101 TyrThrLeuProGlyTyrArgLysTyrAsnLeuThrTyrArgIleleAsnTyrThrPro 120
QY 384 GATATGGACGAGCTGCTGTGATGAGGTATCCAAAGAGGTTTGAAGTGGAGCAAA 443
DB 121 AspMetAlaArgAlaAlaValAspGluAlaIleGlnGluGlyLeuGluValTyrSerLys 140
QY 444 GTCACCTCCACTAAATTCACCAAGATTTCAAAGGGGATTCACACATCATGATTCGCTTT 503
DB 141 ValThrProleuLysPheThrLysIleSerLysGlyIleAlaAspIleMetIleAlaPhe 160
QY 504 AGGACTCGAGTCCATGGTGGTGTCTCGCTATTTTGTAGTGGTCCCTTGGGAGTGTGGC 563
DB 161 ArgThrArgValHisGlyArgCysProArgTyrPheAspGlyProLeuGlyValLeuGly 180
QY 564 CATGCTTTCTCTGGTCCGGGTCTGGGTGGTGTGACACTCATTTGATGAGGATGAAAC 623
DB 181 HisAlaPheProGlyProGlyLeuGlyGlyAspThrHisPheAspGluAspGluAsn 200
QY 624 TGGACCAAGGATGGACGAGATTCACTTGTGTTCTTGTGGTGGTCTCATGATTTGGTCA 683
DB 201 TrpThrLysAspGlyAlaGlyPheAsnLeuPheValAlaAlaHisGluPheGlyHis 220
QY 684 GCACTGGGGCTCTCTCACTCCAATGATCAACAGCGCTTGATGTTCCCAATATGTCCTC 743

DB 221 AlaLeuGlyLeuSerHisSerAsnAspGlnThrAlaLeuMetPheProAsnTyrValSer 240
QY 744 CTGGATCCCAAAAAATACCCACATTTCTCAGGATGATATCAATGAATCCAGTCCATCAT 803
DB 241 LeuAspProArgLysTyrProLeuSerGlnAspAspIleAsnGlyIleGlnSerIleTyr 260
QY 804 GAGGCTCTGCTTAAGTACTCTGCTAAGCCAAAGCAAGCCACTATACCCCATGCTGTGAC 863
DB 261 GlyGlyLeuProLysValProAlaLysProLysGluProThrIleProHisAlaCysAsp 280
QY 864 CTTGACTTCTGCTTTCAGCGTATCAACAATTTCCGAGAGAGTAAATGTTCTTAAAGGC 923
DB 281 ProAspLeuThrPheAspAlaIleThrPheArgArgGluValMetPhePheLysGly 300
QY 924 AGGCACCTATGGAGGATCTATTATGATATCACGGATGTTGAGTTTGAATTAATTTGTTCA 983
DB 301 ArgHisLeuTrpArgIleTyrTyrAspIleThrAspValGluPheGluLeuIleAlaSer 320
QY 984 TTCTGGCCATCTCTGCCAGTGTATCTGCAAGCTGCATACAGAACCCCGAGATTAAGATT 1043
DB 321 PheTrpProSerLeuProAlaAspLeuGlnAlaAlaTyrGluAsnProArgAspLysIle 340
QY 1044 CTGGTTTTTAAAGATCAAAAATCTTCTGGATGATCAGAGGATATGCTGCTTCCAGATTAT 1103
DB 341 LeuValPheLysAspGluAsnPheTrpMetIleArgGlyTyrAlaValLeuProAspTyr 360
QY 1104 CCCAAATCCATCATACATTAGGTTTTCCAGGACGTGTGAAGAAAATAGATGCAGCGTC 1163
DB 361 ProLysSerIleHisThrLeuGlyPheProGlyArgValLysLysIleAspAlaAlaVal 380
QY 1164 TGTGATAAGACCAACAGAAAACCTACTTCTTTGCGGATTTGCTGCTGGAGTTTGAT 1223
DB 381 CysAspLysThrThrArgLysThrTyrPhePheValGlyIleTrpCysTrpArgPheAsp 400
QY 1224 GAAATGACCCAAACCAATGACAAAGATTCCCGCAGAGAGTGTGTAACACACTTTCTCTGGA 1283
DB 401 GluMetThrGlnThrMetAspLysGlyPheProGlnArgValLysHisPheProGly 420
QY 1284 ATCAGTATCCGTTGATGCTGCTTTCAGTACAAAGGATTTCTTTTTCAGCCCTGGA 1343
DB 421 IleSerIleArgValAspAlaAlaPheGlnTyrLysGlyPhePhePheSerArgGly 440
QY 1344 TCAAGCAATTTGAATACAACTTAAGCAAAAGATATATCCCGAATCATAGAACTAAT 1403
DB 441 SerLysGlnPheGluTyrAsnIleLysThrLysAsnIleThrArgIleMetArgThrAsn 460
QY 1404 ACTTGTTTCAATGCAAGAACCAAGAACTCTCATTTGTTGTTGATATCAACAGGAA 1463
DB 461 ThrTrpPheGlnCysLysGluProLysAsnSerSerPheGlyPheAspIleAsnLysGlu 480
QY 1464 AAAGCACATTCAGGAGGCATAAGATATTGTATCATCAAGAGTTTAAGCTTGTATTATTTT 1523
DB 481 LysAlaHisSerGlyGlyIleLysIleLeuTyrHisLysSerLeuSerLeuPheIlePhe 500
QY 1524 GGTATGTTTCATTTCTGTAAGAAACACTTCTATTATCA 1562
DB 501 GlyIleValHisLeuLeuLysAsnThrSerIleTyrGln 513
RESULT 15
ADA61415
ID ADA61415 standard; protein; 513 AA.
XX
AC ADA61415;
XX
DT 20-NOV-2003 (first entry)
XX
DE Homo sapiens.
XX
KW Human; secreted and transmembrane protein; PRO;
KW Tumour necrosis factor alpha release; TNF-alpha release;
KW glucose uptake modulator; FFA uptake modulator;
KW cell proliferation stimulator; cell differentiation stimulator;

KW cell differentiation inhibitor; cytokine release stimulator; tumour;
KW lung tumour; colon tumour; breast tumour; prostate tumour; rectal tumour;
KW cervical tumour; liver tumour; chromosome mapping; gene mapping;
KW gene therapy; chromosome identification; chromosome marker.
XX
OS Novel.
OS human.
OS secreted.
OS and.
OS transmembrane.
OS protein.
OS PRO5992.
XX
PN US2003049816-A1.
XX
PD
XX
XX
XX
PF 15-APR-2002; 2002US-00123262.
XX
PR 31-MAR-1997; 97WO-US005230.
PR 12-JUN-1998; 98WO-US012456.
PR 14-JUL-1998; 98WO-US014552.
PR 28-AUG-1998; 98WO-US017888.
PR 10-SEP-1998; 98WO-US018824.
PR 14-SEP-1998; 98WO-US019093.
PR 14-SEP-1998; 98WO-US019094.
PR 14-SEP-1998; 98WO-US019177.
PR 16-SEP-1998; 98WO-US019330.
PR 17-SEP-1998; 98WO-US019437.
PR 07-OCT-1998; 98WO-US021141.
PR 29-OCT-1998; 98WO-US022991.
PR 29-OCT-1998; 98WO-US022992.
PR 20-NOV-1998; 98WO-US024855.
PR 01-DEC-1998; 98WO-US025108.
PR 05-JAN-1999; 98WO-US000106.
PR 08-MAR-1999; 98WO-US005028.
PR 10-MAR-1999; 98WO-US005190.
PR 20-APR-1999; 98WO-US008615.
PR 14-MAY-1999; 98WO-US010733.
PR 02-JUN-1999; 98WO-US012252.
PR 01-SEP-1999; 98WO-US020111.
PR 08-SEP-1999; 98WO-US020594.
PR 13-SEP-1999; 98WO-US020944.
PR 15-SEP-1999; 98WO-US021090.
PR 15-SEP-1999; 98WO-US021547.
PR 05-OCT-1999; 98WO-US023089.
PR 29-NOV-1999; 98WO-US028214.
PR 30-NOV-1999; 98WO-US028313.
PR 30-NOV-1999; 98WO-US028409.
PR 01-DEC-1999; 98WO-US028301.
PR 01-DEC-1999; 98WO-US028634.
PR 02-DEC-1999; 98WO-US028551.
PR 02-DEC-1999; 98WO-US028554.
PR 02-DEC-1999; 98WO-US028565.
PR 16-DEC-1999; 98WO-US030095.
PR 20-DEC-1999; 98WO-US030911.
PR 20-DEC-1999; 98WO-US030999.
PR 22-DEC-1999; 98WO-US030720.
PR 30-DEC-1999; 98WO-US031243.
PR 30-DEC-1999; 98WO-US031274.
PR 05-JAN-2000; 2000WO-US000219.
PR 06-JAN-2000; 2000WO-US000277.
PR 11-FEB-2000; 2000WO-US000376.
PR 18-FEB-2000; 2000WO-US004341.
PR 18-FEB-2000; 2000WO-US004342.
PR 22-FEB-2000; 2000WO-US004414.
PR 24-FEB-2000; 2000WO-US004914.
PR 24-FEB-2000; 2000WO-US005004.
PR 01-MAR-2000; 2000WO-US005601.
PR 02-MAR-2000; 2000WO-US005746.
PR 02-MAR-2000; 2000WO-US005841.
PR 10-MAR-2000; 2000WO-US006319.
PR 15-MAR-2000; 2000WO-US006884.
PR 20-MAR-2000; 2000WO-US007377.
PR 21-MAR-2000; 2000WO-US007532.
PR 30-MAR-2000; 2000WO-US008439.
PR 17-MAY-2000; 2000WO-US013705.
PR 22-MAY-2000; 2000WO-US014042.
PR 30-MAY-2000; 2000WO-US014941.
PR 02-JUN-2000; 2000WO-US015264.
PR 28-JUL-2000; 2000WO-US020710.
PR 11-AUG-2000; 2000WO-US022031.
PR 23-AUG-2000; 2000WO-US023522.
PR 24-AUG-2000; 2000WO-US023328.
PR 08-NOV-2000; 2000WO-US030952.
PR 10-NOV-2000; 2000WO-US030873.
PR 01-DEC-2000; 2000WO-US032678.
PR 20-DEC-2000; 2000US-00747259.
PR 20-DEC-2000; 2000WO-US034956.
PR 28-FEB-2001; 2001US-00796498.
PR 28-FEB-2001; 2001WO-US006520.
PR 01-MAR-2001; 2001WO-US006666.
PR 09-MAR-2001; 2001US-00802706.
PR 14-MAR-2001; 2001US-00808689.
PR 22-MAR-2001; 2001US-00816744.
PR 05-APR-2001; 2001US-00828366.
PR 10-MAY-2001; 2001US-00854208.
PR 10-MAY-2001; 2001US-00854280.
PR 18-MAY-2001; 2001US-00860216.
PR 25-MAY-2001; 2001US-00866028.
PR 25-MAY-2001; 2001US-00866034.
PR 01-JUN-2001; 2001US-00872035.
PR 01-JUN-2001; 2001WO-US017800.
PR 05-JUN-2001; 2001US-00874503.
PR 14-JUN-2001; 2001US-00882636.
PR 19-JUN-2001; 2001US-00886342.
PR 21-JUN-2001; 2001US-00887879.
PR 22-JUN-2001; 2001WO-US020116.
PR 29-JUN-2001; 2001WO-US021066.
PR 09-JUL-2001; 2001WO-US021735.
PR 18-JUL-2001; 2001US-00908827.
PR 06-AUG-2001; 2001US-00924419.
PR 09-AUG-2001; 2001US-00927796.
PR 16-AUG-2001; 2001US-00931836.
PR 19-DEC-2001; 2001US-00028072.
XX
XX (GETH) GENENTECH INC.
XX
XX Baker KP, Beresini M, Deforge L, Desnoyers L, Filvaroff E, Gao W;
PI Gerritsen ME, Goddard A, Godowski PJ, Gurney AL, Sherwood S;
PI Smith V, Stewart TA, Tumas D, Watanabe CK, Wood WI, Zhang Z;
XX
XX WPI; 2003-695892/66.
DR N-PSDB; ADA61414.
DR
XX
PT New PRO nucleic acid and encode polypeptides, are useful for
PT manufacturing a medicament for diagnosing or treating cancer.
XX
XX Claim 12; Fig 192; 660pp; English.
XX
CC The invention describes 305 nucleic acids encoding PRO (secreted and
CC transmembrane) polypeptides (I). (I) is useful for stimulating the
CC release of TNF-alpha from human blood, for modulating the uptake of
CC glucose or FFA by skeletal muscle cells or adipocyte cells, for
CC stimulating the proliferation or differentiation of chondrocyte cells,
CC for stimulating the proliferation of or gene expression in pericyte
CC cells, for stimulating the release of proteoglycans from cartilage, for
CC stimulating the proliferation of inner ear lymphocyte supporting cells,
CC for stimulating the proliferation of T-lymphocyte cells, for stimulating
CC the release of a cytokine from PMBC cells, for inhibiting the binding of
CC A-peptide to factor VIIA, for inhibiting the differentiation of adipocyte
CC cells, for stimulating proliferation of endothelial cells, for detecting
CC the presence of tumour in a mammal. The tumour is lung, colon, breast,

CC prostate, rectal, cervical or liver tumour. The oligonucleotide probes
 CC are useful for isolating genomic and cDNA nucleotide sequences or
 CC antisense probes. (I) is also useful as therapeutic agent. PRO is useful
 CC in assays to identify other proteins or molecules involved in binding
 CC interaction. A polynucleotide (II) encoding (I) is useful in chromosome
 CC and gene mapping, in generation of antisense RNA and DNA, in the
 CC preparation of PRO polypeptide, for generating transgenic animals or
 CC knockout animals which in turn are useful in the development and
 CC screening of therapeutically useful reagents, in gene therapy, for
 CC chromosome identification, as chromosome marker, and for generating
 CC probes. An anti-(I)-antibody is useful in diagnostic assays for PRO, e.g.
 CC detecting its expression in specific cells, tissues or serum, and for
 CC affinity purification of PRO from recombinant cell culture or natural
 CC sources. (I) and (II) are useful for tissue typing. This is the amino
 CC acid sequence of a novel human secreted and transmembrane PRO
 CC polypeptide.

XX
 SQ Sequence 513 AA;

Alignment Scores:
 Pred. No.: 6.23e-285 Length: 513
 Score: 2752.00 Matches: 512
 Percent Similarity: 99.81% Conservative: 0
 Best Local Similarity: 99.81% Mismatches: 1
 Query Match: 93.92% Indels: 0
 DB: 6 Gaps: 0

US-10-729-807-28 (1-1627) x ADA61415 (1-513)

QY 24 ATGAAGCGCTTCGCTCTGTTGTTTCTTATACATTTCTTCGCAATTCCTTCA 83
 DB 1 MetLysArgLeuLeuLeuPhePhePhePhePhePhePhePhePhePhePhePhe 20
 QY 84 GTCGCGATGACGGAATGAAGAATATGCACTGCTCAGCATATCTCAACAGTTC 143
 DB 21 ValArgMetThrGluAsnGluGluAsnMetGlnLeuAlaGlnAlaTyrLeuAsnGlnPhe 40
 QY 144 TACTCTCTTGAAATAGAGGAATCATCTTGTTCAGAGCAAGAAATAGGAGTCTCATAGAT 203
 DB 41 TyrSerLeuGluLeuGluGluGluGluGluGluGluGluGluGluGluGluGluGlu 60
 QY 204 GACAAATTCGGGAATGCAAGCAATTTTGGATTGACAGTGTGGAAGAACTGGACTCA 263
 DB 61 AspLysLeuArgGluMetGlnAlaPhePheGlyLeuThrValThrGlyLysLeuAspSer 80
 QY 264 AACACCTTCGAGATCATGAGACACCCAGTGTGGGTGCTCATGTGGCCAGTATGGC 323
 DB 81 AsnThrLeuGluLeuMetLysThrProArgCysGlyValProAspValGlyGlnTyrGly 100
 QY 324 TACACCTCCCTCGGTGGAGAAATACACCTCACCTACAGATAATAAATACTACTCCG 383
 DB 101 TyrThrLeuProGlyTrpArgLysTyrAsnLeuThrTyrArgLysLeuAsnTyrThrPro 120
 QY 384 GATATGGCAGAGCTGCTGTGATAGGCTATCCAGAGAGTTTGAAGAGTTTGAAGTGGACAAA 443
 DB 121 AspMetAlaArgAlaAlaValAspGluAlaLeuGlnGluGlyLeuGluValTrpSerLys 140
 QY 444 GTCACCTCCACTAAATTCACCAAGATTTCAGAGGGATTCAGACATCATGCTGCTTT 503
 DB 141 ValThrProLeuLysPheThrLysLeuSerLysGlyLeuAlaAspMetLeuAlaPhe 160
 QY 504 AGGACTTCGAGTCCATGCTCGTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 563
 DB 161 ArgThrArgValHisGlyArgCysProArgTyrPheAspGlyProLeuGlyValLeuGly 180
 QY 564 CATGCTTCCTCTCGGTGGGTCTGGGTGGGTGGGTGGGTGGGTGGGTGGGTGGGTGGGT 623
 DB 181 HisAlaPheProGlyProGlyLeuGlyGlyAspThrHisPheAspGluAspGluAsn 200
 QY 624 TGGACCAAGAGTGGAGCAGGATTCACCTGTTCTTCTGCTGCTGCTGCTGCTGCTGCTGCT 683
 DB 201 TrpThrLysAspGlyAlaGlyPheAsnLeuPheLeuValAlaAlaHisGluPheGlyHis 220

QY 684 GCCTGGGGCTCTCTCACTCAATGATCAACAGCCTTGATGTTCCCAATATATGCTCTCC 743
 DB 221 AlaLeuGlyLeuSerHisSerAsnAspGlnThrAlaLeuMetPheProAsnTyrValSer 240
 QY 744 CTGGATCCCAAGAAATACCCACTTTCTCAGGATCATATCAATGAATCCAGTCCATCTAT 803
 DB 241 LeuAspProArgLysTyrProLeuSerGlnAspPheLeuGlnSerLeuTyr 260
 QY 804 GGAGTCTGCTAGGTACCTGTAAGCCAAAGAACCCACTATACCCCATGCTGCTGAC 863
 DB 261 GlyGlyLeuProLysValProAlaLysProLysGluProThrLeuProHisAlaCysAsp 280
 QY 864 CCTGACTTGACTTTTTCAGCTATCACAACCTTCGCGAGAGAGTAAGTCTTTAAAGGC 923
 DB 281 ProAspLeuThrPheAspAlaLeuThrThrPheArgGluValMetPhePheLysGly 300
 QY 924 AGGCACCTATGAGGATCTATTATGATATCACGGATGTTGAGTTTGAATTAATGCTTCA 983
 DB 301 ArgHisLeuTrpArgLysTyrTyrAspLeuThrAspValGluPheGluLeuLeuAlaSer 320
 QY 984 TTCTGGCCATCTCTGCGAGCTGATCTGCAAGCTGATACGAGAACCCAGAGATAAGATT 1043
 DB 321 PheTrpProSerLeuProAlaAspLeuGlnAlaLysTyrGluAsnProArgAspLysLe 340
 QY 1044 CTGTTTTTAAAGATGAAACTTCTCGATGATCAGAGGATATGCTGCTTCCAGATTAT 1103
 DB 341 LeuValPheLysAspGluAsnPheTrpMetLeuArgGlyTyrAlaValLeuProAspTyr 360
 QY 1104 CCAGAAATCCATCATATAGTGTTCAGAGCAGTGTGAGAGAAATAGATGACGCGCTC 1163
 DB 361 ProLysSerLeuHisThrLeuGlyPheProGlyArgValLysLysLeuAspAlaVal 380
 QY 1164 TGTGATAAGCACAGAAACCTACTCTTTGTGGGCAATTTGGTCTCGAGGTTTGAT 1223
 DB 381 CysAspLysThrThrArgLysThrTyrPhePheValGlyLeuTrpCysTrpArgPheAsp 400
 QY 1224 GAAATGACCCAAACCATGGACAAGGATTCCTCCAGAGAGTGTGTAACACTTTCCTGGA 1283
 DB 401 GluMetThrGlnThrMetAspLysGlyPheProGlnArgValValLysHisPheProGly 420
 QY 1284 ATCAGTATCCGTTGATGCTGCTTCCAGTACAAAGGATTCCTCTTTTTCAGCCGTGGA 1343
 DB 421 IleSerLeuArgValAspAlaAlaPheGlnTyrLysGlyPhePhePheSerArgGly 440
 QY 1344 TCAGCAATTTGAATACACATTAAGACAAAGATATTACCCGAATCATGAGAACTAAT 1403
 DB 441 SerLysGlnPheGluTyrAsnLeuThrLysAsnLeuThrArgLysMetArgThrAsn 460
 QY 1404 ACTTGTTTTCAATGCAAGAACCCAAAGAACTCTCTCATTTGTTTGTATATCAACAGGA 1463
 DB 461 ThrTrpPheGlnCysLysGluProLysAsnSerSerPheGlyPheAspLysLysGlu 480
 QY 1464 AAAGCATTCTCAGGAGGCATTAAGATATTGATCATCAAGAGTTTAAGCTTGTATTATTT 1523
 DB 481 LysAlaHisSerGlyGlyLeuLysLeuTyrHisLysSerLeuSerLeuPheLeuPhe 500
 QY 1524 GGTATTGTTTCATTGCTGAAAACACTTCTTATTATCAA 1562
 DB 501 GlyLeuValHisLeuLeuLysAsnThrSerLeuTyrGln 513

Search completed: November 15, 2004, 20:25:04
 Job time : 156 secs

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GenCore version 5.1.6
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OM nucleic - protein search, using frame_plus_n2p model

Run on: November 15, 2004, 20:03:11 ; Search time 35.5 Seconds
(without alignments)
8819.418 Million cell updates/sec

Title: US-10-729-807-28

Perfect score: 2930

Sequence: 1 gcttcagctgaagaagaga.....aattctgctcaaatagaa 1627

Scoring table:

BLOSUM62
Xgapop 10.0 , Xgapext 0.5
Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 566832

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Command line parameters:

-MODEL=frame+_n2p.model -DEV=xlh
-Q=/cgn2_1/USPTO_spool/US10729807/runat_15112004_131151_14700/app_query.fasta_1.1799
-DB=PIR_79 -QFWT=fastan -SUFFIX=rpr -MINMATCH=0.1 -LOOPEL=0 -LOOPEXT=0
-UNITS=bits -START=1 -END=-1 -MATRIX=blosum62 -TRANS=human40.cdi -LIST=45
-DOALIGN=200 -THR SCORE=pct -THR MAX=100 -THR MIN=0 -ALIGN=15 -MODE=LOCAL
-OUTFWT=ptp -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=2000000000
-USER=US10729807@cgn_1_1_43 @runat_15112004_131151_14700 -NCPU=6 -ICPU=3
-NO_MMAP -LARGQUERY -NEG SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG
-DEV TIMEOUT=120 -WARN TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database :

PIR_79.*
1: pir1.*
2: pir2.*
3: pir3.*
4: pir4.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1271.5	43.4	478	1 KCRBS1	stromelysin 1 (EC
2	1250	42.7	477	1 KCHUS1	stromelysin 1 (EC
3	1243.5	42.4	476	1 JCS505	stromelysin 2 (EC
4	1237.5	42.2	477	1 KCHSS1	stromelysin 1 (EC
5	1234	42.1	476	1 KCHUS2	stromelysin 2 (EC
6	1205	41.1	469	1 KCPGI	interstitial colla
7	1198.5	40.9	476	1 KCHUS2	stromelysin 2 (EC
8	1177.5	40.2	469	1 KCHOI	interstitial colla
9	1173.5	40.1	475	1 KCHTIH	stromelysin 1 (EC
10	1170.5	39.9	468	1 KCRBI	interstitial colla
11	1161.5	39.6	467	1 KCHUI	interstitial colla
12	1161	39.6	469	1 KCHUI	neutrophil colla
13	1141	38.9	471	2 A53711	collagenase 3 (EC
14	1133	38.7	470	2 A49499	metalloelastase HM

15	1126	38.4	466	2 A23685	interstitial colla
16	1119.5	38.2	472	2 S29243	interstitial colla
17	1020.5	34.8	462	2 A42401	macrophage elastat
18	1002.5	34.2	483	2 JCS743	matrix metalloprot
19	798	27.2	384	2 I51267	collagenase (EC 3
20	797	27.2	660	1 A28153	gelatinase A (EC 3
21	790	27.0	662	2 A42496	gelatinase A (EC 3
22	790	27.0	662	2 S34780	gelatinase A (EC 3
23	783	26.7	662	2 S70365	gelatinase A (EC 3
24	769.5	26.3	663	1 S46492	gelatinase A (EC 3
25	715.5	24.4	669	2 I38029	matrix metalloprot
26	713	24.3	582	2 I38028	matrix metalloprot
27	698	23.8	582	2 I84471	matrix metalloprot
28	667	22.8	582	2 I48673	matrix metalloprot
29	626.5	21.4	712	1 I46031	gelatinase B (EC 3
30	603.5	20.6	491	2 JG6197	stromelysin 3 (EC
31	594.5	20.3	267	1 KCHUM	matrilysin (EC 3.4
32	593	20.2	707	1 A34458	gelatinase B (EC 3
33	590	20.1	492	2 A44399	stromelysin 3 (EC
34	590	20.1	707	1 A53796	gelatinase B (EC 3
35	586	20.0	730	2 JCL456	gelatinase B (EC 3
36	585	20.0	730	1 I52580	gelatinase B (EC 3
37	577	19.7	508	2 JCS082	matrix metalloprot
38	574	19.6	488	2 S13423	stromelysin 3 (EC
39	559.5	19.1	708	2 JG4364	gelatinase B (EC 3
40	556	19.0	477	1 I51645	stromelysin 3 (EC
41	551.5	18.8	708	2 S2907	gelatinase B (EC 3
42	550.5	18.8	267	2 A57490	matrilysin (EC 3.4
43	413	14.1	579	2 T3248	probable matrix me
44	413	14.1	598	2 T32166	hypothetical prote
45	400.5	13.7	587	2 S12805	envelysin (EC 3.4

ALIGNMENTS

RESULT 1

KCRBS1

stromelysin 1 (EC 3.4.24.17) precursor - rabbit

N:Alternate names: collagenase activating protein; matrix metalloproteinase 3 (MMP3); pr

C:Species: Oryctolagus cuniculus (domestic rabbit)

C>Date: 30-Sep-1992 #sequence_revision 30-Sep-1992 #text_change 09-Jul-2004

C:Accession: A37306; A29157

R:Finl, M.E.; Karmilowicz, M.J.; Ruby, P.L.; Beeman, A.M.; Borges, K.A.; Brinckerhoff, C

A:Title: Cloning of a complementary DNA for rabbit proactivator. A metalloproteinase tha

ed with collagenase.

A:Reference number: A37306; MUID:88077214; PMID:2825726

A:Accession: A37306

A:Molecule type: mRNA

A:Residues: 1-478 <FIN>

A:Cross-references: UNIPROT:P28863; GB:M25664; NID:g165709; PIDN:AAA31467.1; PID:g165710

R:Whitham, S.E.; Murphy, G.; Angel, P.; Rahmsdorf, H.J.; Smith, B.J.; Lyons, A.; Harris,

Biochem. J. 240, 913-916, 1986

A:Title: Comparison of human stromelysin and collagenase by cloning and sequence analysi

A:Reference number: A90336; MUID:87156645; PMID:3030290

A:Accession: A29157

A>Status: nucleic acid sequence not shown; not compared with conceptual translation

A:Molecule type: mRNA

A:Residues: 1-82,'D','K',129-167,'GNS', <WHI>

C:Comment: This enzyme degrades various extracellular matrix proteins, including fibron

C:Comment: Stromelysin 1 hydrolyzes peptide bonds in plasminogen to yield a fragment wit

C:Comment: Stromelysin 1 activates its proenzyme after cleavage(s) within the activation

C:Comment: Stromelysin 1 is found in glycosylated and unglycosylated forms, both of whi

C:Function:

A:Description: endopeptidase preferentially hydrolyzing peptide bonds on the carboxyl si

C:Superfamily: interstitial collagenase; hemopexin repeat homology; matrix metalloprotei

C:Keywords: calcium; extracellular matrix; fibroblast; glycoprotein; hydrolase; metallo

F:1-17/Domain: signal sequence #status predicted <SIG>

F:18-478/Product: prostromelysin 1 #status predicted <PRO>

F:18-100/Domain: activation peptide #status predicted <ACT>

F:61-265/Domain: matrix metalloproteinase homology <MMP>

F:91-98/Region: autoinhibitory

F:101-478/Product: stromelysin 1 #status predicted <MAT>

A;Accession: A28399

F;218,222,228/Binding site: zinc, catalytic (His) (active) #status experimental
F;219/Active site: Glu #status predicted
F;290-477/Disulfide bonds: #status predicted

Alignment Scores:
Pred. No.: 9,29e-99 Length: 477
Score: 1250.00 Matches: 246
Percent Similarity: 66.04% Conservative: 71
Best Local Similarity: 51.25% Mismatches: 145
Query Match: 42.66% Indels: 18
DB: 1 Gaps: 9

US-10-729-807-28 (1-1627) x KCHUS1 (1-477)

QY	24	ATGAAGCGCCTTCTGCTCTGTGTTGGTTCTTTATAACATTTCCTTCTGCATTTCCCTTA	83
Db	1	MetLysSerLeuProIleLeuLeuLeuCysValAlaValCysSerAlaTyrProLeu	20
QY	84	GTCGGATGACGGAAATGAAGAA---AATATGCAACTGGCTCAGGCATATCTCAACCAG	140
Db	21	AspGlyAlaAlaArgGlyGluAspThrSerMetAsnLeuValGlnLysTyrLeuGluAsn	40
QY	141	TTCCTCTCTTGCAANTAGNAGGATCATCTGTTCAAAGCAAGAATAGGAGTCTCATYA	200
Db	41	TyrtTyAspLeuLysValLysGlnPheValArgLysAspSerGlyProVal	60
QY	201	GATGACAAAATTCGGAAATGCAAGCATTTTTGGATTGACGTGACGTGAMAACTGGAC	260
Db	61	ValLysIleArgGluMetGlnLysPheLeuGlyLeuGluValThrGlyLysLeuAsp	80
QY	261	TCAACACCCCTTGAGATCATGAAGACACCCAGGTGGGGTGCTGATGGGCCAGTAT	320
Db	81	SerAspThrLeuGluValMetArgLysProArgCysGlyValProAspValGlyHisPhe	100
QY	321	GGCTACACCTCCTCGG-----TGGAGAAATACAACCTCACCTACAGAAATAA	371
Db	101	---ArgThrPheProGlyIleProLysTyrArgLysThrHisLeuThrTyrArgIleVal	119
QY	372	AACATACTCCGATATGCGACAGCTGCTGTGGATGAGGTATCCAAGAAGTTTAGAA	431
Db	120	AsnTyThrProAspLeuProLysAspAlaValAspSerAlaValGlnLysAlaLeuLys	139
QY	432	GTGTGGAGCAAAAGTACTCCACTCAATAATTCACCAAGATTTCAAAGGGGATTCAGACATC	491
Db	140	ValTrpGluGluValThrProLeuThrPheSerArgLeuTyrGluGlyGluAlaAspIle	159
QY	492	ATGATTGCCCTTAGGACTCGAGTCCAGTGGTGGTGCCTCGCTAT---TTTGATGGTCCC	548
Db	160	MetIleSerPheAlaValArgGluHisGly-----AspPheTyrProPheAspGlyPro	177
QY	549	TTGGGAGTGCTGGCCATGCTTTCTCTCTGCTGGTCCGGTCTGGGTGTGACATCATTTT	608
Db	178	GlyAsnValLeuAlaHisAlaTyrAlaProGlyProGlyLysGlnAspAlaHisPhe	197
QY	609	GATGAGGATCAAAACTGGACCAAGGATGGAGCAGGATTCACACTTGTTCTTGTGGCTGCT	668
Db	198	AspAspGluGlnTrpThrLysAspThrThrGlyThrAsnLeuPheLeuValAlaAla	217
QY	669	CATGAATTTGGTCATCCACTGGGCTCTCTCACTCCAATGATCAACAGCCTTGATGTTTC	728
Db	218	HisGluIleGlyHisSerLeuGlyLeuPheHisSerAlaAsnThrGluAlaLeuMetTyr	237
QY	729	CAAAATTATGTCTCCCTG---GATCCAGAAAAATACCCACTTCTCAGATGATATCAAT	785
Db	238	ProLeuTyrHisSerLeuThrAspLeuThrArgPheArgLeuSerGlnAspIleAsn	257
QY	786	GGATCCAGTCCATCATATGGA-----GGTCTGCTCAAGGTACCTGCT	827
Db	258	GlyIleGlnSerLeuTyrGlyProProAspSerProGluThrProLeuValProThr	277
QY	828	ANG-----CCAAAGAACCCACTATACCCCATGCTGTGACCTGACTTGACTTTTGAC	881
Db	278	GluProValProGluProGlyThrProAlaAsnCysAspProAlaLeuSerPheAsp	297

```

882 GCTATCACAACTTCCGACAGAGTAATGTTCTTTAAAGCGAGGACCTATCGAGGATC 941
Db |||:||||| ||| |||:||||| ||| |||:||||| ||| |||:||||| ||| |||:|||||
298 AlavalserThrLeuArgGlyGluLeuPheLysAspArgHisPheTrpArgLys 317
QY |||:||||| ||| |||:||||| ||| |||:||||| ||| |||:||||| ||| |||:|||||
942 TATTATGATATCAGGATGTTGAGTTTGAATTAATCTCTTCATCTGGCCATCTCTGCCA 1001
Db |||:||||| ||| |||:||||| ||| |||:||||| ||| |||:||||| ||| |||:|||||
318 SerLeuArgLysLeuGluProGluLeuHisLeuLeuSerSerPheTrpProSerLeuPro 337
QY |||:||||| ||| |||:||||| ||| |||:||||| ||| |||:||||| ||| |||:|||||
1002 GCTGATCTGCAAGTCGATACGAG--AACCCGAGAGTAAGATTCGGTTTAAAGAT 1058
Db |||:||||| ||| |||:||||| ||| |||:||||| ||| |||:||||| ||| |||:|||||
338 SerGlyValAspAlaAlaTrpGluValThrSerLysAspLeuValPheLeuPheLysGly 357
QY |||:||||| ||| |||:||||| ||| |||:||||| ||| |||:||||| ||| |||:|||||
1059 GAAACCTCTGGATGATCAGAGGATATGCTGCTTGGCCGATATATCCCAATCCATCCAT 1118
Db |||:||||| ||| |||:||||| ||| |||:||||| ||| |||:||||| ||| |||:|||||
358 AsnGlnPheTrpAlaLeuArgGlyAsnGluValArgAlaGlyTrpProArgGlyLeuHis 377
QY |||:||||| ||| |||:||||| ||| |||:||||| ||| |||:||||| ||| |||:|||||
1119 ACATTAGTCTTCCAGGACGCTGTGAAGAAATAGATCAGCGCTCTGTGATAAGACCA 1178
Db |||:||||| ||| |||:||||| ||| |||:||||| ||| |||:||||| ||| |||:|||||
378 ThrLeuGlyPheProThrValArgLysLeuAspAlaLeuSerAspLysGluLys 397
QY |||:||||| ||| |||:||||| ||| |||:||||| ||| |||:||||| ||| |||:|||||
1179 AGAAAACTTACTTCTTGTGGGCAATTTGGTGGAGGTTGATGAATGACCCAAACC 1238
Db |||:||||| ||| |||:||||| ||| |||:||||| ||| |||:||||| ||| |||:|||||
398 AsnLysThrTrpPheValGluAspLysTrpArgPheAspGluLysArgAsnSer 417
QY |||:||||| ||| |||:||||| ||| |||:||||| ||| |||:||||| ||| |||:|||||
1239 ATGCAGAAAGATCCCGCAGAGAGTGTAAACACTTCTCGCAATCAGTATCCCGTGT 1298
Db |||:||||| ||| |||:||||| ||| |||:||||| ||| |||:||||| ||| |||:|||||
418 MetGluProGlyPheProLysGlnLeuAlaGluAspPheProGlyLeuAspSerLysLe 437
QY |||:||||| ||| |||:||||| ||| |||:||||| ||| |||:||||| ||| |||:|||||
1299 GATGCTCTTCCAGTCAAAAGGATCTCTTCTTTCAGCGCTGATCAAAAGCAATTTGAA 1358
Db |||:||||| ||| |||:||||| ||| |||:||||| ||| |||:||||| ||| |||:|||||
438 AspAlaValPheGluGluPheGlyPhePheTrpPhePheThrGlySerSerGlnLeuGlu 457
QY |||:||||| ||| |||:||||| ||| |||:||||| ||| |||:||||| ||| |||:|||||
1359 TACAACATTAAGACAAAGATATTACCCGAAATCATGAGAACTAATCTGGTTTCAATGC 1418
Db |||:||||| ||| |||:||||| ||| |||:||||| ||| |||:||||| ||| |||:|||||
458 PheAspProAsnAlaLysLysValThrHisThrLeuLysSerAsnSerTrpLeuAsnCys 477

RESULT 3
JC6505
stromelysin 2 (EC 3.4.24.22) precursor - mouse
N;Alternate names: matrix metalloproteinase 10
C;Species: Mus musculus (house mouse)
C;Date: 16-Oct-1998 #sequence_revision 16-Oct-1998 #text_change 09-Jul-2004
C;Accession: JC6505
R;Madlener, M.; Werner, S.
Gene 202, 75-81, 1997
A;Title: cDNA cloning and expression of the gene encoding murine stromelysin-2 (MMP-10).
A;Reference number: JC6505; MUID:98087420; PMID:9427548
A;Molecule type: mRNA
A;Residues: 1-476 <MAD>
A;Cross-references: UNIPROT:O55123; GB:Y13185; NID:g2791311; PID:G27913
C;Comment: This enzyme degrades various extracellular matrix proteins, including fibronectin.
C;Genetics:
A;Superfamily: interstitial collagenase; hemopexin repeat homology; matrix metalloproteinase;
C;Keywords: calcium; extracellular matrix; fibroblast; glycoprotein; hydrolase; metalloproteinase;
F;1-17/Domain: signal sequence #status predicted <SIG>
F;18-476/Domain: prostromelysin 2 #status predicted <PRO>
F;120-222/Domain: activation peptide #status predicted <ACT>
F;60-264/Domain: matrix metalloproteinase homology <MMP>
F;90-97/Region: autoinhibitory
F;100-476/Domain: stromelysin 2 #status predicted <MAT>
F;283-476/Domain: hemopexin repeat homology <PXN>
F;92,218,222,228/Binding site: zinc, catalytic (Cys, His, His) (inhibited) #status predicted
F;120/Binding site: carboxylate (Asn) (covalent) #status predicted
F;218,222,228/Binding site: zinc, catalytic (His) (active) #status predicted
F;219/Active site: Glu #status predicted
F;289-476/Disulfide bonds: #status predicted

Alignment Scores:
Pred. No.: 3,35e-98 Length: 476
Score: 1243.50 Matches: 244

```

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Percent Similarity: 66.88% Conservative: 77
Best Local Similarity: 50.83% Mismatches: 140
Query Match: 42.44% Indels: 19
DB: 1 Gaps: 9

US-10-729-807-28 (1-1627) x JC6505 (1-476)

QY 24 ATGAGGCGCTTCTGCTCTGCTGCTGCTTCTTATAACATTTCTTCTGCTGCTTCCCTTA 83
Db |||:||||| ||| |||:||||| ||| |||:||||| ||| |||:||||| ||| |||:|||||
1 MetGluProLeuAlaLeuLeuAlaLeuLeuSerLeuProLeuLeuSerLeuProLeu 20
QY 84 ---GTCGGATGACGGAATAAGAAATATGCAACTGGCTCAGGCATATCTCAACAG 140
Db |||:||||| ||| |||:||||| ||| |||:||||| ||| |||:||||| ||| |||:|||||
21 HisGlyAlaValThrGlnGlyHisProSerMetAspLeuAlaGlnGlnTrpLeuGluLys 40
QY 141 TTCTACTCTCTTGAATAGAGGAAATCATCTGTTTCAAGCAAGTAAGAGTCTCAT 200
Db |||:||||| ||| |||:||||| ||| |||:||||| ||| |||:||||| ||| |||:|||||
41 TyrTrpAsnPheLysLysAsnGluLysGlnLeuPheLysArgLysAspSerProVal 60
QY 201 GATGACAAAATTCGGAAATGCAAGCATTTTGGATTGACAGTGAAGTGAAGAACTGAC 260
Db |||:||||| ||| |||:||||| ||| |||:||||| ||| |||:||||| ||| |||:|||||
61 ValLysLysLeuGlnMetGlnLysPheLeuGlyLeuGluMetThrGlyLysLeuAsp 80
QY 261 TCAACACACCTTCAGATCATGAAGACACACCCAGGTGTGGGTGCTGATGTGGGCCAGTAT 320
Db |||:||||| ||| |||:||||| ||| |||:||||| ||| |||:||||| ||| |||:|||||
81 SerAsnThrMetGluLeuMetHisLysProArgCysGlyValProAspValGlyGlyPhe 100
QY 321 GGCTACACCTCTCCCTGGG-----TGAGAAATACAACTCACCCTACCTACAGATAATA 371
Db |||:||||| ||| |||:||||| ||| |||:||||| ||| |||:||||| ||| |||:|||||
101 Ser---ThrPheProGlySerProLysTrpArgLysSerHisLeuThrTrpArgLeuVal 119
QY 372 AACTATCTCTCCGATATGGCAGCAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 431
Db |||:||||| ||| |||:||||| ||| |||:||||| ||| |||:||||| ||| |||:|||||
120 AsnTrpThrProAspLeuProArgGlnSerValAspSerAlaLeuGluLysAlaLeuLys 139
QY 432 GTGTGGAGCAGCAAGTCACTCCACTCAAAATTCACCAAGATTTCAAAGGGGATTTGAGACATC 491
Db |||:||||| ||| |||:||||| ||| |||:||||| ||| |||:||||| ||| |||:|||||
140 ValTrpGluGluValThrProLeuThrPheSerArgLysSerGluGlyGluAlaAspLe 159
QY 492 ATGATTCCTTTAGGACTCGAGTCCATGTCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 548
Db |||:||||| ||| |||:||||| ||| |||:||||| ||| |||:||||| ||| |||:|||||
160 MetIleSerPheAlaValGlyGluHisGly-----AspPheTrpProPheAspGlyPro 177
QY 549 TTGGAGTGTCTCGCCATGCTTTCCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 608
Db |||:||||| ||| |||:||||| ||| |||:||||| ||| |||:||||| ||| |||:|||||
178 GlyClnSerLeuAlaHisAlaTrpProGlyProGlyPheTrpGlyAspValHisPhe 197
QY 609 GATGAGGATGAAACCTGGACCAAGGATTCAGAGGATTCACCTTGTCTTGTGGCTGCT 668
Db |||:||||| ||| |||:||||| ||| |||:||||| ||| |||:||||| ||| |||:|||||
198 AspAspAspGluLysTrpThrLeuAlaProSerGlyThrAsnLeuPheLeuValAlaAla 217
QY 669 CATGAATTTGCTATGACACTGGGCTCTCTCACTCCCAATGATCAACAGCCTTGATGCTTC 728
Db |||:||||| ||| |||:||||| ||| |||:||||| ||| |||:||||| ||| |||:|||||
218 HisGluLeuGlyHisSerLeuGlyLeuPheHisSerAspLysLysGluSerLeuMetTrp 237
QY 729 CCAAAATTTAT---GTCCTCCCTGGATCCAGAAATACCCACTTCTCAGGATGATATCAAT 785
Db |||:||||| ||| |||:||||| ||| |||:||||| ||| |||:||||| ||| |||:|||||
238 ProValTrpArgPheSerThrSerProAlaAsnPheHisLeuSerGlnAspPheGlu 257
QY 786 GGAATCCAGTCCATCTATGGAGGT-----CTGCCCTAAGTA 821
Db |||:||||| ||| |||:||||| ||| |||:||||| ||| |||:||||| ||| |||:|||||
258 GlyLeuGlnSerLeuTrpGlyAlaGlyProSerSerAspAlaThrValValProValLeu 277
QY 822 CTGCTTAAGCAAGAACCCATATACCCATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 881
Db |||:||||| ||| |||:||||| ||| |||:||||| ||| |||:||||| ||| |||:|||||
278 SerValSerProArg---ProGluThrProAspLysCysAspProAlaLeuSerPheAsp 296
QY 882 GCTATCACAACTTCCGACAGAGTAATGTTCTTAAAGCGAGGACCTATCGAGGATC 941
Db |||:||||| ||| |||:||||| ||| |||:||||| ||| |||:||||| ||| |||:|||||
297 SerValSerThrLeuArgGlyGluValLeuPhePheLysAspArgTrpPheTrpArgArg 316
QY 942 TATTATGATATCAGGATGTTGAGTTTGAATTAATCTCTTCATCTGGCCATCTCTGCCA 1001
Db |||:||||| ||| |||:||||| ||| |||:||||| ||| |||:||||| ||| |||:|||||

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Db 256 ValAspGlyIleGlnSerLeuTyrGlyThrProThrAlaSerProAspValLeuValVal 275
 QY 822 CTGTGTAAGCAAG-----GAACCCATPATACCCAGCCCTGTGACCCCTGACTTGAAT 875
 Db 276 ProThrLysSerAsnSerLeuGluProGluThrSerProMetCysSerSerThrLeuPhe 295
 QY 876 TTTGACGCTATCAACTTCCGACAGAGAGTAACTTCTTTAAAGCAGCAGCCTATGG 935
 Db 296 PheAspAlaValSerThrLeuArgGlyGluValLeuPhePheLysAspArgHisPheTrp 315
 QY 936 AGGATCTATTATGATATACAGGATGTGAGTTGAATTAATGCTTCAATCTGCGCATCT 995
 Db 316 ArgLysSerLeuArgThrProGluProGluPheThrLeuLeuSerSerPheTrpProSer 335
 QY 996 CTCGCCAGCTGATCTGCAAGTGTGATACGAG-----AAOCCCCAGAGATAAGATTCTGGTTTT 1052
 Db 336 LeuProSerAsnMetAspAlaIleTyrGluValThrAsnArgAspThrValPheIlePhe 355
 QY 1053 AAGAGTCAAAACTTCTGGATGATCAGAGGATATGCTCTTGGCCAGATTATCCCAATCC 1112
 Db 356 LysGlyAsnGlnPheTrpAlaIleArgGlyHisGluLeuLeuAlaGlyTyrProLysSer 375
 QY 1113 ATCATATACATTAGCTTTTCCAGGACGCTGCAAGAAATAGATGACGCGCTCTGTGATAAG 1172
 Db 376 IleHisThrLeuGlyLeuProAlaThrValLysLysIleAspAlaIleSerAsnLys 395
 QY 1173 ACCACAGAAAACTTCTTTGTTGGGCAATTTGTTGGCTGGAGGTTTGATGAAATGACC 1232
 Db 396 GluLysArgLysThrTyrPhePheValGluAspLysTyrTrpArgPheAspGluLysLys 415
 QY 1233 CAACCATGACAAAGGATTCGCGCAGAGAGTGTAAACACTTTCCTGCGAATCAGTATC 1292
 Db 416 GlnSerMetGluProGlyPheProArgLysIleAlaGluAspPheProGlyValAspSer 435
 QY 1293 CGTGTTCATGCTGTTTCCAGTCAAAAGGATTTCTTTTTCAGCCGTGGATCAAAAGCAA 1352
 Db 436 ArgValAspAlaValPheGluAlaPheGlyPheLeuTyrPhePheSerGlySerSerGln 455
 QY 1353 TTTGATATCAACATTAAAGACAGATATATACCGAATCATGAGAACTAATATCTGTTTT 1412
 Db 456 LeuGluPheAspProAsnAlaLysLysValThrHisIleLeuLysSerAsnSerTrpPhe 475
 QY 1413 CAATGC 1418
 Db 476 AsnCys 477

RESULT 5
 KCHUS2
 stromelysin 2 (EC 3.4.24.22) precursor [validated] - human
 N;Alternate names: matrix metalloproteinase 10 (MMP10); transin-2
 C;Species: Homo sapiens (man)
 C;Date: 30-Sep-1992 #sequence_revision 30-Sep-1992 #text_change 09-Jul-2004
 C;Accession: A28816; A47496
 R;Muller, D.; Quantin, B.; Gesnel, M.C.; Millon-Collard, R.; Abecassis, J.; Breathnach, Biochem. J. 253, 187-192, 1988
 A;Title: The collagenase gene family in humans consists of at least four members.
 A;Reference number: A90339; MUID:88339885; PMID:2844164
 A;Accession: A28816
 A;Molecule type: mRNA
 A;Residues: 1-476 <MUL>
 A;Cross-references: UNIPROT:P09238; EMBL:X07820; NID:G36628; PIDN:CAA30679.1; PID:G36629
 A;Note: mRNA for this protein was detected in several human tumors
 R;Windsor, L.J.; Grenett, H.; Birkedal-Hansen, B.; Borden, M.K.; Engler, J.A.; Birkedal-J. Biol. Chem. 268, 17341-17347, 1993
 A;Title: Cell type-specific regulation of SL-1 and SL-2 genes. Induction of the SL-2 gene
 A;Reference number: A47496; MUID:93352520; PMID:8349617
 A;Accession: A47496
 A;Molecule type: protein
 A;Residues: 17-33 <WIN>
 C;Comment: This enzyme degrades various extracellular matrix proteins, including fibronectin
 A;Gene: GDB:MMP10; STMY2
 A;Cross-references: GDB:120392; OMIM:185260

A;Map position: 11q22.3-11q23
 C;Superfamily: interstitial collagenase; hemopexin repeat homology; matrix metalloproteinase
 F;1-16/Domain: signal sequence #status predicted <SIG>
 F;17-476/Product: stromelysin 2 #status experimental <PRO>
 F;17-98/Domain: activation peptide #status predicted <ACT>
 F;59-263/Domain: matrix metalloproteinase homology <MMP>
 F;89-96/Region: autoinhibitory
 F;99-476/Product: stromelysin 2 #status predicted <MAT>
 F;93-476/Domain: hemopexin repeat homology <PN>
 F;91,217,221,227/Binding site: zinc, catalytic (Cys, His, His, His) (inhibited) #status
 F;119/Binding site: carboxylate (Asn) (covalent) #status predicted
 F;217,221,227/Binding site: zinc, catalytic (His) (active) #status predicted
 F;218/Active site: Glu #status predicted
 F;289-476/Disulfide bonds: #status predicted

Alignment Scores: 2.18e-97 Length: 476
 Pred. No.: 1234.00 Matches: 244
 Score: 67.58% Conservative: 77
 Percent Similarity: 51.37% Mismatches: 136
 Best Local Similarity: 42.12% Indels: 18
 Query Match: 1
 DB: 8

US-10-729-807-28 (1-1627) x KCHUS2 (1-476)

QY 33 CTTCGCTCTGTTGTTGTTCTTTTAAACATTTCTTCGCAATTCCTTAGTCCGGATG 92
 Db 7 LeuValLeuLeuCysLeu-----ProValCysSerAlaTyrProLeuSerGlyAla 23
 QY 93 ACGGAAATCAAGAA--AAATATGCAACTGGCTCAGGCATATCTCAACCAAGTTCTACTCT 149
 Db 24 AlaLysGluGlnAspSerAsnLysAspLeuAlaGlnGlnTyrLeuGluLysTyrTyrAsn 43
 QY 150 CTTGAAATAGAGGGAATCATCTTGTTCAGCAAGCAATAGGAGTCTCATAGATGACAAA 209
 Db 44 LeuGluLysAspValLysGlnPhe---ArgArgLysAspSerAsnLeuLeuValLysLys 62
 QY 210 ATTGGGAAATCAAGCATTTTGGATTGACAGTGCATGCAAGTGGAACTGGACTCAACACC 269
 Db 63 IleGlnGlyMetGlnLysPheLeuGlyLeuGluValThrGlyLysLeuAspThrAspThr 82
 QY 270 CTTGAGATGATGAAGCACCCAGCTGTGGGTGCTGATGTGGCCAGATGAGTAC-- 326
 Db 83 LeuGluValMetArgLysProArgCysGlyValProAspValGlyHisPheSerSerPhe 102
 QY 327 ---ACCTCCCTGGTGGAGAAAATAACACCTCACCTACAGATAATAATACTATACCTCG 383
 Db 103 ProGlyMetProLysTrpArgLysThrHisLeuThrTyrArgIleValAsnTyrThrPro 122
 QY 384 GATATGCGCAGCAGCTGCTGTGGATGAGGCTATCCAGAGGTTTAGAGTGTGGAGCAAA 443
 Db 123 AspLeuProArgAspAlaValAspSerAlaIleGluLysAlaLeuLysValTrpGluGlu 142
 QY 444 GTCACTCCACTAAATTCACCAAGATTCAAGAGGATTCAGACATCATGATGCTCTTT 503
 Db 143 ValThrProLeuThrPheSerArgLeuTyrGluGlyGluAlaAspIleMetIleSerPhe 162
 QY 504 AGGACTCGAGTCCATGCTCGGTGCTCTGCTATTTGATGCTGCTGGAGTGTGGC 563
 Db 163 AlaValLysGluHisGlyAspPhe---TyrSerPheAspGlyProGlyHisSerLeuAla 181
 QY 564 CATGCTCTTCTCTGCTGGTCCGGCTCTGGGTGTGACACTCATTTGATGAGGATGAAC 623
 Db 182 HisAlaTyrProGlyProGlyProGlyLeuTyrGlyAspIleHisPheAspAspGluLys 201
 QY 624 TGGACCAAGGATGAGCAGGATTCACCTGCTTTCTGTGCTGCTCATGATTTGGTCAT 683
 Db 202 TrpThrGluAspAlaSerGlyThrAsnLeuPheLeuValAlaAlaHisGluLeuGlyHis 221
 QY 684 GCATGGGGCTCTCTCATCTCAATGATCAACAGCCTTGATGTCCCAATATGCTCC 743
 Db 222 SerLeuGlyLeuPheHisSerAlaAsnThrGluAlaLeuMetTyrProLeuTyrAsnSer 241

Db 184 AlaPheGlnProGlyProGlyIleGlyGlyAspAlaHisPheAspGluAspGluArgTyr 203
 QY 627 ACCAAGATGAGACAGAGATTCAACTGTTTCTTGTGGCTGCTCATGAATTTGGTCATGCA 686
 Db 204 ThrLysAsnPheArgAspTyrAsnLeuTyrArgValAlaAlaHisGluLeuGlyHisSer 223
 QY 687 CTGGGCTCTCTCACTCCATGATCAACAGCCCTGATGTTCCCAATATGCTCCCTG 746
 Db 224 LeuGlyLeuSerHisSerThrAspIleGlyAlaLeuMetTyrProAsnTyrIleTyrThr 243
 QY 747 GATCCAGAAAATACCCACTTCTCAGGATGATCAATGAATCCAGTCCATCTATGGA 806
 Db 244 Gly-----AspValGlnLeuSerGlnAspAspIleAspGlyIleGlnAlaIleTyrGly 261
 QY 807 GGTCTGCTTAAGTACTGCTTAAGCCAAAGAACCCACTATACCCANGCCTGTGACCT 866
 Db 262 Pro---SerGluAsnProValGlnProSerGlyProGlnThrProGlnValCysAspSer 280
 QY 867 GACTGACTTTTACGCTATCACAACTTCCGAGAGAGTAAATGTTCTTTAAAGGCAGG 926
 Db 281 LysLeuThrPheAspAlaIleThrThrLeuArgGlyGluLeuMetPhePheLysAspArg 300
 QY 927 CACTATGAGAGATATTATGATATCACGATGTTGAGTTGAAATTAATGCTTCATTC 986
 Db 301 PheTyrMetArgThrAsnSerPheTyrProGluValGluLeuAsnPheIleSerValPhe 320
 QY 987 TGGCCATCTCTGCCAGCTGATCTGCAAGCTGCATACGAG---AACCCAGATAGAAATT 1043
 Db 321 TrpProGlnValProAsnGlyLeuGlnAlaAlaTyrGluIleAlaAspArgAspGluVal 340
 QY 1044 CTGGTTTAAAGATGAAACTTCTGATGATCAGAGATATGCTGCTTGCAGATAT 1103
 Db 341 ArgPhePheLysGlyAsnLysTyrTrpAlaValArgGlyGlnAspValLeuTyrGlyTyr 360
 QY 1104 CCCAAATCCATCCAT---ACATTAGTGTTCACGAGCTGTGAAGAAAATAGATGACGCC 1160
 Db 361 ProllysAspIleHisArgSerPheGlyPheProSerThrValLysAsnIleAspAlaAla 380
 QY 1161 GTCTGTGATTAAGACCAAGAAAACCTACTTCTTGTGGCATTTGGTGTGAGGTTT 1220
 Db 381 ValPheGluGluAspThrGlyLysThrPhePheValAlaHisGluCysTrpArgTyr 400
 QY 1221 GATGAATACCCAAACCATGGACAAAGGATTCCTCCGACAGAGTGGTAAACACTTTCCT 1280
 Db 401 AspGluTyrLysGlnSerMetAspThrGlyTyrProllysMetIleAlaGluGluPhePro 420
 QY 1281 GGAATCAGTATCCGTGTGTGCTTTCAGTACAAAGGATTTCTTTTTCAGCCGT 1340
 Db 421 GlyIleGlyAsnLysValAspAlaValPheGlnLysAspGlyPheLeuTyrPhePheHis 440
 QY 1341 GGATCAAGCAATTTGAATACACATTAAGCAAGAAATATTATCCCGAATCATGAGAACT 1400
 Db 441 GlyThrArgGlnTyrGlnPheAspPheLysThrLysArgIleLeuThrLeuGlnLysAla 460
 QY 1401 AATACTTGGTTTCAATGCAAGAA 1424
 Db 461 AsnSerTrpPheAsnCysArgLys 468

RESULT 7

KCRTS2
 N:Alternate names: matrix metalloproteinase 10 (MMP10); transin-2
 C:Species: Rattus norvegicus (Norway rat)
 C>Date: 30-Sep-1992 #sequence revision 30-Sep-1992 #text_change 09-Jul-2004
 C:Accession: B26403; A41775; S26498
 R:Breatnach, R.; Matrisian, L.M.; Gesnel, M.C.; Staub, A.; Leroy, P.
 Nucleic Acids Res. 15, 1139-1151, 1987
 A:Title: Sequences coding for part of oncogene-induced transin are highly conserved in a
 A:Reference number: A26403; MUID:87146421; PMID:3547333
 A:Accession: B26403
 A:Molecule type: mRNA
 A:Residues: 1-476 <BRE>
 A:Cross-references: UNIPROT:P07152; EMBL:X05083; NID:g57388; PIDN:CAA28739.1; PID:g57389

A:Note: intron positions were determined by comparison of the cDNA sequence to genomic DNA
 A:Note: mRNA for this protein was expressed in several transformed rat embryo fibroblasts
 R:Chan, J.C.; Scanlon, M.; Zhang, H.Z.; Jia, L.B.; Yu, D.H.; Hung, M.C.; French, M.; Eas
 J. Biol. Chem. 267, 1099-1103, 1992
 A:Title: Molecular cloning and characterization of v-mos-activated transformation-associ
 A:Reference number: A41775; MUID:92112748; PMID:1370458
 A:Accession: A41775
 A:Molecule type: mRNA
 A:Residues: 1-476 <CHA>
 A:Cross-references: GB:M65253; NID:g207150; PIDN:AAA42202.1; PID:g207151
 A:Note: sequence extracted from NCBI backbone (NCBIP:76184)
 R:de Vouge, M.W.; Mukherjee, B.B.
 Oncogene 7, 109-119, 1992
 A:Title: Transformation of normal rat kidney cells by v-K-ras enhances expression of tra
 A:Reference number: S26496; MUID:92158347; PMID:1741158
 A:Accession: S26498
 A:Status: preliminary; translation not shown
 A:Molecule type: mRNA
 A:Residues: 31-103,'L',241-242,'TQMEBKPH',251,'L',253-254,'CE',293-294,'L',296 <DEV>
 A:Cross-references: EMBL:X64020
 C:Genetics:
 A:Introns: 35/3; 117/2; 167/1; 209/1; 264/1; 311/2; 356/1; 409/2; 444/1
 C:Superfamily: interstitial collagenase; hemopexin repeat homology; matrix metalloprote
 C:Keywords: calcium; extracellular matrix; fibroblast; glycoprotein; hydrolase; metallo
 F:1-17/Domain: signal sequence #status predicted <SIG>
 F:18-476/Product: prostomelysin 2 #status predicted <PRO>
 F:18-99/Domain: activation peptide #status predicted <ACT>
 F:60-264/Domain: matrix metalloproteinase homology <MMP>
 F:90-97/Region: autoinhibitory
 F:100-476/Product: stromelysin 2 #status predicted <MAT>
 F:283-476/Domain: hemopexin repeat homology <PXN>
 F:92,218,222,228/Binding site: zinc, catalytic (Cys, His, His) (inhibited) #status
 F:120/Binding site: carbohydrate (Asn) (covalent) #status predicted
 F:218,222,228/Binding site: zinc, catalytic (His) (active) #status predicted
 F:219/Active site: Glu #status predicted
 F:289-476/Disulfide bonds: #status predicted
 Alignment Scores:
 Pred. No.: 2,4e-94 Length: 476
 Score: 1198.50 Matches: 243
 Percent Similarity: 64.24% Conservative: 66
 Best Local Similarity: 50.52% Mismatches: 151
 Query Match: 40.90% Indels: 21
 DB: 1 Gaps: 9
 US-10-729-807-28 (1-1627) x KCRTS2 (1-476)
 QY 24 ATGAAGCGCTCTGCTCTGCTTCTTTATTAACATTTCTTCTGATTTCCCTTA 83
 Db 1 MetGluProLeuAlaIleLeuValLeuLeuCysPheProIleCysSerAlaTyrProLeu 20
 QY 84 -----GTCCGATGACGGAATAAGAAATATGCAACATGCACTGGCTCAGGCATATCTC 134
 Db 21 HisGlyAlaValArg-----GlnAspHisSerThrMetAspLeuAlaGlnGlnTyrLeu 38
 QY 135 AACCAAGTCTACTCTCTTGAATAAGAGGAATCATCTTGTTCAAAGCAAGAAATAGGAGT 194
 Db 39 GluLysTyrTyrAsnPheArgLysAsnGluLysGlnPhePheLysArgLysAspSerSer 58
 QY 195 CTCATGATGACAAAATTCGGGAAATGCAAGCATTTTTCGATTCAGTCAGTCTGGAAGA 254
 Db 59 ProValValLysLysIleGluGluMetGlnLysPheLeuGlyLeuGluMetThrGlyLys 78
 QY 255 CTGACCTCAACACCTTTCGATCATCAAGACACCCAGAGTGTGGGTGCTGATGTGGGC 314
 Db 79 LeuAspSerAsnThrValGluMetMetHisLysProArgCysGlyValProAspValGly 98
 QY 315 CAGTATGCTACACCTCCCTCTGGG-----TGGAGAAAATACAACTCACCTACAGAGA 365
 Db 99 GlyPheSer---ThrPheProGlySerProLysTrpArgLysAsnHisIleSerTyrArg 117
 QY 366 ATAATAACTATATCTCCGATATGGCAGCACTGCTGTGGATGAGGCTATCAAGAGGT 425

QY 321 GGCTACACCTCCTCTGGG-----TGAGAAATACAACTCCACCTACAGATAATA 371
 Db 101 ValLeuThr-----ProGlySerCysTrpGluAsnThrAsnLeuThrArgGlu 119
 QY 372 AACTATCTCCGATGATGCGACGAGCTGTGTGGATGAGGCTATCCAAAGAGGTGTAGAA 431
 Db 120 AsnTrpThrProAspLeuSerArgAlaAspValAspGlnAlaIleGluAsnAlaPheGln 139
 QY 432 GTGTGGAGCAAGTCACTCCACTAAATTCACCAAGATTTCAAGGGAGTTGAGACATC 491
 Db 140 LeuTrpSerAsnValThrProLeuThrPheThrLysValSerGluGlyGlnAlaAspIle 159
 QY 492 ATGATTCCTTTAGGACTCCAGTCCATGCGTGGTCTCTCGCTATTTTGTATGTCCTTCG 551
 Db 160 MetIleSerPhe---ValArgGlyAspHisArgAspAsnSerProPheAspGlyProGly 178
 QY 552 GGAAGTGTCTGGCATGCTTCTCTCTCGTCCGGGTCTGGGTGGTGGTGGTGGTGGTGGT 611
 Db 179 GlyAsnLeuAlaHisAlaPheGlnProGlyAlaGlyIleGlyGlyAspAlaHisPheAsp 198
 QY 612 GAGGATGAACCTGGACCAAGGATGGAGAGGATTCACCTGTTTCTTGTGGTGGTGGTGGT 671
 Db 199 AspAspGluTrpTrpThrSerAsnPheGlnAspTrpAsnLeuTrpArgValAlaAlaHis 218
 QY 672 GAATTTGGTATGCACCTGGGCTCTCTCACTCCAAATGATCAACAGAGCTTGATGTTCCCA 731
 Db 219 GluPheGlyHisSerLeuGlyLeuAlaHisSerThrAspIleGlyAlaLeuMetTrpPro 238
 QY 732 AATTTATGTC---TCCCTGGATCCAGAAATACCCACTTCTCAGGATGATATCAATGGA 788
 Db 239 SerTrpThrPheSerGlyAspValGln-----LeuSerGlnAspAspIleAspGly 255
 QY 789 ATCCAGTCCATCTATGAGGCTCTGCTAAGTACTCTGTAAGCAAGCAAGGACCCACTATA 848
 Db 256 IleGlnAlaIleTrpGlyPro---SerGlnAsnProThrGlnProValGlyProGlnThr 274
 QY 849 CCCATGCTGTGACCTGACTGCTTTCACCTATCACTTCCGAGAGAGTGAAGTA 908
 Db 275 ProGluValCysAspSerLysLeuThrPheAspAlaIleThrIleArgGlyGluVal 294
 QY 909 ATGTCTCTTTAAAGCCAGCCACTATGGAGGATCTATTATGATATCAGCGATGTTGAGTT 968
 Db 295 MetPhePheLysAspArgPheTrpMetArgThrAsnProLeuTrpProGluValGluLeu 314
 QY 969 GAATTAATGCTTCATCTGCGCATCTGCGACGCTGATCGAAGCTGCATAGAG--- 1025
 Db 315 AsnPheIleSerValPheTrpProGlnLeuProAsnGlyLeuGlnAlaAlaTrpGluVal 334
 QY 1026 AACCCAGAGATAAGATCTGTTTAAAGATGAAACTTCTGGATGATCAGAGGATAT 1085
 Db 335 AlaAspArgAspGluValArgPhePheLysGlyAsnLysTrpTrpAlaValLysGlyGln 354
 QY 1086 GCTGCTTGGCAGATATCCCAATCCATCCAT---ACATTAGGTTTCCAGGAGCTGTG 1142
 Db 355 AspValLeuArgGlyTrpProArgAspIleTrpArgSerPheGlyPheProArgThrVal 374
 QY 1143 AAGAAATAGATGAGCGCTGTGTATGAGACCAAGCAAGAAACCTACTCTTTGTGGGC 1202
 Db 375 LysSerIleAspAlaAlaValSerGluGluAspThrGlyLysTrpTrpPhePheValAla 394
 QY 1203 ATTTGGTCTGAGGTTTGTAGATGATGACCAACCAAGGATTCAGGAGAGAG 1262
 Db 395 AsnLysCysTrpArgTrpAspGluTrpLysGlnSerMetAspAlaGlyTrpProLysMet 414
 QY 1263 GTGGTAAACACTTCTCTGGATCAGTATCCGTGTGTATGCTGCTTCAGGTACAAAGGA 1322
 Db 415 IleAlaGluAspPheProGlyIleGlyAsnLysValAspAlaValPheGlnLysGlyGly 434
 QY 1323 TTCTCTTTTTCAGCGGTGGATCAAGCAATTTGATACACATTAAGACAAAGATATT 1382
 Db 435 PhePheTrpPhePheHisGlyArgArgGlnTrpLysPheAspProGlnThrLysArgIle 454
 QY 1383 ACCCGAATCATGAGAACTAATACTTGGTTTCAATGCAAGAA 1424

Db 455 LeuThrLeuLysAlaAsnSerTrpPheAsnCysArgLys 468
 RESULT 9
 KCRTIH
 Stromelysin 1 (EC 3.4.24.17) precursor - rat
 N;Alternate names: collagenase activating protein; matrix metalloproteinase 3 (MMP3);
 C;Species: Rattus norvegicus (Norway rat)
 C;Date: 13-Aug-1986 #sequence revision 13-Aug-1986 #text_change 09-Jul-2004
 C;Accession: A00997; PS0150; S22767
 R;Matrisian, L.M.; Glaichenhaus, N.; Gesnel, M.C.; Breathnach, R.
 EMBO J. 4, 1435-1440, 1985
 A;Title: Epidermal growth factor and oncogenes induce transcription of the same cellular
 A;Reference number: A00997; MUID:85284930; PMID:3875482
 A;Accession: A00997
 A;Molecule type: mRNA
 A;Residues: 1-475 <NAL>
 A;Cross-references: UNIPROT:P03957; GB:X02601; NID:G57460; PIDN:CA26448.1; PID:G57461
 R;Umenishi, F.; Yasumitsu, H.; Ashida, Y.; Yamauti, J.; Umeda, M.; Miyazaki, K.
 J. Biochem. 108, 537-543, 1990
 A;Title: Purification and properties of extracellular matrix-degrading metallo-proteinase
 A;Reference number: PS0150; MUID:91154156; PMID:1963430
 A;Accession: PS0150
 A;Molecule type: protein
 A;Residues: 19-20,'X',22-28;110-112,'X',114-115,'X',117,'X',119;309-325 <UME>
 R;Breathnach, R.; Matrisian, L.M.; Gesnel, M.C.; Staub, A.; Leroy, P.
 Nucleic Acids Res. 15, 1139-1151, 1987
 A;Title: Sequences coding for part of oncogene-induced transin are highly conserved in
 A;Reference number: A26403; MUID:87146421; PMID:3547333
 A;Contents: annotation; introns
 A;Note: Intron positions were determined by comparison of the previously reported cDNA
 R;Sanchez-Lopez, R.; Nicholson, R.; Gesnel, M.C.; Matrisian, L.M.; Breathnach, R.
 J. Biol. Chem. 263, 11892-11899, 1988
 A;Title: Structure-function relationships in the collagenase family member transin.
 A;Reference number: S22767; MUID:88298869; PMID:2841336
 A;Contents: annotation; active site; activation
 A;Note: molecules with mutations in the autoinhibitory region showed a much increased
 A;Note: mutations of His-216, Glu-217, and His-226 inactivate the enzyme
 R;Park, A.J.; Matrisian, L.M.; Kells, A.F.; Pearson, R.; Yuan, Z.; Navre, M.
 J. Biol. Chem. 266, 1584-1590, 1991
 A;Title: Mutational analysis of the transin (rat stromelysin) autoinhibitor region dem
 A;Reference number: A43028; MUID:91107652; PMID:1988438
 A;Contents: annotation; autoinhibitory region
 A;Note: Arg-89 and Cys-92 are essential for maintaining latency
 C;Comment: This enzyme degrades various extracellular matrix proteins, including fibrin
 C;Comment: Stromelysin 1 hydrolyzes peptide bonds in plasminogen to yield a fragment wi
 C;Comment: Stromelysin 1 activates its proenzyme after cleavage(s) within the activatio
 C;Comment: Prostromelysin is found in glycosylated and unglycosylated forms, both of wh
 C;Genetics:
 A;Introns: 33/3; 115/2; 165/1; 207/1; 262/1; 310/2; 355/1; 408/2; 443/1
 C;Function:
 A;Description: endopeptidase preferentially hydrolyzing peptide bonds on the carboxyl s
 C;Superfamily: interstitial collagenase; hemopexin repeat homology; matrix metalloprote
 C;Keywords: calcium; extracellular matrix; fibroblast; glycoprotein; hydrolase; metallo
 F;1-17/Domains: signal sequence #status predicted <SIG>
 F;18-475/Product: prostromelysin 1 #status predicted <PRO>
 F;18-97/Domains: activation peptide #status predicted <ACT>
 F;58-262/Domains: matrix metalloproteinase homology <MMP>
 F;88-95/Region: autoinhibitory
 F;98-475/Product: stromelysin 1 #status predicted <MAT>
 F;282-475/Domains: hemopexin repeat homology <PXN>
 F;90.216,220,226/Binding site: zinc, catalytic (Cys, His, His, His) (inhibited) #status
 F;118/Binding site: carboxylate (Asn) (covalent) #status predicted
 F;216,220,226/Binding site: zinc, catalytic (His) (active) #status predicted
 F;217/Active site: Glu #status experimental
 F;288-475/Disulfide bonds: #status predicted
 Alignment Scores:
 Pred. No.: 3,32e-92 Length: 475
 Score: 1173.50 Matches: 236
 Percent Similarity: 64.86% Conservative: 76
 Best Local Similarity: 49.06% Mismatches: 148
 Query Match: 40.05% Indels: 21

[illegible]

Db	335	ProSerAsnMetAspAlaAlaTyrGluValThrAsnArgAspThrValPheIleLeuLys	354
QY	1056	GATGAAACCTTCGTGATCAGAGGATATGCTCTTGGCAGATTATCCAAATCCATC	1115
Db	355	GlyAsnGlnIleTrpAlaIleArgGlyHisGluGluLeuAlaGlyTyrProLysSerIle	374
QY	1116	CATACATTAGGTTTCCAGGACGTGTCAGAAATATAGATCAGCCGCTGTGATAAGACC	1175
Db	375	HisThrLeuGlyLeuProGluThrValGlnIlyIleAspAlaIleSerLeuLysAsp	394
QY	1176	ACAAGAAAAACCTACTTCTTTGTGGGCATTGTGGTCTGGAGGTTTGATGAAATGACCCAA	1235
Db	395	GlnIlyIlyThrTyrPhePheValGluAspLysPheTrpArgPheAspGluLysLysGln	414
QY	1236	ACCATGCACAAAGATTCCCGCAGAGAGTGGTAAACACTTCTCTGGAATCATGATCCGT	1295
Db	415	SerMetAspProGluPheProArgLysIleAlaGluAsnPheProGlyIleGlyThrLys	434
QY	1296	GTTTCATGCTGCTTCCAGTACAAAGGATTCTCTTTTCAGCCGTGATCAAAAGCAATTT	1355
Db	435	ValAspAlaValPheGluAlaPheGlyPheLeuTyrPhePheSerGlySerSerGlnLeu	454
QY	1356	GAATPACAACTTAAGACAAAGATATPACCGCAATCATGAGAACTAATCTGGTTTCAA	1415
Db	455	GluPheAspProAsnAlaGlyLysValThrHisIleLeuLysSerAsnSerTrpPheAsn	474
QY	1416	TGC	1418
Db	475	Cys	475
RESULT 10			
KCRBI			
N;Alternate names: fibroblast collagenase (EC 3.4.24.7) precursor - rabbit			
C;Species: Oryctolagus cuniculus (domestic rabbit)			
C;Date: 30-Sep-1992 #sequence revision 30-Sep-1992 #text_change 09-Jul-2004			
C;Accession: A27500; B27500; I46694			
R;Finl, M.E.; Plucinska, I.M.; Mayer, A.S.; Gross, R.H.; Brinckerhoff, C.E.			
Biochemistry 26, 6156-6165, 1987			
A;Title: A gene for rabbit synovial cell collagenase: member of a family of met			
A;Reference number: A27500; MUID:88077876; PMID:2825772			
A;Accession: A27500			
A;Molecule type: mRNA			
A;Residues: 1-468 <FIN>			
A;Cross-references: UNIPROT:PI3943; GB:M19240			
A;Accession: B27500			
A;Molecule type: DNA			
A;Residues: 1-391;399-468 <FI2>			
A;Cross-references: GB:M17820			
A;Note: the location of the intron between exons 7 and 8 is approximate			
R;Finl, M.E.; Austin, S.D.; Holt, P.T.; Ruby, P.L.; Gross, R.H.; White, H.D.; B			
Coll. Relat. Res. 6, 239-248, 1986			
A;Title: Homology between exon-containing portions of rabbit genomic clones for			
A;Reference number: I46694; MUID:87029174; PMID:3021384			
A;Accession: I46694			
A;Status: translated from GB/EMBL/DBJ			
A;Molecule type: mRNA			
A;Residues: 449-468 <FI3>			
A;Cross-references: GB:M25663; NID:G531211; PIDN:AAA31203.1; PID:G531212			
C;Comment: This enzyme cleaves collagens of types I, II, and III at a Gly-Ile si			
C;Comment: Procollagenase can be activated without removal of the activation pep			
tion peptide by other proteinases.			
C;Comment: Procollagenase is found in glycosylated and unglycosylated forms, bot			
C;Genetics: 34/3; 116/2; 166/1; 208/1; 260/1; 299/2; 344/1; 398/1; 433/1			
A;Introns: 34/3; 116/2; 166/1; 208/1; 260/1; 299/2; 344/1; 398/1; 433/1			
C;Function:			
A;Description: hydrolyzes collagens, in particular types I, II, III, and X, serp			
C;Superfamily: interstitial collagenase; hemopexin repeat homology; matrix metal			
C;Keywords: calcium; extracellular matrix; fibroblast; glycoprotein; hydrolase;			
F;1-18/Domain: signal sequence #status predicted <SIG>			
F;19-468/Product: procollagenase #status predicted <PRO>			
F;19-98/Domain: activation peptide #status predicted <ACT>			

[illegible]

981 TCATCTCTGGCCATCTCTGCCAGCTGATCTGCAAGTGTCAACGAG--AACCCACAGAGAT 1037
 318 ValPheTrpProHisLeuProAsnGlyLeuGlnAlaAlaIaty-GluValAlaHisA-Gasp 337
 1038 AAGATCTCGTGTTTTAAAGATGAAACCTCTCGATGATCAGAGGATATGCTGCTCTGCCA 1097
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and

QY	1	2	3	4	5	6	7	8	9	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25	26	27	28	29	30	31	32	33	34	35	36	37	38	39	40	41	42	43	44	45	46	47	48	49	50	51	52	53	54	55	56	57	58	59	60	61	62	63	64	65	66	67	68	69	70	71	72	73	74	75	76	77	78	79	80	81	82	83	84	85	86	87	88	89	90	91	92	93	94	95	96	97	98	99	100
QY	1	2	3	4	5	6	7	8	9	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25	26	27	28	29	30	31	32	33	34	35	36	37	38	39	40	41	42	43	44	45	46	47	48	49	50	51	52	53	54	55	56	57	58	59	60	61	62	63	64	65	66	67	68	69	70	71	72	73	74	75	76	77	78	79	80	81	82	83	84	85	86	87	88	89	90	91	92	93	94	95	96	97	98	99	100

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U
TGGATCATAGCAATTGCTATACATAAAGCGTTTAA
1333 AGCCGTGAATCATAAGCAATTCATATACATTAAGCGTTTAA

438 PHEHVBGLTHIAIGGTHLYGLYSFNEASRPTODYSMLLPYSKATGTTCEGAMLTTCGGM AS

QY 1395 AGAACTAAATACTTGGTTTCAATGCAAGAA 1424

DB 458 LysAlaAsnSerTyrPheAsnCysArgLys 467

RESULT 11

interstitial collagenase (EC 3.4.24.7) precursor [validated] - human

C;Species: Homo sapiens (man)

C;Accession: A37308; S22766; I57620; A00996; D29157; A44518; S06132; B60964; S1

Cancer Res. 50, 5431-5437, 1990

A;Reference number: A37308; MUID:90352587; PMID:2167156

A:Molecule type: mRNA

A:Cross-references: UNIPROT:P03956; GB:X54925; NID:g30125; PIDN:CAA38691.1; PID

J. Clin. Invest. 79, 542-546, 1987

A: TITLE: MOLECULAR CLONING OF HUMAN c-fos GENE
A: Reference number: S22766: MUID:87109799; PMID:3027129

A;ACCESSION: 522700
A:Molecule type: DNA

A;RESIDUES: I-63, 63-70 (BK12)
 A;Cross-references: EMBL:M15996: NTD:g180666: PIDN:AAA35700.1; PID:g180667

R;Angel, P.; Baumann, I.; Stern, B.; Petrus, H., KAMMSOGLER, M.G.; ROSENBERG, J.
Vol Coll picl 7 2266-2266 1987

A;Title: 12-O-tetradecanoyl-phorbol-13-acetate induction of the human collagenase gene; number: 157620; MID: 87267941; PMID: 3037355

A;Accession: I57620

A;Molecule type: DNA

A;Gene: GDB:MMPI1; CUG
A;Cross-references: GDB:119783; OMIM:120353
A;Map position: 11q22.2-11q22.3
C;Function:
C;Description: hydrolyzes collagens, in particular types I, II, III, and X, esse
C;Superfamily: interstitial collagenase; hemopexin repeat homology; matrix m
C;Keywords: calcium; extracellular matrix; fibroblast; glycoprotein; hydrolase
F;1-19/Domain: signal sequence #status predicted <SIG>
F;20-469/Product: procollagenase #status experimental <PRO>
F;20-99/Domain: activation peptide #status experimental <ACT>
F;60-261/Domain: matrix metalloproteinase homology <MMP>
F;90-97/Region: autoinhibitory
F;100-469/Product: interstitial collagenase #status experimental <MAT>
F;272-466/Domain: hemopexin repeat homology <PXN>
F;92,218,222,228/Binding site: zinc, catalytic (Cys, His, His) (inhibited
F;120,143/Binding site: carbohydrate (Asn) (covalent) #status predicted
F;218,222,228/Binding site: zinc, catalytic (His) (active) #status predicted
F;219/Active site: Glu #status predicted
F;269-270/Cleavage site: Pro-Ile (autolytic) #status experimental
F;278-466/Disulfide bonds: #status experimental

Alignment Scores:

Pred. No.:	3 53e-91	Length:	469
Score:	1161.50	Matches:	234
Percent Similarity:	66.45%	Conservative:	77
Best Local Similarity:	50.00%	Mismatches:	146
Query Match:	39.64%	Indels:	11
DB:	1	Gaps:	8

US-10-729-807-28 (1-1627) x KCHUI (1-469)

QY	36	CTGCTTCGTGTGGTTCCTTTATACAAATTTCTTCGCATTCCCTTAGTCCCGATGACG	95
Db <td>7</td> <td>LeuLeuLeuLeuPheTiglyValValSerHisserPheProAlaThrLeuGluThr</td> <td>26</td>	7	LeuLeuLeuLeuPheTiglyValValSerHisserPheProAlaThrLeuGluThr	26
QY <td>96</td> <td>GAATATGAAGAAAATATGCAATCGCTCAGCATATCTCACAGTGTTCTACTCTCTTGA</td> <td>155</td>	96	GAATATGAAGAAAATATGCAATCGCTCAGCATATCTCACAGTGTTCTACTCTCTTGA	155
Db <td>27</td> <td>Gln--GlutInaspValaspLeuValGlnIstyrLeuGluLysTyrtyrAsnLeuLys</td> <td>45</td>	27	Gln--GlutInaspValaspLeuValGlnIstyrLeuGluLysTyrtyrAsnLeuLys	45
QY <td>156</td> <td>ATAGAAGGGAATCANCTTGTTCAAAGCAAGATAGGAGTCTCATAGATGACAAATTCGG</td> <td>215</td>	156	ATAGAAGGGAATCANCTTGTTCAAAGCAAGATAGGAGTCTCATAGATGACAAATTCGG	215
Db <td>46</td> <td>AsnaspGlyArgglnValgluIstyArgargAsnSerGlyProValValGluLysLeuLys</td> <td>65</td>	46	AsnaspGlyArgglnValgluIstyArgargAsnSerGlyProValValGluLysLeuLys	65
QY <td>216</td> <td>GAATATGAAGCAATTTTTGGATTGACAGTACAGTACGAAAACTGGACTCAAACACCTTGAG</td> <td>275</td>	216	GAATATGAAGCAATTTTTGGATTGACAGTACAGTACGAAAACTGGACTCAAACACCTTGAG	275
Db <td>66</td> <td>GlnMetGlnGluPhePheGlyLeuLysValThrGlyLysProaspAlaGluThrLeuLys</td> <td>85</td>	66	GlnMetGlnGluPhePheGlyLeuLysValThrGlyLysProaspAlaGluThrLeuLys	85
QY <td>276</td> <td>ATCATGAAGACACCAGGTGTGGGTGCTGATGTGGGCCAGTATGGGTACACC-----</td> <td>329</td>	276	ATCATGAAGACACCAGGTGTGGGTGCTGATGTGGGCCAGTATGGGTACACC-----	329
Db <td>86</td> <td>ValMetLysGlnProArgCysglyValProaspValalaglnPheValLeuThrGluGly</td> <td>105</td>	86	ValMetLysGlnProArgCysglyValProaspValalaglnPheValLeuThrGluGly	105
QY <td>330</td> <td>CTCCCTGGGTGGAGAAATACAACCTCACCTACAGATAATAAATACTACTCCGGATATG</td> <td>389</td>	330	CTCCCTGGGTGGAGAAATACAACCTCACCTACAGATAATAAATACTACTCCGGATATG	389
Db <td>106</td> <td>AsnProArgtprgluglnThrHisleuthrtyrargileGluasnTyrThrProaspLeu</td> <td>125</td>	106	AsnProArgtprgluglnThrHisleuthrtyrargileGluasnTyrThrProaspLeu	125
QY <td>390</td> <td>GCACGAGCTGCTGTGGATGAGCTATCCAAAGAGGTTTGAAGTGTGGAGCAAGTCACCT</td> <td>449</td>	390	GCACGAGCTGCTGTGGATGAGCTATCCAAAGAGGTTTGAAGTGTGGAGCAAGTCACCT	449
Db <td>126</td> <td>ProArgAlaaspValaspHisalaileglulysalaphelglnleuTrpSerAsnValThr</td> <td>145</td>	126	ProArgAlaaspValaspHisalaileglulysalaphelglnleuTrpSerAsnValThr	145
QY <td>450</td> <td>CCACTAAATATCCACAGATTCCAAGGGATTCGACATCATGATGTCCTTAGGACT</td> <td>509</td>	450	CCACTAAATATCCACAGATTCCAAGGGATTCGACATCATGATGTCCTTAGGACT	509
Db <td>146</td> <td>ProLeuThrPheThrLysValSerGluGlyGlnAlaaspIleMetIleSerPhe--Val</td> <td>164</td>	146	ProLeuThrPheThrLysValSerGluGlyGlnAlaaspIleMetIleSerPhe--Val	164
QY <td>510</td> <td>CGAGTCCATGTCGTGTCTCGCTATTATTCATGGTCCCTGGGAGTGCTTGGCCATGCC</td> <td>569</td>	510	CGAGTCCATGTCGTGTCTCGCTATTATTCATGGTCCCTGGGAGTGCTTGGCCATGCC	569
Db <td>165</td> <td>ArgGlyAspHisArgaspAsnSerProPheaspGlyProGlyGlyAsnLeuAlaHisala</td> <td>184</td>	165	ArgGlyAspHisArgaspAsnSerProPheaspGlyProGlyGlyAsnLeuAlaHisala	184
QY <td>570</td> <td>TTCCTCTGGTCCGGGTCTGGGTGGTGACACTCATTTTGTATGAGGATGAAATCGAAC</td> <td>629</td>	570	TTCCTCTGGTCCGGGTCTGGGTGGTGACACTCATTTTGTATGAGGATGAAATCGAAC	629
Db <td>185</td> <td>PheGlnProGlyProGlyIleGlyGlyAspAlaHisPheaspGluaspGluArgTrpThr</td> <td>204</td>	185	PheGlnProGlyProGlyIleGlyGlyAspAlaHisPheaspGluaspGluArgTrpThr	204
QY <td>630</td> <td>RAAGATGGACGAGGATTAACATTTGTTCTTGTGGCTGCTCATGAATTTGTCATGCAC</td> <td>689</td>	630	RAAGATGGACGAGGATTAACATTTGTTCTTGTGGCTGCTCATGAATTTGTCATGCAC	689

Db 205 AsnAsnPheArgGluTyrAsnLeuHisArgValAlaAlaHisGluLeuGlyHisSerLeu 224
QY 690 GGGCTCTCTCACTCAATGATCAAAACAGCTTGATGTTCCCAATTATGTC---TCCTGT 746
Db 225 GlyLeuSerHisSerThrAspIleGlyAlaLeuMetTyrProSerTyrThrPheSerGly 244
QY 747 ATCCCAAGAAATACCCCACTTTCAGGATGATATCAATGAATCCAGTCCATCATTCATGGA 806
Db 245 AspValGln-----LeuAlaGlnAspIleAspGlyIleGlnAlaIleTyr--- 260
QY 807 GGTCTGCTGAAGTACCTGCTTAAGCCAAAGAACCCACTATACCCCATGCTGTGACCCCT 866
Db 261 GlyArgSerGlnAsnProValGlnProIleGlyProGlnThrProLysAlaCysAspSer 280
QY 867 GACTTGACTTTGACGCTATCACAACTTTCGCGAGAGAGTAATGTTCTTTAAAGGAGG 926
Db 281 LysLeuThrPheAspAlaIleThrIleArgGlyGluValMetPhePheLysAspArg 300
QY 927 CACCTATGGAGATCTATTATGATATCACGATGCTGAGTTTGAATTAATTCGCTTCATTC 986
Db 301 PheTyrMetArgThrAsnProPheTyrProGluValGluLeuAsnPheIleSerValPhe 320
QY 987 TGGCCATCTCTGCCAGTGTACTCCAGCTGCATACGAG---AACCCAGAGATAGATT 1043
Db 321 TrpProGlnLeuProAsnGlyLeuGluAlaIleTyrGluPheAlaAspArgAspGluVal 340
QY 1044 CTGGTTTAAAGATGAAACTTCTGGATGATCATCAGATATGCTGCTGCCAGATTAT 1103
Db 341 ArgPhePheLysGlyAsnLysTyrTrpAlaValGlnGlyGlnAsnValLeuHisGlyTyr 360
QY 1104 CCAAAATCCATCCAT---ACATAGTGTTCAGGAGCTGTGAAGAAATAGATGCAGCC 1160
Db 361 ProllysAspIleTyrSerPheGlyPheProArgThrValLysHisIleAspAlaAla 380
QY 1161 GTCTGTGATAGACCAAGAAACCTACTTCTTTGGGCATTTGGTGTGCGAGTTT 1220
Db 381 LeuSerGluGluAsnThrGlyLysThrTyrPhePheValAlaAsnLysTyrTrpArgTyr 400
QY 1221 GATGAATGACCCAAACATCGACAAAGGATTCGCGAGAGTGGTAAACACTTTCCCT 1280
Db 401 AspGluTyrLysArgSerMetAspProGlyTyrProllysMetIleAlaHisAspPhePro 420
QY 1281 GGAATCATGATCCGTGTGTGCTGCTTCCAGTACAAAGATTCCTCTTTTCCAGCCGT 1340
Db 421 GlyIleGlyHisLysValAspAlaValPheMetLysAspGlyPheTyrPhePheHis 440
QY 1341 GGATCAAGCAATTTGAATACCAATTAAGACAAAGAAATATACCGAATCATGAGAACT 1400
Db 441 GlyThrArgGlnTyrLysPheAspProllysThrLysArgIleLeuThrLeuGlnLysAla 460
QY 1401 AATACTTGGTTTCAATCAAGAA 1424
Db 461 AsnSerTrpPheAsnCysArgLys 468
RESULT 12
KCHUN
N;Alternate names: matrix metalloproteinase 8
C;Species: Homo sapiens (man)
C;Date: 30-Sep-1992 #sequence revision 30-Sep-1992 #text_change 09-Jul-2004
C;Accession: A37073; A61175; A36230; S09680; S11026; S19576; S27225; S62
R;Hasty, K.A.; Pourmotabbed, T.F.; Goldberg, G.I.; Thompson, J.P.; Spinella, D.G.; Steve
J. Biol. Chem. 265, 11421-11424, 1990
A;Title: Human neutrophil collagenase. A distinct gene product with homology to other ma
A;Reference number: A37073; MUID:90307647; PMID:2164002
A;Accession: A37073
A;Molecule type: mRNA
A;Residues: 1-467 <HAS>
A;Cross-references: UNIPROT:p22894; GB:J05556; NID:g180617; PIDN:AAA88021.1; PID:g180618
R;Devarajan, P.; Mookhtiar, K.; Van Wart, H.; Berliner, N.
Blood 77, 2731-2738, 1991
A;Title: Structure and expression of the cDNA encoding human neutrophil collagenase.
A;Reference number: A61175; MUID:91255696; PMID:1646048

A;Accession: A61175
A;Status: not compared with conceptual translation
A;Molecule type: mRNA
A;Residues: 1-31, 'I', 33-86, 'E', 88-467 <DEV>
A;Accession: B61175
A;Molecule type: protein
A;Residues: 263-264, 'X', 266-270, 'X', 272-273, 'X', 275, 'X', 277 <DE2>
R;Mallva, S.K.; Mookhtiar, K.A.; Gao, Y.; Brew, K.; Dioszegi, M.; Birkedal-Hansen, H.; V
Biochemistry 29, 10628-10634, 1990
A;Title: Characterization of 58-kilodalton human neutrophil collagenase: comparison with
A;Reference number: A36230; MUID:91104978; PMID:2176876
A;Accession: A36230
A;Molecule type: protein
A;Residues: 'X', 86-87, 'X', 89-90, 'X', 92-97, 'X', 99-111, 'X', 113-120 <MAL>
R;Knaeuper, V.; Kraemer, S.; Reinke, H.; Tschesche, H.
Eur. J. Biochem. 189, 295-300, 1990
A;Title: Characterization and activation of procollagenase from human polymorphonuclear
A;Reference number: S09680; MUID:90249372; PMID:2159879
A;Accession: S09680
A;Molecule type: protein
A;Residues: 21-31, 'I', 33-39, 'I', 41-47, 'V', 49-53, 'I', 55-72, 'G', 74-86, 'E', 88-111, 'X', 113-1
A;Note: 67-Lys was also found
R;Knaeuper, V.; Kraemer, S.; Reinke, H.; Tschesche, H.
Biochem. Hoppe-Seyler 371, 733, 1990
A;Title: Corrigendum. Partial amino-acid sequence of human PMN leukocyte procollagenase
A;Reference number: S11026; MUID:91000455; PMID:2169766
A;Note: Original publication was Biol. Chem. Hoppe-Seyler 371(Suppl.), 295-304, 1990
A;Accession: S11026
A;Molecule type: protein
A;Residues: 21-31, 'I', 33-53, 'I', 55-72, 'G', 74-111, 'X', 113-140;183-203, 'X', 205-209;248-2
A;Note: 87-Glu was also found
R;Blaeser, J.; Knaeuper, V.; Osthus, A.; Reinke, H.; Tschesche, H.
Eur. J. Biochem. 202, 1223-1230, 1991
A;Title: Mercurial activation of human polymorphonuclear leucocyte procollagenase.
A;Reference number: S19576; MUID:92111500; PMID:1662606
A;Accession: S19576
A;Molecule type: protein
A;Residues: 69-103 <BL2>
R;Blaeser, J.; Triebel, S.; Reinke, H.; Tschesche, H.
FEBS Lett. 313, 59-61, 1992
A;Title: Formation of a covalent Hg-Cys-bond during mercurial activation of PMNL procol
A;Reference number: S27225; MUID:93050220; PMID:1330697
A;Accession: S27225
A;Molecule type: protein
A;Residues: 68-103 <BLA>
R;Knaeuper, V.; Osthus, A.; DeClerck, Y.A.; Langley, K.E.; Blaeser, J.; Tschesche, H.
Biochem. J. 291, 847-854, 1993
A;Title: Fragmentation of human polymorphonuclear-leucocyte collagenase.
A;Reference number: S32527; MUID:93256897; PMID:8489511
A;Accession: S32527
A;Molecule type: protein
A;Residues: 100-112;263-276 <KN3>
R;Knaeuper, V.; Murphy, G.; Tschesche, H.
Eur. J. Biochem. 235, 187-191, 1996
A;Title: Activation of human neutrophil procollagenase by stromelysin 2.
A;Reference number: S62608; MUID:96202934; PMID:8631328
A;Accession: S62608
A;Molecule type: protein
A;Residues: 21-39, 'I', 41-47, 'V', 49-122 <KN4>
R;Stams, T.; Spurlino, J.C.; Smith, D.L.; Rubin, B.
submitted to the Brookhaven Protein Data Bank, January 1994
A;Reference number: A67078; PDB:1MNC
A;Contents: annotation; X-ray crystallography, 2.1 angstroms, residues 'G', 106-149, 'G',
R;Stams, T.; Spurlino, J.C.; Smith, D.L.; Wahl, R.C.; Ho, T.F.; Qoronfleh, M.W.; Banks,
Nat. Struct. Biol. 1, 119-123, 1994
A;Title: Structure of human neutrophil collagenase reveals large S1' specificity pocket
A;Reference number: A58274; MUID:95384762; PMID:7656015
A;Contents: annotation; X-ray crystallography, 2.1 angstroms, residues 'G', 106-149, 'G',
C;Comment: This protein is more highly glycosylated than interstitial collagenase and i
C;Genetics:
A;Gene: GDB:MMP8; CLG1
A;Cross-references: GDB:128173; OMIM:120355
A;Map position: 11q22.2-11q22.3

C:Genetics:

A;Gene: GDB:MMP13; CLG3
 A;Cross-references: GDB:373966; OMIM:600108
 A;Map position: 11q22.2-11q22.3
 C;Superfamily: interstitial collagenase; hemopexin repeat homology; matrix metalloproteinase
 C;Keywords: hydrolase; metalloproteinase; zinc; zymogen
 F;64-267/Domain: matrix metalloproteinase homology <MMP>
 F;278-471/Domain: hemopexin repeat homology <PN>
 F;96,222,226,232/Binding site: zinc, catalytic (Cys, His, His, His) (inhibited) #status
 F;222,226,232/Binding site: zinc, catalytic (His) (active) #status predicted
 F;223/Active site: Glu #status predicted

Alignment Scores:
 Pred. No.: 2,01e-89 Length: 471
 Score: 1141.00 Matches: 222
 Percent Similarity: 63.68% Conservative: 62
 Best Local Similarity: 49.78% Mismatches: 150
 Query Match: 38.94% Indels: 12
 DB: 2 Gaps: 8

US-10-729-807-28 (1-1627) x AS3711 (1-471)

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Db 32 SerGluGluAspLeuGlnPheAlaGluArgTyrLeuArgSerTyrHisProThrAsn 51
QY 156 ATAGAGGGAATCATCTGTGTTCAAGCAAGAAATAGAGTCTCTAGATGACAAATTCGG 215
Db 52 LeuAlaGly-----IleLeuLysGluAsnAlaSerSerMetThrGluArgLeuArg 69
QY 216 GAAATGCAAGCATTTTGTGATTGACAGTCACTGGAATCGACTCAACACACCTTGAG 275
Db 70 GluMetGlnSerPhePheGlyLeuGluValThrGlyLysLeuAspAspAsnThrLeuAsp 89
QY 276 ATCATGAAGACACCCAGGTGGGGTCCCTGATGTGGCCAGTATGCTAC----- 326
Db 90 ValMetLysLysProArgCysGlyValProAspValGlyGluTyrAsnValPheProArg 109
QY 327 ACCTCGCTGGGAGAAATACACCTCACCTACAGATATTAACATATCTACCTCGAT 386
Db 110 ThrLeuLys---TrpSerLysMetAsnLeuThrTyrArgIleValAsnTyrThrProAsp 128
QY 387 ATGGCAGCATGCTGTGGATGAGGCTATCCAAAGGTTTAGAAGTGTGGCAAGATGC 446
Db 129 MetThrHisSerGluValGluLysAlaPheLysLysAlaPheLysValTrpSerAspVal 148
QY 447 ACTCCACTAAATTCACCAAGATTTCAAAGGGATTCGACATCATGATGATGCTTTAGG 506
Db 149 ThrProLeuAsnPheThrArgLeuHisAspGlyIleAlaAspIleMetIleSerPheGly 168
QY 507 ACTCGAGTCCATGCTGGTCTCTCGCTAT---TTTGATGCTCCCTGGGAGTGTGGC 563
Db 169 IleLysGluHisGly-----AspPheTyrProPheAspGlyProSerGlyLeuLeuAla 186
QY 564 CATGCTCTTCTCTGCTCGGGTCTCGGTGGTGACACTCATTTGATGAGGATGAAAC 623
Db 187 HisAlaPheProGlyProAsnTyrGlyGlyAspAlaHisPheAspAspGluThr 206
QY 624 TGGACCAAGATGAGCAGGATTCACCTGTTTCTTGTGGCTGCTCATGAATTTGGTCAT 683
Db 207 TrpThrSerSerLysGlyTyrAsnLeuPheLeuValAlaAlaHisGluPheGlyHis 226
QY 684 GCATCGGGCTCTCACTCAATGATCAACAGCCTGTGTGTCCTCAATATGCTCC 743
Db 227 SerLeuGlyLeuAspHisSerLysAspProGlyAlaLeuMetPheProIleTyrThrTyr 246
QY 744 CTGGATCCCAAGAAATACCACTTCTCAGGATGATATCAATGAATCCAGTCCATCAT 803
Db 247 ThrGlyLysSerHisPheMetLeuProAspAspValGlnGlyIleGlnSerLeuTyr 266
QY 804 GGAGGTCTGCTAAGTACTGTGTAAGCAAGAAACCACTATACCCCATGCTGTGAC 863
Db 267 GlyProGlyAspGluAspPro---AsnProLysHisProLysThrProAspLysCysAsp 285

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QY 864 CQTGACTGACTTTTTCAGCGCTATCACAACCTTTCCGACAGAGTAATGTTCTTTAAAGGC 923
Db 286 ProSerLeuSerLeuAspAlaIleThrSerLeuArgGlyGluThrMetIlePheLysAsp 305
QY 924 AGCCACCTATGAGGAGTATATATATATATATATATATATATATATATATATATATATAT 983
Db 306 ArgPhePheTrpArgLeuHisProGlnGlnValAspAlaGluLeuPheLeuThrLysSer 325
QY 984 TTTGCGCATCTCTGCGCAGTCTGATCTGCAAGCTGATACGACGATACGACGACCC---AGAGTAAG 1040
Db 326 PheTrpProGluLeuProAsnArgIleAspAlaAlaTyrGluHisProSerHisAspLeu 345
QY 1041 ATTCTGTTTAAAGATGAAACCTTCTGATGATCAGAGGATATGCTGCTTGGCCAGAT 1100
Db 346 IlePheIlePheArgGlyArgLysPheTrpAlaLeuAsnGlyTyrAspIleLeuGluGly 365
QY 1101 TATCCCAATCCATCCATACATAGTGTTCAGGACGTGTGAAGAAATAGATGACGCC 1160
Db 366 TyrProLysLysIleSerGluLeuGlyLeuProLysGluValLysLysIleSerAlaAla 385
QY 1161 GTCTGTGATAGACCAACCAAGGATTCCTTCTTGTGGCATTTGGTCTCGAGGTTT 1220
Db 386 ValHisPheGluAspThrGlyLysThrLeuLeuPheSerGlyAsnGlnValTrpArgTyr 405
QY 1221 GATGAATGACCCAAACCATGGAAGGATTCCTCCGACAGAGTGTGTAACACACTTTCTCT 1280
Db 406 AspAspThrAsnHisIleMetAspLysAspTyrProArgLeuIleGluGluAspPhePro 425
QY 1281 GGAATCAGTATCCGTGTGATGCTGCTTCCAGTCAAAAGGATTTCTTTTTCAGCCGT 1340
Db 426 GlyIleGlyAspLysValAspAlaValTyrGluLysAsnGlyTyrIleTyrPheAsn 445
QY 1341 GGATCAAGCAATTTGATACACATTAAGACAAAGATATATCCGGAATCATGAGACT 1400
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QY 1401 AATACTTGGTTTCAATGC 1418
Db 466 AsnSerIleLeuTrpCys 471

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RESULT 14

A49499
 metalloelastase HME (EC 3.4.24.-) - human
 C;Species: Homo sapiens (man)
 C;Date: 07-Apr-1994 #sequence_revision 18-Nov-1994 #text_change 09-Jul-2004
 C;Accession: A49499
 R;Shapiro, S.D.; Kobayashi, D.K.; Ley, T.J.
 J. Biol. Chem. 268, 23824-23829, 1993
 A;Title: Cloning and characterization of a unique elastolytic metalloproteinase produced
 A;Reference number: A49499; MUID:94043200; PMID:8226919
 A;Accession: A49499
 A;Status: preliminary
 A;Molecule type: mRNA
 A;Residues: 1-470 <SHA>
 A;Cross-references: UNIPROT:P39900; GB:L23808; NID:g435969
 A;Experimental source: alveolar macrophage
 A;Note: sequence extracted from NCBI backbone (NCBI:139457, NCBI:139458)
 C;Genetics:
 A;Gene: GDB:MMP12; HME
 A;Cross-references: GDB:266582; OMIM:601046
 A;Map position: 11q22.2-11q22.3
 C;Superfamily: interstitial collagenase; hemopexin repeat homology; matrix metalloproteinase
 C;Keywords: hydrolase; metalloproteinase; zinc; zymogen
 F;60-263/Domain: matrix metalloproteinase homology <MMP>
 F;276-470/Domain: hemopexin repeat homology <PN>
 F;92,218,222,228/Binding site: zinc, catalytic (Cys, His, His, His) (inhibited) #status
 F;218,222,228/Binding site: zinc, catalytic (His) (active) #status predicted
 F;219/Active site: Glu #status predicted

Alignment Scores:

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 Score: 1133.00 Matches: 229

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 Query Match: 38.67% Indels: 16
 DB: 2 Gaps: 10

US-10-729-807-28 (1-1627) x A49499 (1-470)

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 QY 90 ATGACGGAATAATGAAGAAATATGCAACTG---GCTCAGGCATATCTCAACCACTTCTAC 146
 DB 22 SerThrSerLeuGluLysAsnValLeuPheGlyGluArgTyrLeuGluLysPheTyr 41
 QY 147 TCTCTGTAATAGAGGGAATCATCTTGTGTTCAAGCAAGAATAGG-----AGTCTC 197
 DB 42 GlyLeuGluLeu-----AsnLysLeuProValThrLysMetLysTyrSerGlyAsnLeu 59
 QY 198 ATAGATGACAAATTCGGGAATGCAAGCATTTTGTGATTGACAGTCACTGGAACACTG 257
 DB 60 MetLysGluLysIleGlnGluMetGlnHisPheLeuGlyLeuLysValThrGlyGlnLeu 79
 QY 258 GACTCAAAACACCTTTGAGATCATGAGACACCCAGGTGTGGGGTGCCTGATGTGGGCCAG 317
 DB 80 AspThrSerThrLeuGluMetMetHisAlaProArgCysGlyValProAspValHis 99
 QY 318 TATGCTACACCTCCCTGGG-----TGAGAAATATACACTCACTACAGAAATA 368
 DB 100 Phe---ArgGluMetProGlyGlyProValThrArgLysHisTyrIleThrTyrArgIle 118
 QY 369 ATAACTATCTCCGATATGACAGAGCTGCTGTGGATGAGGCTATCCAAAGGTTTA 428
 DB 119 AsnAsnTyrThrProAspMetAsnArgGluAspValAspTyrAlaIleArgLysAlaPhe 138
 QY 429 GAAGTGTGGAGCAAAAGTCACTCCATTAATAATTCACCAAGATTTCAAAGGGATTCGACAC 488
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 QY 489 ATCATGATGCTTTAGACTGCTAGTCCATGCTCGGTGCTCGCTGCTATTTGATGCTGCC 548
 DB 159 IleLeuValValPheAlaArgGlyAlaHisGlyAspPhe---HisAlaPheAspGlyLys 177
 QY 549 TTGGAGAGTGTGGCCATGCTCTCTCTGCTCGGCTGGGTGGGTGACACTCATTTT 608
 DB 178 GlyGlyIleLeuAlaHisAlaPheGlyProGlySerGlyIleGlyAspAlaHisPhe 197
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 DB 198 AspGluAspGluPheTyrThrThrHisSerGlyGlyThrAsnLeuPheLeuThrAlaVal 217
 QY 669 CATGATTTGTCATGCACTGGGCTCTCTCACTCAATGATCAACAGCCCTTGATGTC 728
 DB 218 HisGluIleGlyHisSerLeuGlyLeuGlyHisSerSerAspProLysAlaValMetPhe 237
 QY 729 CCAATTTATGTCCTCCGTGATCCAGAAATACCCACTTCTCAGATGATATCAATGGA 788
 DB 238 ProThrTyrLysTyrValAspIleAsnThrPheArgLeuSerAlaAspIleArgGly 257
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 DB 258 IleGlnSerLeuTyrGlyAsp---ProLysGluAsnGlnArgLeuProAsnProAspAsn 276
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 DB 277 SerGluProAlaLeuCysAspProAsnLeuSerPheAspAlaValThrThrValGlyAsn 296
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RESULT 15

A23685
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 N:Alternate names: matrix metalloproteinase 1 (MMP1); vertebrate collagenase
 C:Species: Rattus norvegicus (Norway rat)
 C:Date: 04-Oct-1991 #sequence_revision 04-Oct-1991 #text_change 09-Jul-2004
 C:Accession: A23685
 R:Quinn, C.O.; Scott, D.K.; Brinckerhoff, C.E.; Matrisian, L.M.; Jeffrey, J.J.; Partridge
 J. Biol. Chem. 265, 22342-22347, 1990
 A:Title: Rat collagenase. Cloning, amino acid sequence comparison, and parathyroid hormone
 A:Reference number: A23685; MUID:91093077; PMID:2176215
 A:Accession: A23685
 A>Status: preliminary
 A:Molecule type: mRNA
 A:Residues: 1-466 <QUL>
 A:Cross-references: UNIPROT:P23097; GB:M60616; GB:M36452; NID:g203498; PIDN:AAAY2124.1;
 C:Superfamily: interstitial collagenase; hemopexin repeat homology; matrix metalloprotei
 C:Keywords: hydrolase; metalloproteinase; zinc; zymogen
 F:59-262/Domain: matrix metalloproteinase homology <MMP>
 F:273-466/Domain: hemopexin repeat homology <HPN>
 F:91,217,221,227/Binding site: zinc, catalytic (Cys, His, His) (inhibited) #status 1
 F:217,221,227/Binding site: zinc, catalytic (His) (active) #status predicted
 F:218/Active site: Glu #status predicted

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 Query Match: 38.43% Indels: 10
 DB: 2 Gaps: 7

US-10-729-807-28 (1-1627) x A23685 (1-466)

QY 99 AATGAAGAAATATGCAACTGGCTCAGGCATATCTCAACCACTTCTACTCTTGAATA 158
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 QY 159 GAAGGAATCATCTTGTTCAAAGCAAGAAATAGGAGTCTCATAGATGACAAATTCGGAA 218
 DB 47 LeuAlaGlyIleLeuLysLysSerThrValThrSerThrVal---AspArgLeuArgGlu 65
 QY 219 ATGCAAGCATTTTGTGGATTGACAGTGCAGTGGAAACCTGGAACCTTGCAGATC 278

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Db      66 MetGlnSerPhePheGlyLeuAspValThrGlyLysLeuAspPProThrLeuAspIle 85
QY      279 ATGAAGACACCCAGGTGTGGGGTCCCTGATGTGGCCAGTATGCTATAC-----ACC 329
Db      86 MetArgLysProArgCysGlyValProAspValGlyValTyrAsnValPheProArgThr 105
QY      330 CTCCTCGGTGGAGAAATACACCTCACCTACAGATAATAAATACTATATCTCGGATATG 389
Db      106 LeuLys---TrpSerGlnThrAsnLeuThrTyrArgIleValAsnTyrThrProAspIle 124
QY      390 GCACGAGCTCTGTGGATGAGGTATCCAAAGAGTTTGAAGTGTGGAGTGCACAAAGTCACT 449
Db      125 SerHisSerGluValGluLysAlaPheArgLysAlaPheLysValTrpSerAspValThr 144
QY      450 CCACATAAATTCACCAAGATTTCAAAGGGGATTGCAGACATCATGATTCGCTTTAGGACT 509
Db      145 ProLeuAsnPheThrArgIleHisAspGlyThrAlaAspIleMetIleSerPheGlyThr 164
QY      510 CGAGTCCATGGTGGTGTCTCGCTAT---TTTGTGTTGCTCCCTGGAGTGTGGCCAT 566
Db      165 LysGluHisGly-----AspPheTyrProPheAspGlyProSerGlyLeuLeuAlaHis 182
QY      567 GCCTTTCTCTCTGTCCTGGGTCTCGGTGTGACACTCATTTTGATGAGGATGAAACTGG 626
Db      183 AlaPheProGlyProAsnLeuGlyGlyAspAlaHisPheAspAspGluThrTrp 202
QY      627 ACCAAGATGGAGCAGGATCAACTCTTTCTGTGGCTGCTCATGAATTTGTCATGCA 686
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QY      687 CTGGGGCTCTCTCACTCAATGATCAACAGCCCTGTGATGTTCCCAATTTATGTCCTCGT 746
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Db      282 AlaLeuSerLeuAspAlaIleThrSerLeuArgGlyGluThrMetIlePheLysAspArg 301
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Db      362 ProArgLysIleSerAspLeuGlyPheProLysGluValLysArgLeuSerAlaVal 381
QY      1164 TGTGATAAGACCAACAAGAAACCTACTTCTTTGTTGGGCACTTGTGCTGGAGTTTGTAT 1223
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QY      1224 GAATGACCCCAACCATCGACAAAGGATTCCCGCAGAGAGTGGTAAACACACTTTCTCTGA 1283
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Db      422 IleGlyAspLysValAspAlaValTyrGluLysAsnGlyTyrIleTyrPhePheAsnGly 441
QY      1344 TCAAGCAATTTCAATACACACATTAGACACAAAGATATTACCCGAATCATGAGAACTAAT 1403
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QY      1404 ACTTGGTTTCAATGC 1418
Db      462 SerLeuLeuTrpCys 466
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GenCore version 5.1.6
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OM nucleic - protein search, using frame_plus_n2p model

Run on: November 15, 2004, 18:33:02 ; Search time 180.5 Seconds
(without alignments)
10372.682 Million cell updates/sec

Title: US-10-729-807-28

Perfect score: 2930

Sequence: 1 gcttcagctgaagaagaga.....aattcgtctcaaatagaa 1627

Scoring table:

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Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 1825181 seqs, 575374646 residues

Total number of hits satisfying chosen parameters: 3650362

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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-UNITS=bits -START=1 -END=1 -MATRIX=biosum62 -TRANS=human40.cdi -LIST=45
-DOALIGN=200 -THR SCORE=pct -THR MAX=100 -THR MIN=0 -ALIGN=15 -MODE=LOCAL
-OUTFMT=ptc -NORM=ext -HEAPSIZ=500 -MINLEN=0 -MAXLEN=2000000000
-USER=US10729807 @CGN_1_1_165 @runat_15112004_131150_14688 -NCPU=6 -ICPU=3
-NO_WMAP -LARGEQUERY -NEG SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG
-DEV_TIMEOUT=120 -WARN_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database :

Uniprot_02 : *
1: uniprot_sprot : *
2: uniprot_trembl : *

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	ID	Description
1	2752	93.9	513	2 Q6UWK6	Q6UWK6 homo sapien
2	2752	93.9	513	2 AAQ89112	AAQ89112 homo sapi
3	2731	93.2	513	2 Q9H306	Q9H306 homo sapien
4	2347	80.1	512	2 Q9GKE1	Q9GKE1 tupaiia glis
5	1520.5	51.9	472	2 Q93342	Q93342 gallus gall
6	1286.5	43.9	478	2 Q6Y4Q5	Q6Y4Q5 canis faml
7	1286.5	43.9	478	2 AA063580	AA063580 canis fam
8	1271.5	43.4	478	1 MM03_RABIT	MM03_RABIT
9	1254	42.8	477	2 AAH69676	AAH69676 homo sapi
10	1254	42.8	477	2 AAH69716	AAH69716 homo sapi
11	1250	42.7	477	1 MM03_HUMAN	MM03_HUMAN
12	1247	42.6	483	2 Q98857	Q98857 cynops pyrr
13	1244	42.5	477	1 MM03_HORSE	MM03_HORSE
14	1243.5	42.4	476	1 MM10_MOUSE	MM10_MOUSE
15	1238.5	42.3	479	2 Q922W6	Q922W6 mus musculu
16	1237.5	42.2	477	1 MM03_MOUSE	MM03_MOUSE

17	1234	42.1	476	1 MM10_HUMAN	P09238 homo sapien
18	1234	42.1	476	2 AAF36110	AAF36110 homo sapi
19	1229	41.9	472	2 Q10833	Q10833 xenopus lae
20	1219.5	41.6	469	1 MM13_XENLA	Q10835 xenopus lae
21	1205	41.1	469	1 MM01_PIG	P21692 sus scrofa
22	1200.5	41.0	464	1 MM12_RABIT	P79227 oryctolagus
23	1200.5	41.0	464	2 Q9TV75	Q9TV75 oryctolagus
24	1198.5	40.9	476	1 MM10_RAT	P07152 rattus norv
25	1196	40.8	469	1 MM01_HORSE	Q95825 equus cabal
26	1195	40.8	469	2 Q98858	Q98858 cynops pyrr
27	1190.5	40.6	466	2 Q7SYX1	Q7SYX1 xenopus lae
28	1183.5	40.4	471	2 Q98859	Q98859 cynops pyrr
29	1177.5	40.2	469	1 MM01_BOVIN	P28053 bos taurus
30	1173.5	40.1	475	1 MM03_RAT	P03957 rattus norv
31	1170.5	39.9	468	1 MM01_RABIT	P13943 oryctolagus
32	1167	39.8	467	1 MM18_XENLA	O13065 xenopus lae
33	1161.5	39.6	469	1 MM01_HUMAN	P03956 homo sapien
34	1161.5	39.6	469	2 AAP35520	AAP35520 homo sapi
35	1161	39.6	467	1 MM08_HUMAN	P22894 homo sapien
36	1159	39.6	465	2 AAH42742	AAH42742 mus muscu
37	1159	39.6	465	2 BAC40805	BAC40805 mus muscu
38	1158.5	39.5	471	1 MM13_RABIT	O62806 oryctolagus
39	1155	39.4	472	1 MM13_HORSE	O18927 equus cabal
40	1154	39.4	465	2 Q8C209	Q8C209 mus musculu
41	1154	39.4	465	2 Q8C230	Q8C230 mus musculu
42	1150	39.2	465	1 MM08_MOUSE	O70138 mus musculu
43	1143.5	39.0	466	1 MM08_RAT	O88766 rattus norv
44	1141	38.9	471	1 MM13_HUMAN	P45452 homo sapien
45	1141	38.9	471	2 AAH67522	AAH67522 homo sapi

ALIGNMENTS

RESULT 1

Q6UWK6 PRELIMINARY; PRT; 513 AA.
AC Q6UWK6;
DT 05-JUL-2004 (TREMBLrel. 27, Created)
DT 05-JUL-2004 (TREMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TREMBLrel. 27, Last annotation update)
DE MRP27.
GN ORFNames=UNQ2503;
OS Homo sapiens (Human)
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]

RP SEQUENCE FROM N.A.
RX MEDLINE=22887296; PubMed=12975309;
RA Clark H.F., Gurney A.L., Abaya E., Baker K., Baldwin D., Brush J.,
Chen J., Chow B., Chui C., Crowley C., Currell B., Deuel B., Dowd P.,
Eaton D., Foster J., Grimaldi C., Gu Q., Hass P.E., Heldens S.,
Huang A., Kim H.S., Klimowski L., Jin Y., Johnson S., Lee J.,
Lewis L., Liao D., Mark M., Robbie E., Sanchez C., Schoenfeld J.,
Seshagiri S., Simmons L., Singh J., Smith V., Stinson J., Vagts A.,
Vandlen R., Watanabe C., Wieand D., Woods K., Xie M.H., Yansura D.,
Yi S., Yu G., Yuan J., Zhang M., Zhang Z., Goddard A., Wood W.I.,
Godowski P.;
RA "The secreted protein discovery initiative (SPDI), a large-scale
effort to identify novel human secreted and transmembrane proteins: a
bioinformatics assessment";
RL Genome Res. 13:2265-2270(2003).
DR EMBL; AY358752; AAQ89112.1; -
DR InterPro; IPR000585; Hemopexin.
DR InterPro; IPR006026; Peptidase M.
DR InterPro; IPR001818; Pept M10A_M12B.
DR InterPro; IPR006025; Pept_M_Zn_BS.
DR Pfam; PF00045; Hemopexin; 4.
DR Pfam; PF00413; Peptidase M10; 1.
DR Pfam; PF03933; Peptidase M10_N; 1.
DR PRINTS; PR00138; MATRXIN.
DR SMART; SM00120; HX; 4.
DR SMART; SM00235; ZnMc; 1.

RT Bioinformatics Assessment.*;
 RL Genome Res. 13:2265-2270(2003).
 DR EMBL; AY358752; AAQ89112.1; -. 1B1D55699553DCD CRC64;
 SQ SEQUENCE 513 AA; 58994 MW; 1B1D55699553DCD CRC64;

Alignment Scores:

Pred. No.: 9,1e-236 Length: 513
 Score: 2752.00 Matches: 512
 Percent Similarity: 99.81% Conservative: 0
 Best Local Similarity: 99.81% Mismatches: 1
 Query Match: 93.92% Indels: 0
 DB: 2 Gaps: 0

US-10-729-807-28 (1-1627) x AAQ89112 (1-513)

QY 24 ATGAAGCCCTCTCTGCTCTCTGTTGTTCTTTTAAACATTTTCTTCGCAATTCCTCTTA 83
 DB 1 MetLysArgLeuLeuLeuLeuPheLeuPhePheLeuThrPheSerSerAlaPheProLeu 20
 QY 84 GTCCGGATGACGGAATAAGAAATATGCAACTGGCTCAGGCATATCTCAACAGTTC 143
 DB 21 ValArgMetThrGluAsnGluGluAsnMetGlnLeuAlaGlnAlaTyrLeuAsnGlnPhe 40
 QY 144 TACTCTCTTGAATAAGAGGAATCATCTTGTTCAAAGCAAGATAGGAGTCTCATAGAT 203
 DB 41 TyrSerLeuGluLeuGluGluAsnHisLeuValGlnSerLysAsnArgSerLeuLeuLeuLeu 60
 QY 204 GACAAATTCGGAAATGCAAGCATTTTGTGATGACAGTACCTGAGTGGAAACCTGACTCA 263
 DB 61 AspLysIleLeuGluMetGlnAlaPhePheGlyLeuThrValThrGlyLysLeuAspSer 80
 QY 264 AACACCTTGTAGATCATCAAGACACCCAGGTGGGTGGCTGAGTGGCGAGTATGCG 323
 DB 81 AsnThrLeuGluLeuLeuLeuLysThrProArgCysGlyValProAspValGlyGlnTyrGly 100
 QY 324 TACACCTCTCTGCGTGGAGAAATACAACTCCTACAGAAATATAAATATACTCCG 383
 DB 101 TyrThrLeuProGlyTyrArgLysTyrAsnLeuThrTyrArgIleAsnTyrThrPro 120
 QY 384 GATATGGCAGAGCTGTGTGATGAGGTATCCAAAGGTTTGAAGTGTGGAGCAAA 443
 DB 121 AspMetAlaArgAlaAlaValAspGluAlaIleGlnGluGlyLeuGluValTyrSerLys 140
 QY 444 GTCACTCCACATAAATTCACCAAGATTCACAGGGGATTCAGACATCATGATTCCTTT 503
 DB 141 ValThrProLeuLysPheThrLysIleSerLysGlyIleAlaAspIleMetIleAlaPhe 160
 QY 504 AGGACTCGAGTCCATGCTGCTGCTCTCTCTATTTTGTGCTCCCTTGGGAGTGTCTGCG 563
 DB 161 ArgThrArgValHisGlyArgCysProArgTyrPheAspGlyProLeuGlyValLeuGly 180
 QY 564 CATGCTTCTCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 623
 DB 181 HisAlaPheProGlyProGlyLeuGlyGlyAspThrHisPheAspGluAspGluAsn 200
 QY 624 TGGACCAAGATGAGCAGGATTCACATTTGTTCTTGTGGCTGCTCATGAATTTGCTAT 683
 DB 201 TrpThrLysAspGlyAlaGlyPheAsnLeuPheLeuValAlaAlaHisGluPheGlyHis 220
 QY 684 GCACCTGGGCTCTCTCACTCCCAATGATCAACAGCCTTGATGTTCCCAATATATCTCTCC 743
 DB 221 AlaLeuGlyLeuSerHisSerAsnAspGlnThrAlaLeuMetPheProAsnTyrValSer 240
 QY 744 CTGGATCCAGAAATACCCATTTCTCAGGATGATATCAATCGAATCCAGTCCATCAT 803
 DB 241 LeuAspProArgLysTyrProLeuSerGlnAspAspIleAsnGlyIleGlnSerIleTyr 260
 QY 804 GGAGTCTGCTAAGTACCTGCTAAGCAAGGACCCACTATATACCCATGCTCTGCTAC 863
 DB 261 GlyGlyLeuProLysValProAlaLysProLysGluProThrIleProHisAlaCysAsp 280
 QY 864 CTTGACTTGTGCTTGTGCTGCTTGTGCTTGTGCTTGTGCTTGTGCTTGTGCTTGTGCTT 923

DB 281 ProAspLeuThrPheAspAlaIleThrThrPheArgArgGluValMetPhePheLysGly 300
 QY 924 AGGCACCTATGAGGATCTTATATGATATCAGGATGTGATTTGAATTAATTTGCTTCA 983
 DB 301 ArgHisLeuTrpArgIleTyrTyrAspIleThrAspValGluPheGluLeuIleAlaSer 320
 QY 984 TTCTGCCATCTCTGCCAGCTGATCTGCAAGCTGATCAGACGATCAGAGAACCCAGACATAGATT 1043
 DB 321 PheTrpProSerLeuProAlaAspLeuGlnAlaIleTyrGluAsnProArgAspLysIle 340
 QY 1044 CTGGTTTTAAAGATGAAAACTTCTGGATGATCAGAGGATATGCTGTCTTGGCCAGATTAT 1103
 DB 341 LeuValPheLysAspGluAsnPheTrpMetIleArgGlyTyrAlaValLeuProAspTyr 360
 QY 1104 CCCAATCCATCCATACATATTAGTTTCCAGACCTGTGAAGAAATAGATGACCCGTC 1163
 DB 361 ProLysSerIleHisThrLeuGlyPheProGlyArgValLysLysIleAspAlaAlaVal 380
 QY 1164 TGTGATAAGACACCAAGAAACCTCTTCTTGTGGCATTTGCTGGAGGTTTGTAT 1223
 DB 381 CysAspLysThrThrArgLysThrThrPhePheValGlyIleTrpCysTrpArgPheAsp 400
 QY 1224 GAAATGACCCCAACCATCGACAAAGGATTCGCCGACAGAGATGCTAAACACTTTCTCTGGA 1283
 DB 401 GluMetThrGlnThrMetAspLysGlyPheProGlnArgValValLysHisPheProGly 420
 QY 1284 ATCAGTATCGTGTGTGATGCTGCTTCCAGTACAAAGGATTTCTTTTTCAGCCGTGGA 1343
 DB 421 IleSerIleLeuArgValAspAlaPheGlnTyrLysGlyPhePhePheSerArgGly 440
 QY 1344 TCAAGCAATTTGAATCAACATTAAGCAAGATATATCCGCAATCATGAGAACTAAT 1403
 DB 441 SerLysGlnPheGluTyrAsnIleLysThrLysAsnIleThrArgIleMetArgThrAsn 460
 QY 1404 ACTTGGTTTCAATGCAAGAACCAAGAACTCTCATTTGTTTGAATCAACAAAGAA 1463
 DB 461 ThrTrpPheGlnCysLysGluProLysAsnSerSerPheGlyPheAspIleAsnLysGlu 480
 QY 1464 AAAGCAGATTCAGAGGATTAAGATATTTGATATCATAAGATTTAAGCTTTGTTATTTT 1523
 DB 481 LysAlaHisSerGlyGlyIleLysIleLeuTyrHisLysSerLeuSerLeuPheIlePhe 500
 QY 1524 GGTATGTTTCAATTTGCTGCAAAACACTCTCTATTTATCAA 1562
 DB 501 GlyIleValHisLeuLeuLysAsnThrSerIleTyrGln 513
 RESULT 3
 Q9H306 PRELIMINARY; PRT; 513 AA.
 AC Q9H306;
 DT 01-MAR-2001 (TrEMBLrel. 16, Created)
 DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
 DE Matrix metalloprotease MMP-27.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Benoit de Colnag A., Elson G., Magistrelli G., Jeannin P.,
 RA Delneste Y., Aubry J.P., Berthier O., Bonnefoy J.Y., Gauchat J.F.;
 RL Submitted (OCT-1999) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AF195192; AAG28453.1; -.
 DR HSSP; P08254; 1HY7.
 DR MEROPS; M10.027; -.
 DR Genew; HGNC:14250; MMP27.
 DR GO; GO:0005578; C:extracellular matrix; IEA.
 DR GO; GO:0004222; F:metalloendopeptidase activity; IEA.
 DR GO; GO:0006508; P:proteolysis and peptidolysis; IEA.
 DR InterPro; IPR000585; Hemopexin.
 DR InterPro; IPR006026; Peptidase M.
 DR InterPro; IPR001818; Pept_M10A_M12B.

DR InterPro; IPR006025; Pept M Zn Bs.
 DR InterPro; IPR009070; PGBD_like.
 DR Pfam; PF00045; Hemopexin; 4.
 DR Pfam; PF00413; Peptidase M10; 1.
 DR Pfam; PF03933; Peptidase M10_N; 1.
 DR PRINTS; PR00138; MATRIXIN.
 DR SMART; SM00120; HX; 4.
 DR SMART; SM00235; ZnMc; 1.
 DR PROSITE; PS00546; CYSTEINE SWITCH; 1.
 DR PROSITE; PS00024; HEMOPEXIN; 1.
 DR PROSITE; PS00142; ZINC PROTEASE; UNKNOWN_1.
 KW Metalloprotease; Protease.
 SQ SEQUENCE 513 AA; 59023 MW; ED3C9B175C014683 CRC64;

Alignment Scores:
 Pred. No.: 6,74e-234 Length: 513
 Score: 2731.00 Matches: 508
 Percent Similarity: 99.42% Conservative: 2
 Best Local Similarity: 99.03% Mismatches: 3
 Query Match: 93.21% Indels: 0
 DB: 2 Gaps: 0

US-10-729-807-28 (1-1627) x Q9H306 (1-513)

QY 24 ATGAAGCGCTCTGCTTCTGTGTTCTTTTATACATTTCTTCTGCAATTCCTCTTA 83
 DB 1 MetLysArgLeuLeuLeuLeuPheLeuPhePheLeuThrPheSerSerAlaPheProLeu 20
 QY 84 GTCGGATGACGGAATAAGAAATATCAACTGGCTCAGGCATATCTCAACCACTTC 143
 DB 21 ValArgMetMetGluAsnGluGluAsnValGlnLeuAlaGlnAlaTyrLeuAsnGlnPhe 40
 QY 144 TACTCTCTCAATAGAGGATCATCTTGTTCGAAGCAAGATAGGATCTCATAGAT 203
 DB 41 TyrSerLeuGluLeuGluGlyAsnHisLeuValGlnSerLysAsnArgSerLeuLeuLeuAsp 60
 QY 204 GACAAATTCGGAAATCGAAGCATTTTTCGATTGACAGTGTGAGAACTGGACTCA 263
 DB 61 AspLysLeuArgGluMetGlnAlaPhePheGlyLeuThrValThrGlyLysLeuAspSer 80
 QY 264 AACACCTTCAGATCATGAGACACCCAGGTGTGGGTGCTGATGGCCAGATGGC 323
 DB 81 AsnThrLeuGluLeuMetLysThrProArgCysGlyValProAspValGlyGlnTyrGly 100
 QY 324 TACACCTCCCTCGGTGGAGAAATCAACTCCTACAGATTAATAACTATCTCCG 383
 DB 101 TyrThrLeuProGlyTyrPheGlyTyrAsnLeuThrTyrArgLeuLeuLeuLeuLeuLeuLeu 120
 QY 384 GATATGCGCAGCTGCTGTGATGAGCTATCCAGAAGGTTTAGAAGTGTGGAGCAAA 443
 DB 121 AspMetAlaArgAlaAlaValAspGluAlaIleGlnGluGlyLeuGluValTyrSerLys 140
 QY 444 GTCACCTCAATAAATTCACAAAGATTCAAAGGGATTCAGACATCATGATGGCTTT 503
 DB 141 ValThrProLysLysPheThrLysIleSerLysGlyIleAlaAspIleMetIleAlaPhe 160
 QY 504 AGGACTCGATCCATGCTCGGTGTCCTGCTATTTGATGTCCTGGGAGTGGTGGC 563
 DB 161 ArgThrArgValHisGlyArgCysProArgTyrPheAspGlyProLeuGlyValLeuGly 180
 QY 564 CATGCTCTTCTCTGCTCGGGTCTGGGTGGTGCACACTCATTTTGTAGAGGATGAAAC 623
 DB 181 HisAlaPheProGlyProGlyLeuGlyGlyAspThrHisPheAspGluAspGluAsn 200
 QY 624 TGGACCAAGATGAGCAGGATTCACATGTTTCTGTGGCTGCTCATGATTTGGTCAT 683
 DB 201 TrpThrLysAspGlyAlaGlyPheAsnLeuPheLeuValAlaAlaHisGluPheGlyHis 220
 QY 684 GCATGGGGCTCTCTCACTCAATGATCAACAGCCTTGATGTTCCCAAAATATGTCCTC 743
 DB 221 AlaLeuGlyLeuSerHisSerAsnAspGlnThrAlaLeuMetPheProAsnTyrValSer 240
 QY 744 CTGGATCCCAAGAAATACCCACTTCTTCAGGATGATATCAATGAATCCAGTCCATCTAT 803

DB 241 LeuAspProArgLysTyrProLeuSerGlnAspAspIleAsnGlyIleGlnSerIleTyr 260
 QY 804 GGAGGTCTGCTTAAGTACTGCTTAAGCCAAAGAACCCACTATACCCCATGCTGTGAC 863
 DB 261 GlyGlyLeuProLysGluProAlaLysProLysGluProThrIleProHisAlaCysAsp 280
 QY 864 CCTGACTGCTACTTTTTCAGCGCTATCAAACTTTCCGAGAGAGATTAATGTTCTTTAAAGGC 923
 DB 281 ProAspLeuThrPheAspAlaIleThrThrPheArgArgGluValMetPhePheLysGly 300
 QY 924 AGGCACCTATGGAGGATCTATTATGATATCACCGATGTTGAGTTGAATTAATGCTTCA 983
 DB 301 ArgHisLeuTrpArgIleTyrTyrAspIleThrAspValGluPheGluLeuLeuAlaSer 320
 QY 984 TTCTGGCATCTCTGCCAGCTGATCTGCAAGCTGCATACAGAACCCAGAGATTAAGATT 1043
 DB 321 PheTrpProSerLeuProAlaAspLeuGlnAlaAlaTyrGluAsnProArgAspLysIle 340
 QY 1044 CTGGTTTAAAGATGAAAACTTCTGATGATCAGAGGATATGCTGCTTTCGCCAGATTAT 1103
 DB 341 LeuValPheLysAspGluAsnPheTrpMetIleArgGlyTyrAlaValLeuProAspTyr 360
 QY 1104 CCATAATCCATCCATCATATTAGTTCAGGACGTGTGAAGAAATAGATGAGCGCTC 1163
 DB 361 ProLysSerIleHisThrLeuGlyPheProGlyArgValLysLysIleAspAlaAlaVal 380
 QY 1164 TGTGATAAGACCCACAGAAAACCTACTTCTTGTGGCATTTGCTGCGAGGTTTGAT 1223
 DB 381 CysAspLysThrThrArgLysThrTyrPhePheValGlyIleTyrCysThrPheAsp 400
 QY 1224 GAAATCACCACCAACCATGGAAGGATTCGCCAGAGAGTGTGAAGAACTTTCCTGGA 1283
 DB 401 GluMetThrGlnThrMetAspLysGlyPheProGlnArgValValLysHisPheProGly 420
 QY 1284 ATCAGTATCCGTGTTGATGCTGCTTCCAGTACAAAGGATCTCTTTTTCAGCCGTGGA 1343
 DB 421 IleSerIleArgValAspAlaAlaPheGlnTyrLysGlyPhePhePheSerArgGly 440
 QY 1344 TCAAGCAATTTCAATACATTAACATTAAGCAAGATATTAACCAATCATGAGAACTAAT 1403
 DB 441 SerLysGlnPheGluTyrAspIleLysThrLysAsnIleThrArgIleMetArgThrAsn 460
 QY 1404 ACTTGGTTTCAATGCAAGAAACCAAGAACTCTCATTTGCTTTTGCATCAACAGGAA 1463
 DB 461 ThrTrpPheGlnCysLysGluProLysAsnSerSerPheGlyPheAspIleAsnLysGlu 480
 QY 1464 AAAGCACTTCAGAGGCATAAAGATTTGATCATTAAGGTTTAAAGCTTGTATTATTTT 1523
 DB 481 LysAlaHisSerGlyGlyIleLysIleLeuTyrHisLysSerLeuSerLeuPheIlePhe 500
 QY 1524 GSTATTGTTTCATTTGCTGAAAACACTTCTATTATCA 1562
 DB 501 GlyIleValHisLeuLeuLysAsnThrSerIleTyrGln 513

RESULT 4
 Q9GKE1 PRELIMINARY; PRT; 512 AA.
 ID Q9GKE1
 AC Q9GKE1 (TrEMBLrel. 16, Created)
 DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
 DT 01-MAR-2001 (TrEMBLrel. 26, Last annotation update)
 DE Matrix metalloproteinase-27.
 OS Tupia glis belangeri (Common tree shrew).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Scandentia; Tupaiidae; Tupai.
 OX NCBI_TaxID=37347;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Sciera;
 RA Guggenheim J.A., To C.H., Frost M.R.;
 RL Submitted (JUN-2000) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AF281673; AAC44844.1; -.

Db	201	TrpThrLysAspThrAlaGlyPheSerLeuPheLeuValAlaAlaHisGluPheGlyHis	220
QY	684	GCACCTGGGGCTCTCTCACTCCAAATGATCAAAACAGCCTTGATGTTCACAAATATGATGTCTCC	743
Db	221	AlaLeuGlyLeuSerHisSerAsnAspGlnThrAlaLeuMetPheProAsnIyrValSer	240
QY	744	CTGGATCCCAGAAAATACCCACTTTCTCAGGATGATATCAATGAAGATCCAGTCCATCTAT	803
Db	241	LeuAspProSerLysIyrProLeuSerGlnAspAspIleAspGlyIleGlnSerIleIyr	260
QY	804	GGAGGTCTGCTTAAGTACCTGCTAAAGCCAAAGAAACCCACTATACCCCATGCTGTGAC	863
Db	261	GlyGlyLeuProThrProSerLysProLysGlyProLysIleProHisAlaCysAsp	280
QY	864	CCTGACTTGACTTTTGACGCTATCACAACTTTCGCGAGAGAAGTAATGTTCTTTTAAAGGC	923
Db	281	ProAspLeuThrPheAspAlaIleThrAsnIleArgArgGluValMetPhePheLysGly	300
QY	924	AGGCACCTATGAGGATCTATATGATATCACCGATGTTGAGTTTGAATTAATGCTTCA	983
Db	301	ArgHisLeuTyrAspGlyIleIyrHisAspIleThrAspValGluPheGluLeuIleAlaSer	320
QY	984	TTCTGCGCATCTCTGCGACGTGATCTGCAAGCTGCATACGAGACCCAGAGATAAGATT	1043
Db	321	PheTrpProSerLeuProAlaAspLeuGlnAlaAlaIyrGluAsnProArgAspLysIle	340
QY	1044	CTGGTTTTTAAAGATGAATACTCTGATGATCAGAGATATGCTGCTGCCAGATTAT	1103
Db	341	LeuValPheLysAspGluAsnPheTrpMetIleGlyAlaIyrAsnValLeuProArgTyr	360
QY	1104	CCCAAAATCCATCCATACATTAGGTTTTCCAGGACGTGTGAAGAAAAATAGATGACGCGCTC	1163
Db	361	ProArgSerIleHisIleLeuGlyPheProArgTyrValLysLysIleAspAlaAlaVal	380
QY	1164	TGTGATTAAGACCACAAAGAAAACCTACTCTTCTGTGGCATTTGGTCTCGAGGTTTGAT	1223
Db	381	CysAspGlnAspThrArgLysThrTyrPhePheValGlyIleIyrCysTrpArgTyrAsp	400
QY	1224	GAATGACCCAAACCATGCGCAAAAGGATTCGCGCAGAGAGTGTGAACAACTTTTCCTGGA	1283
Db	401	GluMetThrArgThrMetAspArgGlyIyrProGlnArgIleValArgHisPheProGly	420
QY	1284	ATCAGTATCCGTGTGTGCTGCTTTCCAGTACAAAGGATTTCTTTTTCAGCCGCTGGA	1343
Db	421	IleGlyLeuArgValAspAlaAlaPheGlnHisLysGlyPhePheTyrPhePheArgGly	440
QY	1344	TCAAGCAATTTGNATACACATTAACAGAAAGATATTACCGAATCATGAGAGACTAAT	1403
Db	441	SerLysGlnPheGluTyrAspIleLysAlaLysSerIleThrArgIleMetArgThrAsn	460
QY	1404	ACTTGGTTTCAATGCAAAAGAACCAAGAACTCCCTCAATTTGGTTTGATATCAACAAGAA	1463
Db	461	ThrTrpPheGlnCysLysGluProLeuAsnSerSerLeuAspPheHisPheAsnGlnGlu	480
QY	1464	AAAGCAATTCAGGAGGCATAAAGATATTGATCATAGAGTTTAAAGCTTTGTTATTTT	1523
Db	481	LysAlaIyrSerGlyGluValGluThrLeuHisGlnSerLeuSerLeuLeuIlePhe	500
QY	1524	GGTATTGTTTCAATTCGTGAAAAACACTTCTATTAT	1559
Db	501	GlyIleValHisLeuLeuAsnLysIleCysSerTyr	512
RESULT 5			
QY	093342	PRELIMINARY;	PRT; 472 AA.
AC	093342;		
DT	01-NOV-1998 (TrEMBLrel. 08, Created)		
DT	01-NOV-1998 (TrEMBLrel. 08, Last sequence update)		
DT	01-MAR-2004 (TrEMBLrel. 26, Last annotation update)		
DE	Matrix metalloproteinase.		
OS	Gallus gallus (Chicken).		
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
OC	Archosauria; Aves; Neornathae; Galliformes; Phasianidae; Phasianinae;		

167	GlyThrLysAlaHisGlyHisCysProArgTyrPheAspGlyProLeuGlyValLeuAla	186
564	CATGCTTTCTCTCGTCCGGTCTGGGTGTGTGACACTCATTTTGTATGAGTGAATAAC	623
187	HisAlaPheProGlySerGlyPheGlyGlyAspValHisPheAspGluAspGluAsp	206
624	TGGACCAAGGATGGACAGGATTCACTTGTCTTCTGTGTGCTGCTCATGAATTTGTCAT	683
207	TrpThrMetGlySerAspGlyPheAsnLeuPheLeuValAlaAlaHisGluValGlyHis	226
684	GCATGGGGCTCTCTACATCCCAATGATCAAAACAGCCCTTGATGTTCCTCAATATGCTCC	743
227	AlaLeuGlyLeuSerHisProAsnAspGlnArgAlaPheMetPheProAsnTyrAlaTyr	246
744	CTGGATCCCAAGAAATACCCACTTTCTCAGGATGATATCAATGGGAATCCAGTCCATCTAT	803
247	IleSerProSerGluPheProLeuSerProAspPheSerGlyIleGlnSerIleTyr	266
804	GGAGGTCTGCCTAAGTACTCTGCTAAG---CCAAAGGAACCCACTATACCCCATGCTGT	860
267	GlySerAlaThrLysThrProGlyLysArgProThrValProThrSerProAsnThrCys	286
861	GACCTGACTGACTTTTGACCGTATCAACAATCTCCGACAGAGAAGTAATGTTCTTTAA	920
287	GlyProGlnIleSerPheAspAlaValThrThrLeuArgArgGluValIlePheLeuLys	306
921	GCACGCACTATGGAGGATCTATTATGATATACCGGATGTTGAGTTTCAATTAATGCT	980
307	GlyArgHisLeuTrpArgValTyrProAsnSerGluValGluLeuGluLeuIleSer	326
981	TCATTTGGCCATCTCTGCCAGTGTCTGCAAGTCGATACGAGACACCCAGAGATAAG	1040
327	AlaPheTrpProPheLeuProSerGlyIleGlnAlaAlaTyrGluAsnMetLysAspArg	346
1041	ATTCTGTTTAAAGATCAAAACTTCTGGATCATCAGAGGATATGCTGCTTGCAGAT	1100
347	IleLeuPhePheLysGlyAsnAsnPheTrpValSerGlyTyrLysValLeuLeuGly	366
1101	TATCCAAATCCATCCATACATTAGGTGTTTCCAGGACGTGTGAAGAAAATAGATGAGCC	1160
367	TyrProLysAsnIleAsnThrLeuGlyPheProLysGlyValLysLysIleAspAlaAla	386
1161	GTCTGTGATAGACACACAGAAAACCTACTTCTTGTGGGCATTTGGTGCTGGAGTTT	1220
387	ValCysAsnLysAsnThrGlyLysThrAspPheValGlyAspLysTyrTrpArgTyr	406
1221	GATGAATCACCACCAACCATGACAAAGATTCCCCACAGAGTGTGTAACACTTTCCT	1280
407	AspGluSerThrGlnSerMetGluLysGlyTyrProArgArgThrValAsnAspPhePro	426
1281	GGAATCAGTATCCGTGTTGATGCTGTTCCAGTACAAAGGATCTTCTTTTTCACCCGT	1340
427	GlyIleSerGlnArgIleAspAlaValPheGlnHisLysGlyLeuPheTyrPheHis	446
1341	GGATCAAGCAATTTCAATACACATTAAAGACAAAGAATATTACCCGAATCATGGAAC	1400
447	GlySerArgGlnLeuLysPheAspProThrAlaLysArgValIleSerGluIleLysSer	466
1401	AATACTTGGTTTCAATGC	1418
467	AsnSerTrpPheAsnCys	472
RESULT 6		
Q6V4Q5	PRELIMINARY;	Q6V4Q5
ID	Q6V4Q5	PRT; 478 AA.
AC	Q6V4Q5;	
DT	05-JUL-2004 (TrEMBLrel. 27, Created)	
DT	05-JUL-2004 (TrEMBLrel. 27, Last sequence update)	
DT	05-JUL-2004 (TrEMBLrel. 27, Last annotation update)	
DE	Stromelysin 1.	
GN	Name=WMF3;	
OS	Canis familiaris (Dog).	

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.
 OX NCBI_TaxID=9615;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Sarcoma;
 RA Sorensen K.C., Balkin R.G., Kticheil B.E., Siegel A.M., Schaeffer D.,
 RL Submitted (NOV-2002) to the EMBL/GenBank/DBJ databases.
 DR EMBL: AV183143; AA063580.1; -
 DR InterPro: IPR000585; Hemopexin.
 DR InterPro: IPR006026; Peptidase M.
 DR InterPro: IPR001818; Pept M10A M12B.
 DR InterPro: IPR006025; Pept M Zn_BS.
 DR Pfam: PF00045; Hemopexin; 4
 DR Pfam: PF00413; Peptidase M10; 1.
 DR Pfam: PF03933; Peptidase M10_N; 1.
 DR PRINTS: PR00130; MATRIXIN.
 DR SMART: SM00120; HX; 4.
 DR SMART: SM00235; ZmC; 1.
 DR PROSITE: PS00546; CYSTEINE SWITCH; 1.
 DR PROSITE: PS00024; HEMOPEXIN; 1.
 DR PROSITE: PS00142; ZINC PROTEASE; UNKNOWN 1.
 SQ SEQUENCE 478 AA; 53633 MW; 5D1B9DA9D57BC041 CRC64;
 Alignment Scores:
 Pred. No.: 2,62e-105 Length: 478
 Score: 1286.50 Matches: 254
 Percent Similarity: 67.29% Conservative: 69
 Best Local Similarity: 52.92% Mismatches: 140
 Query Match: 43.91% Indels: 17
 DB: 2 Gaps: 8
 US-10-729-807-28 (1-1627) x Q6Y4Q5 (1-478)
 QY 24 ATGAGCGCTTCTGCTTCTGTTGTTCTTTTAAACATTTCTTCTGATTTCCCTTA 83
 Db 1 MetGlnAsnLeuProAlaLeuLeuLeuPheCysGlyValValCysSerAlaTyrProVal 20
 QY 84 GTCGGATGACGGAATGAA---GAAATATGCAACTGCTGCTCAGCATATCTCAACCAG 140
 Db 21 AspArgAlaAlaGluAspGluAsnAsnMetGluLeuThrGlnGlnTyrLeuGluAsn 40
 QY 141 TTCTACTCTCTGAAATAGAGGAATCATCTGTTCAAAGCAAGATAGGAGTCTCAT 200
 Db 41 TyrTyrAsnLeuGlyLysAspValLysProPheValArgArgAsnSerGlyProVal 60
 QY 201 GATGCAAAATTCGGAAATGCAAGCATTTTGGATTGACAGTGTGCAAAATCGGAC 260
 Db 61 ValGluLysIleArgGluMetGlnLysPheLeuGluValThrGlyLysValAsp 80
 QY 261 TCAACACCCCTTGAGATCATGAGACACCCAGGTGTGGGTGCTGATGCGCCAGTAT 320
 Db 81 SerAspThrLeuAlaMetMetArgProArgProArgCysGlyValProAspValGlyAspPhe 100
 QY 321 GGCTACCCCTCCCTGGG-----TGGAGAAATACAACTCACCTACAGAAATAA 371
 Db 101 ---ThrThrPheProGlyMetProLysTyrArgLysThrHisLeuThrTyrArgIleMet 119
 QY 372 AACTATATCCGGATATGCGACGAGCTGTGTGATGAGCTATCCAGAAAGTTTAGAA 431
 Db 120 AsnTyrThrProAspLeuProArgAspAlaValAspSerAlaIleGluLysAlaLeuAsn 139
 QY 432 GTGTGAGCAAGTCACTCACTAAATTCACCAAGATTTCAGGGGATTCGACGACATC 491
 Db 140 ValTrpLysGluValThrProLeuThrPheSerArgThrAspGlyGluAlaAspIle 159
 QY 492 ATGATTCCTTTAGGACTCGAGTCCATGCTGCTGCTGCTGCTGCTGCTGCTGCTG 551
 Db 160 LysIleSerPheAlaValArgAspHisGlyAspPhe---AsnProPheAspGlyProGly 178
 QY 552 GGAGTGTGGCAGCCCTTCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 611
 Db 179 AsnValLeuGlyHisAlaTyrProProGlyProGlyIleTyrGlyAspAlaHisPheAsp 198

QY 612 GAGGATGAAACTGGACCAAGGATGAGCAGGAGATTCAACTGTTTCTTGTGGTGTCTCAT 671
 Db 199 AspAspGluGlnTrpThrSerAspThrSerGlyThrAsnLeuPheLeuValAlaHis 218
 QY 672 GAATTTGGTTCATGCACTGGGGTCTCTCACTCCAATGATCAAAACAGCCTTGATGTTCCCA 731
 Db 219 GluLeuGlyHisSerLeuGlyLeuPheHisSerAlaAspProSerAlaLeuMetTyrPro 238
 QY 732 AATTAT---GTCTCCCTGGATCCAGAAATATCCCACTTTCTCAGGATGATATCAATGGA 788
 Db 239 ValTyrAsnValLeuAlaAspLeuAlaArgPheHisLeuSerGlnAspValAsnGly 258
 QY 789 ATCCAGTCCATCTATGAGGTCTGCTCAAG-----GTACCTGCT 827
 Db 259 IleGlnSerLeuTyrGlyGlyProSerAspSerSerAsnAspProValValProThr 278
 QY 828 AAG-----CCAAAGGAACCACTATATACCCCATGCTGTGACCTGACTTGTGAC 881
 Db 279 GluSerValProGlyProGlyThrProAlaAlaCysAspProThrLeuSerPheAsp 298
 QY 882 GCTATCACAACCTTCGCGAGAGAAGTAATGTTTAAAGCGCAGGACCTATGAGGATC 941
 Db 299 AlaIleSerThrLeuArgGlyGluPheLeuPhePheLysAspArgHisPheTyrAspLys 318
 QY 942 TATTATGATATCACCGATGTTGAGTTTGAATTAATGTTCTTCTGCGCATCTCTGCCA 1001
 Db 319 SerLeuArgThrLeuGluProGlyPheTyrLeuLeuSerSerPheTyrProSerLeuPro 338
 QY 1002 GCTGATCTCAAGCTGCATAC---GAGAACCCAGAGATTAAGATTCTGTTTAAAGAT 1058
 Db 339 SerGlyLeuAspAlaAlaTyrGluThrSerLysAspIleValPheIlePheLysGly 358
 QY 1059 GAAACTTCTGATGATCAGAGATATGCTGTTTCCAGATTTATCCAAATCCATCCAT 1118
 Db 359 AsnGlnPheTyrPheAlaMetArgGlyThrGluValGlnAlaGlyTyrProLysGlyIleHis 378
 QY 1119 ACATTAAGTTCCTCAGGAGCTGTGAGAAATAGATGACGCGCTGTGTATAGACCACA 1178
 Db 379 ThrLeuGlyPheProProThrValLysLysIleAspAlaAlaValPheAspLysGluLys 398
 QY 1179 AGAAACCTACTCTTCTTGTGGCATTTGCTGCTGAGGTTTGTGTAATGACCCAAACC 1238
 Db 399 LysLysThrTyrPhePheValGlyAspLysTyrTyrPheAspGluLysArgGlnSer 418
 QY 1239 ATGCAAAAGGATTCGCGAGAGTGGTAAACACTTTCTCGAATCAGTATCCGTGTT 1298
 Db 419 MetGluProGlyPheProLysGlnIleAlaGluAspPheProGlyValAspSerLysVal 438
 QY 1299 GATGCTGCTTCCAGTACAAAGGATTTCTTTTTCAGCGGTGGATCAAGCAATTTGAA 1358
 Db 439 AspAlaAlaPheGluAlaPheGlyPheTyrTyrPhePheAsnGlySerGlnLeuGlu 458
 QY 1359 TACAACATTAAAGCAAGAAATATTATCCCGAATCATGAGAACTAATCTGTTTCAATGC 1418
 Db 459 PheAspProAsnAlaLysLysValThrHisValLeuLysSerAsnSerTrpLeuAsnCys 478
 RESULT 7
 ID AA063580 PRELIMINARY; PRT; 478 AA.
 AC AA063580;
 DT 02-MAR-2004 (TrEMBLrel. 27, Created)
 DT 02-MAR-2004 (TrEMBLrel. 27, Last sequence update)
 DT 02-MAR-2004 (TrEMBLrel. 27, Last annotation update)
 DE Stromelysin 1.
 GN MMP3.
 OS Canis familiaris (Dog).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.
 OX NCBI_TaxID=9615;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Sarcoma;

RA Sorensen K.C., Balkin R.G., Kitchell B.E., Siegel A.M., Schaeffer D.;
RT "Isolation, Characterization and Expression of Stromelysin-1 (MMP3) in
RT Canine Tumors";
RL Submitted (NOV-2002) to the EMBL/GenBank/DBDJ databases.
DR EMBL; AY183143; AAC63580.1; --
SQ SEQUENCE 478 AA; 53633 MW; 5D1B9DA9D57BC041 CRC64;

Alignment Scores:	2.62e-105	Length:	478
Pred. No.:	Score:	Matches:	254
	1286.50	Conservative:	69
Percent Similarity:	67.29%	Mismatches:	140
Best Local Similarity:	52.92%	Indels:	17
Query Match:	43.91%	Gaps:	8
DB:	2		

US-10-729-807-28 (1-1627) x AAO63580 (1-478)

Qy	24	ATGAAGCGCCCTTCGCTCTCTGTGGTTGTGTTCTTTATAACATTTTCTTCGCATTTCCCTTTA	83
Db	1	MetGlnAsnLeuProAlaLeuLeuLeuPheCysGlyValValCysSerAlaTyrProVal	20
Qy	84	GTCCGGATGACGGAAAAATGAA---GAAATATGCAACTGGCTCAGCGCATATCTCAACACG	140
Db	21	AspArgAlaAlaGluAspGluAsnAsnMetGluLeuThrGlnGlnTyrLeuGluAsn	40
Qy	141	TTCTACTCTCTTGAATAGAGGGGAATCATCTGTTTCAAAGCAAGAAATAGGAGTCTCAT	200
Db	41	TyrTyrAsnLeuGlyAspValIysPropheValArgArgAsnSerGlyProVal	60
Qy	201	GATGACAAAATTCGGAAATGCAAGCATTTTGTGATTGACAGTCACTCGGAAAACTGGAC	260
Db	61	ValGluIysIleArgGluMetGlnIysPheLeuGlyLeuGluValThrGlyIysValAsp	80
Qy	261	TCAAACACCCCTTGACATCATGAAGACACCCAGGTGTGGGTCCCTGATGTGGCCAGTAT	320
Db	81	SerAspThrLeuAlaMetMetArgProArgCysGlyValProAspValGlyAspPhe	100
Qy	321	GGCTACACCCCTCCCTGGG-----TGGAGAAAATACAACCTCACCTACAGAATAATA	371
Db	101	--ThrThrPheProGlyMetProIysTrpArgLysThrHisLeuThrTyrArgIleMet	119
Qy	372	AACATATCTCCGGATATGGCAGACGCTGCTGGGATGAGGCTATCCAAGAGTTTGA	431
Db	120	AsnTyrThrProAspLeuProArgAspAlaValAspSerAlaIleGluIysAlaLeuAsn	139
Qy	432	GTGTGGAGCAAAAGTCACATCCATCAAAATTCACCAAGATTCAAAGGGGATTCGACACATC	491
Db	140	ValTrpLysGluValThrProLeuThrPheSerArgThrAspGluGlyGluAlaAspIle	159
Qy	492	ATGATTGGCTTTAGGACTGATCGATGGTCCGGTGTCCCTCGCTATTTTGATGGTCCCTG	551
Db	160	LysIleSerPheAlaValArgAspHisGlyAspPhe---AsnProPheAspGlyProGly	178
Qy	552	GGAGTGTCTGGCATGCCCTTCTCCTGTCTCGGTCTCGGGTGTGCACACTCATTTTGAT	611
Db	179	AsnValLeuGlyHisAlaTyrProGlyProGlyIleTyrGlyAspAlaHisPheAsp	198
Qy	612	GAGGATGAAACTGGACCAAGGATGAGCAGGATCAACTGCTTTCTTGTGCTGCTCAT	671
Db	199	AspAspGluGlnTrpThrSerAspThrSerGlyThrAsnLeuPheLeuValAlaAlaHis	218
Qy	672	GAATTTGGTCATGCATGGGGTCTCTCACTCCAATGATCAACAGCCTTGATGTTCCCA	731
Db	219	GluLeuGlyHisSerLeuGlyLeuPheHisSerAlaAspProSerAlaLeuMetTyrPro	238
Qy	732	AATTAT---GTCTCCTCGATCCCGAAATATCCCAATTTCTTCAGGATGATATCAATGA	788
Db	239	ValTyrAsnValLeuAlaAspLeuAlaArgPheHisLeuSerGlnAspAspValAsnGly	258
Qy	789	ATCCAGTCCATCTATGGAGGTCTGCGCTAAG-----GTACCTGCT	827
Db	259	IleGlnSerLeuTyrGlyGlyProSerAspSerSerAsnAspProValValProThr	278

QY	828	AAG-----CCAAAGGAACCCATACATACCCCATGCTGTGACCTGACTTTGACTTTTGAC	881
Db	279	GluservValProProGlyProGlyThrProAlaAlaCysaspProThrLeuSerPheasp	298
QY	882	GCTATCACAACTTTCCGCAGAGAAGTAATGTTCTTTAAAGCGAGGCACCTATGGAGGATC	941
Db	299	AlaIleSerThrLeuArgGlyGluPheLeuPhePheLysaspArgHisPheTrpArgLys	318
QY	942	TATTATGATATCAGGATGTTTGAGTTTGAATTAATTCCTTCATCTGGCCCATCTCTGCCA	1001
Db	319	SerLeuArgThrLeuGluProGlyPheTyLeuIleSerSerPheTrpProSerLeuPro	338
QY	1002	GCTGATCTGCAAGCTGCATAC---GAGAACCCAGCAGATAGAATTCGTGTTTAAAGAT	1058
Db	339	SerGlyLeuAspAlaAlaTyThrGluThrSerLysaspIleValPheIlePheLysGly	358
QY	1059	GAATACTTCGGATGATCAGAGATATGCTGCTTGGCAGATTTATCCCAATCATTCAT	1118
Db	359	AsnGlnPheTrpAlaMetArgGlyThrGluValGlnAlaGlyTyProLysGlyIleHis	378
QY	1119	ACATTAGTGTTCACGAGACGCTGTGAAGAAATATAGATCACCGCTCTGTATAGAACCA	1178
Db	379	ThrLeuGlyPheProProThrValLysIleAspAlaAlaValPheAspLysGluLys	398
QY	1179	AGAAAAACCTACTTCTTTGTGGGCATTGCTGTGGAGGTTTGATGAAATGACCCAAACC	1238
Db	399	LysLysThrTyThrPheValGlyAspLysTyTrpArgPheaspGluLysArgGlnSer	418
QY	1239	ATGCAAAAGGATCCCGCAGAGAGTGTAACACACTTCTCTGGAATCAGTATCCGTGTT	1298
Db	419	MetGluProGlyPheProLysGlnIleAlaGluaspPheProGlyValaspSerLysVal	438
QY	1299	GATGCTGCTTCCAGTACAAAGGATCTCTCTTTTCAGCCGTGGATCAAAAGCAATTTCAA	1358
Db	439	AspAlaAlaPheGluAlaPheGlyPheTyTyTrpPheAsnGlySerSerGlnLeuGlu	458
QY	1359	TACAACATTAAAGACAAAGAATATPACCCGAATCATGAGAACTAATCTTGTTTCAATGC	1418
Db	459	PheAspProAsnAlaLysLysValThrHisValLeuLysSerAsnSerTrpLeuAsnCys	478
RESULT 8			
MM03	RABIT	STANDARD;	PRT; 478 AA.
ID	MM03	RABIT	
AC	P28863;		
DT	01-DEC-1992 (Rel. 24, Created)		
DT	01-DEC-1992 (Rel. 24, Last sequence update)		
DT	05-JUL-2004 (Rel. 44, Last annotation update)		
DE	Stromelysin-1 precursor (EC 3.4.24.17) (Matrix metalloproteinase-3)		
DE	(MMP-3) (Transin-1) (SL-1).		
GN	Name=MMP3;		
OS	Oryctolagus cuniculus (Rabbit).		
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
OC	Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.		
OX	NCBI_TaxID=9986;		
RN	[1]		
RP	SEQUENCE FROM N.A.		
RX	MEDLINE=88077214; PubMed=2825726;		
RA	Finl M.E., Karmaliowicz M.J., Ruby P.L., Beeman A.M., Borges K.A.,		
RA	Brinckerhoff C.E.;		
RT	"Cloning of a complementary DNA for rabbit proactivator. A		
RT	metalloproteinase that activates synovial cell collagenase, shares		
RT	homology with stromelysin and transin, and is coordinately regulated		
RT	with collagenase.";		
RL	Arthritis Rheum. 30:1254-1264 (1987).		
RN	[2]		
RP	SEQUENCE OF 1-167 FROM N.A.		
RX	MEDLINE=87156645; PubMed=3030290;		
RA	Whitham S.E., Murphy G., Angel P., Rahmedorf H.J., Smith B., Lyons A.,		
RA	Harris T.R., Reynolds J.J., Herrlich P., Docherty A.J.P.;		
RT	"Comparison of human stromelysin and collagenase by cloning and		
RT	sequence analysis.";		
RL	Biochem. J. 240:913-916 (1986).		
CC	!- FUNCTION: Can degrade fibrinectin, laminin, gelatins of type I,		

CC	III, IV, and V; collagens III, IV, X, and IX, and cartilage proteoglycans. Activates procollagenase.
CC	-1- CATALYTIC ACTIVITY: Preferential cleavage where P1', P2' and P3' are hydrophobic residues.
CC	-1- COFACTOR: Binds 2 zinc ions and 4 calcium ions per subunit (By similarity).
CC	-1- SIMILARITY: Belongs to peptidase family M10A.
CC	-1- SIMILARITY: Contains 1 hemopexin-like domain.
CC	-----
CC	This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/ or send an email to license@sb-sib.ch).
CC	-----
DR	EMBL; M25664; AAA31467.1; --
DR	PIR; A37306; KCRBS1.
DR	HSP; P08254; IG05.
DR	MEROPS; M10.005; --
DR	InterPro; IPR000585; Hemopexin.
DR	InterPro; IPR006026; Peptidase M.
DR	InterPro; IPR001818; Pept_M10A_M12B.
DR	InterPro; IPR006025; Pept_M_Zn_BS.
DR	InterPro; IPR009070; PGSD like.
DR	Pfam; PF00405; Hemopexin; 4.
DR	Pfam; PF03933; Peptidase M10; 1.
DR	Pfam; PF03933; Peptidase M10_N; 1.
DR	PRINTS; PR00138; MATRXIN.
DR	SMART; SM00120; HX; 4.
DR	SMART; SM00235; ZnMc; 1.
DR	PROSITE; PS00546; CYSTEINE SWITCH; 1.
DR	PROSITE; PS00024; HEMOPEXIN; 1.
DR	PROSITE; PS00142; ZINC PROTEASE; 1.
KW	Calcium-binding; Collagen degradation; Extracellular matrix;
KW	Glycoprotein; Hydrolyase; Metal-binding; Metalloprotease; Signal; Zinc;
KW	Zymogen.
FT	SIGNAL 1 17 Probable.
FT	PROPEP 18 100 Activation peptide.
FT	CHAIN 101 478 Stromelysin-1.
FT	DOMAIN 288 478 Hemopexin-like.
FT	SITE 93 93 Cysteine switch (Potential).
FT	METAL 125 125 Calcium 1 (By similarity).
FT	METAL 159 159 Calcium 2 (By similarity).
FT	METAL 169 169 Zinc 1 (By similarity).
FT	METAL 171 171 Zinc 1 (By similarity).
FT	METAL 176 176 Calcium 3 (By similarity).
FT	METAL 177 177 Calcium 3 (via carbonyl oxygen) (By similarity).
FT	METAL 179 179 Calcium 3 (via carbonyl oxygen) (By similarity).
FT	METAL 181 181 Calcium 3 (via carbonyl oxygen) (By similarity).
FT	METAL 184 184 Zinc 1 (By similarity).
FT	METAL 191 191 Calcium 2 (via carbonyl oxygen) (By similarity).
FT	METAL 193 193 Calcium 2 (via carbonyl oxygen) (By similarity).
FT	METAL 195 195 Calcium 2 (By similarity).
FT	METAL 197 197 Zinc 1 (By similarity).
FT	METAL 199 199 Calcium 3 (By similarity).
FT	METAL 200 200 Calcium 1 (By similarity).
FT	METAL 202 202 Calcium 1 and 3 (By similarity).
FT	METAL 219 219 Zinc 2 (catalytic) (By similarity).
FT	ACT_SITE 220 220 By similarity.
FT	METAL 223 223 Zinc 2 (catalytic) (By similarity).
FT	METAL 229 229 Zinc 2 (catalytic) (By similarity).
FT	METAL 298 298 Calcium 4 (via carbonyl oxygen) (By similarity).
FT	METAL 390 390 Calcium 4 (via carbonyl oxygen) (By similarity).
FT	METAL 439 439 Calcium 4 (via carbonyl oxygen) (By similarity).
FT	METAL 439 439 Calcium 4 (via carbonyl oxygen) (By similarity).

similarity).

N-linked (GlcNAc. .) (Potential).
By similarity.
N -> D (in Ref. 2).
R -> K (in Ref. 2).

CARBOHYD 121 121
FT DISULFID 291 478
FT CONFLICT 83 83
FT CONFLICT 128 128
SQ SEQUENCE 478 AA, 53942 MW, CA742E31A4549D40 CRC64;

Alignment Scores:
Pred. No.: 5,68e-104 Length: 478
Score: 1271.50 Matches: 250
Percent Similarity: 67.43% Conservative: 75
Best Local Similarity: 51.87% Mismatches: 136
Query Match: 43.40% Indels: 21
DB: 1 Gaps: 9

US-10-729-807-28 (1-1627) x MM03_RABIT (1-478)

QY 24 ATGACGGCGCTTCTGCTTCGTGGTTGTTTATAACAATTTCTCTGCATTTCCTTA 83
Db 1 MetLysThrLeuProThrLeuleuLeuLeuCysValAlaLeuCysSerAlaTyProLeu 20
QY 84 GTCCGGATCACGGAATAAGAA-----AATATGCAACTGGCTCAGGCATATCTCAAC 137
Db 21 AspGlyAlaSerArgAspAlaaspThrThrAsnMetAspLeuLeuGlnTyrLeuGlu 40
QY 138 CAGTCTACTCTCTTGAAATGAAGGAATCATCTGTGTCAAAGAAGATPAGAGTCTC 197
Db 41 AsnTyrTyrAsnLeuGluLysAspValLysGlnPheValLysArgLysAspSerSerPro 60
QY 198 AVATAGTACAAAATTCGGSAATGCAACATTTTTCGATTGACAGTCACTGGAAAACTG 257
Db 61 ValValLysLeuIleGlnGluMetGlnLysPheLeuGlyLeuGluValThrGlyLysLeu 80
QY 258 GACTCAAACACCCTTGAGATCATGAAGACACCCAGGTGTGGGTGCCGTATGGGGCAG 317
Db 81 AspSerAsnThrLeuGluValIleArgLysProArgCysGlyValProAspValGlyHis 100
QY 318 TATGCTACACCCTCCCTGGG-----TGGAGAAAATACACCTCACCTACAGATA 368
Db 101 PheSer---ThrPheProGlyThrProLysTrpThrLysThrHisLeuThrTyrArgile 119
QY 369 ATAACCTATACTCCGATATGCAGAGCTCTGTGGATGAGGCTATCCAAGAGGTTTA 428
Db 120 ValAsnTyrThrProAspLeuProArgAspAlaValAspAlaIleGluLysAlaLeu 139
QY 429 GAAGTGTGGAGCAAAAGTCACCTCACTAAAATTCACCAAGATPTCAAAGGGGATTCAGAC 488
Db 140 LysValTrpGluGluValThrProLeuThrPheSerArgLysTyrGlyGlyGluAlaAsp 159
QY 489 ATCATGATTCCTTTAGGACTCGAGTCATCGTCCG---TGTCTCTCGCTATTTTGATGT 545
Db 160 IleMetIleSerPheGlyValArgGluHisGlyAspPheIlePro-----PheAspGly 177
QY 546 CCCTTGGGAGTCTCTGGCCATCGCTTCTCCTCGTCCGGTCTGGGTGTGACACTCAT 605
Db 178 ProGlyAsnValLeuAlaHisAlaTyraAlaProGlyProGlyIleAsnGlyAspAlaHis 197
QY 606 TTGTATGAGGATGAAATCTGGACCAAGATGGACGAGATTCAACTGTTTCTTTGGCT 665
Db 198 PheAspAspGluGlnTrpThrLysAspThrThrGlyThrAsnLeuPheLeuValAla 217
QY 666 GCTCATGATTTGGTCATGCACTGGGCTCTCTCACTCCAATGATCAAAAGCAGCTTGATG 725
Db 218 AlaHisGluLeuGlyHisSerLeuGlyLeuPheHisSerAlaAsnProGluAlaLeuMet 237
QY 726 TTCCCCAATAATGTCTCCCTG---GATCCCAGAAAAATACCCACTTTTCTCAGGATGATC 782
Db 238 TyrProValTyrAsnAlaPheThrAspLeuAlaargPheArgLeuSerGlnAspAspVal 257
QY 783 AATGAATCCAGTCCATCTATGGA-----GGTCTGCCT 815
Db 258 AspGlyIleGlnSerLeuTyrGlyProAlaProAlaSerProAspAsnSerGlyValPro 277

QY 816 AAGTACCTGCTAGCCAAAGGACCCACCATATACCCCATGCTGCTGACCTGACT 875
 Db 278 MetGluProValProGlySerGlyThr---ProValMetCysAspProAspLeuSer 296
 QY 876 TTGACGCTATCAACATTTCCGAGAGAGTAGTATGTTCTTAAAGCAGCAGCCTATGG 935
 Db 297 PheAspAlaIleSerThrLeuArgGlyGluLeuPhePheLysAspAsgTyrPheTyr 316
 QY 936 AGGATCTATTATGATATACCGAGTGTGAGTTGAATTAATGCTTCATCTGCCCATCT 995
 Db 317 ArgLysSerLeuArgIleLeuGluProGluPheHisLeuIleSerSerPheTyrProSer 336
 QY 996 CTGCCACTGATCTGCAAGCTGCATAGAG---AACCCAGAGATAGATCTCGTTT 1052
 Db 337 LeuProSerAlaValAspAlaAlaTyrGluValIleSerArgAspThrValPheIlePhe 356
 QY 1053 AAAGATGAAAACTCTCGATGATCAGAGGATATGCTGCTGCGAGGTTTGAATGACC 1112
 Db 357 LysGlyThrGlnPheTyrPhePheValGluAsnGluValGlnAlaGlyTyrProArgSer 376
 QY 1113 ATCCATCATAGTATGTTTCCAGGACGTGTGAAGAAATAGATGAGCGGCTCTGTGATAAG 1172
 Db 377 IleHisThrLeuGlyPheProSerThrIleArgLysIleAspAlaAlaIleSerAspLys 396
 QY 1173 ACCACAGAAAACTCTTCTGCTGGCATTTGCTGCTGAGGTTTGAATGACC 1232
 Db 397 GluArgLysLysThrTyrPhePheValGluAspLysTyrTyrPheAspGluLysArg 416
 QY 1233 CAACACATGAGCAAGATTCGCCAGAGAGTGTGAAGAACTTCTCGGATCAGTATC 1292
 Db 417 GlnSerLeuGluProGlyPheProArgHisIleAlaGluAspPheProGlyIleAsnPro 436
 QY 1293 CGTGTGATGCTGCTTCCAGTACAAGAGATCTCTTTTCACGCCGTGAGTCAAGCAA 1352
 Db 437 LysIleAspAlaValPheGluAlaPheGlyPheTyrPhePheSerGlySerSerGln 456
 QY 1353 TTTCAATACACATTAAGACAAAGATATTACCGGAATCATGAGAACTAATCTTGGTTT 1412
 Db 457 SerGluPheAspProAsnAlaLysLysValThrHisValLeuLysSerAsnSerTyrPhe 476
 QY 1413 CAATGC 1418
 Db 477 GlnCys 478
 RESULT 9
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 AC AAH69676;
 DT 20-MAY-2004 (TrEMBLrel. 27, Created)
 DT 20-MAY-2004 (TrEMBLrel. 27, Last sequence update)
 DE Matrix metalloproteinase 3, preproprotein.
 OS MMP3.
 GN Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OC NCBI_taxid=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=PCR rescued clones;
 RX MEDLINE=22389257; PubMed=12477932;
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
 RA Klausner R.D., Collins F.S., Wagner L., Schenker C.M., Schuler G.D.,
 RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
 RA Hopkins R.F., Jordan M., Moore T., Max S.I., Wang J., Hsieh F.,
 RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
 RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
 RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
 RA Raba S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullany S.J.,
 RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
 RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
 RA Fahey J., Helton E., Kettner M., Madan A., Rodriguez S., Sanchez A.,

RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butlerfield Y.S.,
 RA Krzywinski M.I., Skalska U., Smallus D.E., Schnerch A., Schein J.E.,
 RA Jones S.J., Marra M.A.;
 RT "Generation and initial analysis of more than 15,000 full-length human
 RT and mouse cDNA sequences";
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC TISSUE=PCR rescued clones;
 RA Strausberg R.;
 RL Submitted (APR-2004) to the EMBL/GenBank/DBJ databases.
 DR EMBL; BC969676; AAH69676.1; -; 7497490A861DEBA9 CRC64;
 SQ SEQUENCE 477 AA; 53978 MW; 7497490A861DEBA9 CRC64;

Alignment Scores:
 Pred. No.: 2,05e-102 Length: 477
 Score: 1254.00 Matches: 247
 Percent Similarity: 66.04% Conservative: 70
 Best Local Similarity: 51.46% Mismatches: 145
 Query Match: 42.80% Indels: 18
 DB: 2 Gaps: 9

US-10-729-807-28 (1-1627) x AAH69676 (1-477)

QY 24 ATGAAGCGCCTCTGCTTCTGTTGTTCTTTATACATTTCTTCTGCAATTCCTTA 83
 Db 1 MetLysSerLeuProIleLeuLeuLeuCysValAlaValCysSerAlaTyrProLeu 20
 QY 84 GTCCGGATGACGGGAAATGAAGAA---AATATGCACTGGCTCAGGCATATCTCAACAG 140
 Db 21 AspGlyAlaAlaArgGlyGluAspThrSerMetAsnLeuValGlnLysTyrLeuGluAsn 40
 QY 141 TTCTACTCTCTGAAATAGAGGAATCATCTTGTTCAAAGCAAGATAGGAGTCTATA 200
 Db 41 TyrTyrAspLeuGluLysAspValLysGlnPheValArgLysAspSerGlyProVal 60
 QY 201 GATCACAATAATCGGAAATCGACAGCATTTTGGATTGACAGTCTGGAAGAACTGGAC 260
 Db 61 ValLysLysIleArgGluMetGlnLysPheLysGluValThrGlyLysLeuAsp 80
 QY 261 TCAACACCCCTTGAGATCATGACACACCCAGGTGTGGGTGCTGTATGTGGGCAGTAT 320
 Db 81 SerAspThrLeuGluValMetArgLysProArgCysGlyValProAspValGlyHisPhe 100
 QY 321 GCCTACACCTCTCCCTGGG-----TGGAGAAAATACAACTCCTACAGATAATA 371
 Db 101 ---ArgThrPheProGlyIleProLysTyrArgLysThrHisLeuThrTyrArgIleVal 119
 QY 372 AACTATACTCCGATATGGCAGAGCTGCTGTGATGAGGCTATCCAGAGAGTTAGAA 431
 Db 120 AsnTyrThrProAspLeuProLysAspAlaValAspSerAlaValGluLysAlaLeuLys 139
 QY 432 GTGTGGAGCAAAAGTCACTCCACTAAAATTTCAACAGATTTTCAAGAGGATTCAGACATC 491
 Db 140 ValTyrGluGluValThrProLeuThrPheSerArgLeuTyrGluGlyGluAlaAspIle 159
 QY 492 ATGATGCTTTTAGGATCTGAGTCCATGCTCGGTGCTCTCGCTAT---TTTGATGGTCCC 548
 Db 160 MetIleSerPheAlaValArgGluHisGly-----AspPheTyrProPheAspGlyPro 177
 QY 549 TTGGAGTGTGTGGCCATGCTTTCTCTCGGTGCTGGGTGCTGGGTGACACATTTT 608
 Db 178 GlyAsnValLeuAlaHisAlaTyrAlaProGlyProGlyIleAsnGlyAspAlaHisPhe 197
 QY 609 GATGAGGATGAAAATCGACCAAGATGAGGAGATTCACACTTGTCTTTGTGCTGCT 668
 Db 198 AspAspAspGluGlnTyrThrLysAspThrThrGlyThrAsnLeuPheLeuValAlaAla 217
 QY 669 CATGAATTTGGTATGACTGGGCTCTCTCCTCAATGATCAACAGCCCTGATGTC 728
 Db 218 HisGluIleGlyHisSerLeuGlyLeuPheHisSerAlaAsnThrGluAlaLeuMetTyr 237


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QY 729 CCAAAATTATGCTCCCTG---GATCCAGAAATACCCACTTCTCAGGATGATATCAAT 785
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238 ProLeuTyHisSerLeuThrArgPheArgLeuSerGlnAspAspIleAsn 257
QY 786 GGAATCCAGTCCATCTATGGA-----GGTCTGCTAAGGTACCTGCT 827
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
258 GlyIleGlnSerLeuTyrGlyProProAspSerProGluThrProLeuValProThr 277
QY 828 AAG-----CCAAAGAAACCACTATACCCATGCTGTGACCTGACTTGACTTTTGAC 881
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
278 GluProValProProGluProGlyThrProAlaAsnCysAspProAlaLeuSerPheAsp 297
QY 882 GCTATCACAACTTTCGCGAGAGAAGTAATGTTCTTTAAAGCGAGCACCTATGGAGGATC 941
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
298 AlaValSerThrLeuArgGlyGluIleLeuPheLysAspArgHisPheTrpArgLys 317
QY 942 TATTATGATATCACGGATGTGAGTTGTAATTGCTTCAATTCGGCCATCTCTGCCA 1001
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
318 SerLeuArgLysLeuGluProGluLeuHisLeuSerSerPheTrpProSerLeuPro 337
QY 1002 GCTGATCTCCAGTGCATACAG---AACCCAGAGATAAGATTCGTGTTTAAAGAT 1058
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
338 SerGlyValAspAlaAlaTyrGluValThrSerLysAspLeuValPheIlePheLysGly 357
QY 1059 GAAAACCTTCTGATGATCAGAGATATGCTGCTTCCAGATTTATCCCAAATCCATCCAT 1118
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
358 AsnGlnPheTrpAlaIleArgGlyAsnGluValArgAlaGlyTyrProArgLysIleHis 377
QY 1119 ACATTAGTGTTCAGGACGTGTGAAGAAATAGATGCAGCGCTCTGTGATAAGACCACA 1178
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
378 ThrLeuGlyPheProProThrValArgLysIleAspAlaIleSerAspLysGluLys 397
QY 1179 AGAAAACCTACTCTTTTGGCATTTGCTGCTGGAGTTTGATGAATGACCCAAACC 1238
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398 AsnLysThrTyrPhePheValGluAspLysTyrTrpArgPheAspGluLysArgAsnSer 417
QY 1239 ATGGCAAAAGGATTCGCGAGAGAGTGTAAACACTTTCTCGGAATCAGTATCGTGTT 1298
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
418 MetGluProGlyPheProLysGlnIleAlaGluAspPheProGlyIleAspSerLysIle 437
QY 1299 GATGCTGCTTTCCAGTACAAAGATTTCTTTTTCAGCGGTGATCAAGCAATTTGAA 1358
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
438 AspAlaValPheGluGluPheGlyPhePheTyrPhePheThrGlySerSerGlnLeuGlu 457
QY 1359 TACAACATTAAACAAAGAAATATTACCAATCATCAGACAACTAATACITGGTTTCAATGC 1418
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
458 PheAspProAsnAlaLysLysValThrHisThrLeuLysSerAsnSerTrpLeuAsnCys 477

RESULT 10
AAH69716
ID AAH69716 PRELIMINARY; PRT; 477 AA.
AC AAH69716;
DT 20-MAY-2004 (TrEMBLrel. 27, Created)
DT 20-MAY-2004 (TrEMBLrel. 27, Last sequence update)
DE 20-MAY-2004 (TrEMBLrel. 27, Last annotation update)
DE Matrix metalloproteinase 3, preproprotein.
GN MMP3.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=PCR rescued clones;
RX MEDLINE=22388257; PubMed=12477932;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Ustin T.B., Toshiyuki S., Carninci P., Prange C.,

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RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gumaratne P.H.,
RA Richards D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs S.W.,
RA Villalón S., Muzny D.M., Sodergren E.J., Lu X., Gibbs S.W.,
RA Fahey J., Helton E., Kettman M., Madan A., Rodrigues S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA Krzywinski M.I., Skalska U., Schmutz J., Schnerch A., Schein J.E.,
RA Jones S.J., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences."
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=PCR rescued clones;
RA Strausberg R.;
RL Submitted (APR-2004) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC069716; AAH69716.1; -.
SQ SEQUENCE 477 AA; 53978 MW; 7497490A861DEEA9 CRC64;

Alignment Scores:
Pred. No.: 2,05e-102 Length: 477
Score: 1254.00 Matches: 247
Percent Similarity: 66.04% Conservative: 70
Best Local Similarity: 51.46% Mismatches: 145
Query Match: 42.80% Indels: 18
DB: Gaps: 9

US-10-729-807-28 (1-1627) x AAH69716 (1-477)
QY 24 ATGAGAGCGCTTCTCTCTGTTGTTTCTTTATAACATTTTCTCTGCAATTCCTTTA 83
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
1 MetLysSerLeuProIleLeuLeuLeuLeuLeuLeuLeuLeuLeuLeuLeuLeuLeuLeu 20
QY 84 GTCCGATGACGGAATAAGAA---AATATGCACTGGCTCAGGCATATCTCAACCAG 140
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21 AspGlyAlaAlaArgGlyGluAspThrSerMetAsnLeuValGlnLysTyrLeuGluAsn 40
QY 141 TTCTACTCTTGAATAAGAGGAATCATCTTGTCAAAGCAAGAAATAGGAGTCTCAT 200
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QY 201 GATGACAAATTCGGGAATGCAAGCATTTTGTGATGACAGTCACTGGAACCTGGAC 260
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61 ValLysLysIleArgGluMetGlnLysPheLeuGlyLeuGluValThrGlyLysLeuAsp 80
QY 261 TCAAAACACCTTTGAGATCATGAAGACACCCAGGTGTGGGGTGCCTGATGTGGCCAGTAT 320
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81 SerAspThrLeuGluValMetArgLysProArgCysGlyValProAspValGlyHisPhe 100
QY 321 GGCTACACCTCCCTGGG-----TGGAGAAATACACCTCACTACAGATAATA 371
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101 ---ArgThrPheProGlyIleProLysTrpArgLysThrHisLeuThrTyrArgIleVal 119
QY 372 AACTATCTCCGATATGGCAGAGCTCTGTGGATGAGGCTATCCAGAAAGTTAGNA 431
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140 ValTrpGluGluValThrProLeuThrPheSerArgLeuTyrGluGlyGluAlaAspIle 159
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160 MetIleSerPheAlaValArgGluHisGly-----AspPheTyrProPheAspGlyPro 177
QY 549 TTGGAGAGTCTTGGCCATGCTTCTCTGTCGGGTCTGGGTGGTGGACACTCATTT 608
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
178 GlyAsnValLeuAlaHisAlaTyrAlaProGlyProGlyIleAsnGlyAspAlaHisPhe 197
QY 609 GATGAGGATGAAAACCTGACCAAGATGAGCAGGATTCMACTCTTCTTCTGTGCTGCT 668
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Db 198 AspAspAspGluGlnTrpThrLysAspThrGlyThrAsnLeuPheLeuValAlaAa 217
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Db 218 HisGluIleGlyHisSerLeuGlyLeuPheHisSerAlaAsnThrGluAlaLeuMetTyr 237
QY 729 CCAAAATATGTCCTCCGNG--GATCCAGAGAAATACCCATCTTCTCAGGATGATATCAAT 785
Db 238 ProLeuTyrHisSerLeuThrAspLeuThrArgPheArgLeuGlnAspPheAsn 257
QY 786 GGAATCCAGTCCATCTATGGA-----GGTCTGCTCAAGGTACCTGCT 827
Db 258 GlyIleGlnSerLeuTyrGlyProProAspSerProGluThrProLeuValProThr 277
QY 828 AAG-----CCAAAGAACCCATATACCCCATGCCCTGACCTGACCTGACTTGTGAC 881
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QY 882 GCTATCACACTTTCGCGAGAGAGTAAATGTTCTTTAAAGCGACGACCTATGAGGATC 941
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QY 1239 ATGACAAAGATTCGCGAGAGTGTGAACACACTTCTGCTGAATCAGTATCCGTGT 1298
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Db 438 AspAlaValPheGluGluPheGlyPhePheTyrPhePheThrGlySerSerGlnLeuGlu 457
QY 1359 TACAACATTAAGACAAAGATATATACCGAATCATGAACTAATCTGTTTCAATGC 1418
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RESULT 11
MW03 HUMAN
ID MW03 HUMAN STANDARD; PRT; 477 AA.
AC P08254;
DT 01-AUG-1988 (Rel. 08, Created)
DT 01-FEB-1991 (Rel. 17, Last sequence update)
DT 01-OCT-2004 (Rel. 45, Last annotation update)
DE Stromelysin-1 precursor (EC 3.4.24.17) (Matrix metalloproteinase-3)
DE (MMP-3) (Transin-1) (SL-1).
GN Name=MMP3; Synonyms=STW1;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A., AND SEQUENCE OF 18-24.
RX MEDLINE=88198243; PubMed=3360803;
RA Saus J., Quinones S., Otani Y., Nagase H., Harris E.D. Jr.,
RA Kurkinen M.;

RT "The complete primary structure of human matrix metalloproteinase-3.
RT Identity with stromelysin.";
RL J. Biol. Chem. 263:6742-6745 (1988).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Fibroblast;
RX MEDLINE=87156645; PubMed=3030290;
RA Whitam S.E., Murphy G., Angel P., Rahmsdorf H.J., Smith B., Lyons A.,
RA Harris T.J.R., Reynolds J.J., Herrlich P., Docherty A.J.P.;
RA "Comparison of human stromelysin and collagenase by cloning and
RT sequence analysis.";
RL Biochem. J. 240:913-916 (1986).
RN [3]
RP SEQUENCE FROM N.A.
RX MEDLINE=88016164; PubMed=3477804;
RA Wilhelm S.M., Collier I.E., Kronberger A., Eisen A.Z., Marner B.L.,
RA Grant G.A., Bauer E.A., Goldberg G.I.;
RA "Human skin fibroblast stromelysin: structure, glycosylation,
RT substrate specificity, and differential expression in normal and
RT tumorigenic cells.";
RL Proc. Natl. Acad. Sci. U.S.A. 84:6725-6729 (1987).
RN [4]
RP SEQUENCE FROM N.A.
RX Lin D., Duncan M., Allen E., Araujo R., Aparicio A., Chai A.,
RA Chung E., Davis K., Federspiel N., Hyman R., Kalman S., Komp C.,
RA Kurdi O., Lashkari D., Lew H., Namath A., Oefner P., Roberts D.,
RA Heller R., Davis R.W.;
RL Submitted (DEC-1996) to the EMBL/GenBank/DBJ databases.
RN [5]
RP SEQUENCE FROM N.A., AND VARIANT GLU-45.
RX Rieder M.J., Carrington D.P., Chung M.-W., Lee K.L., Poel C.L., Yi Q.,
RA Nickerson D.A.;
RA "SeattleSNPs: NHLBI HUG66682 program for genomic applications, UW-
RT FHCRC, Seattle, WA (URL: http://pga.gs.washington.edu);"
RL Submitted (AUG-2001) to the EMBL/GenBank/DBJ databases.
RN [6]
RP ZYMOGEN ACTIVATION.
RX MEDLINE=90344802; PubMed=2383557;
RA Nagase H., Englund J.J., Suzuki K., Salvesen G.;
RT "Stepwise activation mechanisms of the precursor of matrix
RT metalloproteinase 3 (stromelysin) by proteinases and (4-
RT aminophenyl)mercuric acetate.";
RL Biochemistry 29:5783-5789 (1990).
RN [7]
RP STRUCTURE BY NMR OF CATALYTIC DOMAIN.
RX MEDLINE=95384761; PubMed=7656014;
RA Gooley P.R., O'Connell J.F., Marcy A.I., Cuca G.C., Salowe S.P.,
RA Bush B.L., Hermes J.D., Esser C.K., Hagmann W.K., Springer J.P.,
RA Johnson B.A.;
RT "The NMR structure of the inhibited catalytic domain of human
RT stromelysin-1.";
RL Nat. Struct. Biol. 1:111-118 (1994).
RN [8]
RP STRUCTURE BY NMR OF 100-267.
RX MEDLINE=90433696; PubMed=9827994;
RA Stockman B.J., Waldon D.J., Gates J.A., Schall T.A.,
RA Kloosterman D.A., Mizsak S.A., Jacobsen E.J., Belonga K.L.,
RA Mitchell M.A., Mao B., Petke J.D., Goodman L., Powers E.A.,
RA Ledbetter S.R., Kaytes P.S., Vogel G., Marshall V.P., Petzold G.L.,
RA Poorman R.A.;
RT "Solution structures of stromelysin complexed to thiazole
RT inhibitors.";
RL Protein Sci. 7:2281-2286 (1998).
RN [9]
RP X-RAY CRYSTALLOGRAPHY (1.9 ANGSTROMS) OF 18-272.
RX MEDLINE=96117647; PubMed=8535233;
RA Becker J.W., Marcy A.I., Rokosz L.L., Axel M.G., Burbaum J.J.,
RA Fitzgerald P.M.D., Cameron P.M., Esser C.K., Hagmann W.K.,
RA Hermes J.D., Springer J.P.;
RT "Stromelysin-1: three-dimensional structure of the inhibited catalytic
RT domain and of the C-truncated proenzyme.";
RL Protein Sci. 4:1966-1976 (1995).
RN [10]


```

Db      122 AspMetAlaGluAlaAspValAspThrAlaIleAArgAlaPheLysValTrpSerAsp 141
QY      444 GTCACTCCACATAAATTCCACCAAGATTCAAAGGGAGTTGCAGACATCATGATTCGCTTT 503
Db      142 ValThrProLeuThrPheSerArgIleTyrGluGlyThrAlaAspIleGlnIleSerPhe 161
QY      504 AGGACTCGAGTCAGTCGGTGGTCTCGCTAT---TTTGATGGTCCCTTGGAGTGGTCT 560
Db      162 GlyAlaGlyValHisGly-----AspPheTyrProPheAspGlyProHisGlyThrLeu 179
QY      561 GGCCATGCTTTCCTCTGCTCGGCTCTGGTGTGTCGACACTCATTTTGATGAGGATGAA 620
Db      180 AlaHisAlaPheAlaProGlyAsnSerIleGlyGlyAspAlaHisPheAspGluAspGlu 199
QY      621 AACTGGACCAAGATGAGGACAGATTCAACTTGTCTTCTTGTGCTGCTCATGAATTGT 680
Db      200 ThrTrpThrAlaGlySerAlaGlyTyrAsnLeuPheLeuValAlaAlaHisGluPheGly 219
QY      681 CATGCACTGGGCTCTCTCACTCCATGATCAACAGCCTTGATGTGCCAAATATATGTC 740
Db      220 HisSerLeuGlyLeuSerHisSerGlyAspArgSerAlaLeuMetTyrProThrTyrSer 239
QY      741 TCCTGGATCCCAAGAAATACCCACTTCTCAGGATGATATCAATGGAATCCAGTCCATC 800
Db      240 TyrIleAspProAlaArgPheArgLeuProGlnAspAspValAspGlyIleGlnAlaLeu 259
QY      801 ATGAGAGTCTGCTTAAG---GTACTGCTAAGCAAAG----- 836
Db      260 TyrGlyAlaSerProAsnProValProThrThrProGlnAlaThrThrProThrThrThr 279
QY      837 -----GAACCACTATATACCCATCGCTGTGACCCCTGAC 869
Db      280 ValSerThrThrThrThrThrSerSerProIleAsnProSerIleCysAspProThr 299
QY      870 TTGACTTTTGAGCTATCAACAATTCCCGCAGAGAAAGTATGTTCTTTAAAGCAGGCAC 929
Db      300 LeuValPheAspAlaIleThrThrLeuArgGlyGluIleLeuPhePheLysAspSerSer 319
QY      930 CTATGAGAGATCATATATGATATCAGGATGAGTTGAGTTGAATTAATGCTTCATCTGG 989
Db      320 PheTrpArgValProThrIleGlyGluValTyrAsnTyrProIleSerThrSerTrp 339
QY      990 CATCTCTCCAGCTATCGAAGCTGCATAGCAGAACCCAGAA---GATAGATTCTG 1046
Db      340 ProSerLeuProSerGlyIleGlnAlaTyrGluAsnProGluThrAspGlnIlePhe 359
QY      1047 GTTTTAAAGATGAAAACTCTGGATGATCAGAGGATATGCTCTTGTCCAGATTAATCC 1106
Db      360 LeuPheLysGlySerLysTyrTrpAlaLeuGlnGlyPheAspIleLeuProAsnTyrPro 379
QY      1107 AATCATCATCATATAGTTTTCAGGACGTTGAGAAATAGATAGCAGCGCTCTGT 1166
Db      380 LysAsnIleAspLysLeuGlyPheProArgThrValLysHisIleAsnAlaAlaValTyr 399
QY      1167 GATAACACACAGAAACAACTACTTCTTTGCGGATTTGGTGTGGAGTTTGTATGAA 1226
Db      400 LeuGlnSerThrGlnLysThrTyrPhePheAlaGlyGluGlnTyrTrpSerTyrAspGlu 419
QY      1227 ATGACCCCAACACATGACAAAGGATTCCTCCGACAGAGATGGTGAACACATTTCTCGAATC 1286
Db      420 AlaArgLysThrMetAspLysGluSerProArgGluGluAspAspPheProGlyIle 439
QY      1287 AGTATCGGTGTTGATGCTTTCAGTACAAAGGATCTCTTTTTCAGCCGCTGGATCA 1346
Db      440 GlyLysLysValHisAlaValPheGluAspAsnGlyLeuLeuTyrPhePheSerGlyHis 459
QY      1347 AAGCAATTCAATACAACTTATAGACAAAGAAATATACCCGAATCATGAGAACTAATACT 1406
Db      460 LysGlnPheGluPheAsnMetLysSerLysValThrArgThrLeuLysAsnThrSer 479
QY      1407 TGGTTTCAATGC 1418
Db      480 TrpLeuGlyCys 483

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RESULT 13
 MM03 HORSE
 ID MM03 HORSE STANDARD; PRT; 477 AA.
 AC Q28397;
 DT 30-MAY-2000 (Rel. 39, Created)
 DT 30-MAY-2000 (Rel. 39, Last sequence update)
 DT 01-OCT-2004 (Rel. 45, Last annotation update)
 DE Stromelysin-1 precursor (EC 3.4.24.17) (Matrix metalloproteinase-3) (MMP-3).
 GN Name=MMP3;
 OS Equus caballus (Horse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Perissodactyla; Equidae; Equus.
 OX NCBI_TaxID=9796;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Cartilage;
 RX MEDLINE=99074117; PubMed=9858406;
 RA Richardson D.W., Dodge G.R.;
 RT "Molecular characteristics of equine stromelysin and the tissue
 inhibitor of metalloproteinase 1.";
 RL Am. J. Vet. Res. 59:1557-1562(1998).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Cartilage;
 RX MEDLINE=98104320; PubMed=9442239;
 RA Balkman C.E., Nixon A.J.;
 RT "Molecular cloning and cartilage gene expression of equine stromelysin
 1 (matrix metalloproteinase 3).";
 RL Am. J. Vet. Res. 59:30-36(1998).
 RN [3]
 RP 3D-STRUCTURE MODELING
 RA Mallena S.C., Sharma J.A.R.P.;
 RL Submitted (MAR-2002) to the PDB data bank.
 CC -!- FUNCTION: Can degrade fibronectin, laminin, gelatins of type I,
 CC III, IV, and V; collagens III, IV, X, and IX, and cartilage
 CC proteoglycans. Activates procollagenase.
 CC -!- CATALYTIC ACTIVITY: Preferential cleavage where P1', P2' and P3'
 CC are hydrophobic residues.
 CC -!- COFACTOR: Binds 2 zinc ions and 4 calcium ions per subunit (By
 CC similarity).
 CC -!- SIMILARITY: Belongs to peptidase family M10A.
 CC -!- SIMILARITY: Contains 1 hemopexin-like domain.
 CC
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 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
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 CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
 CC or send an email to license@isb-sib.ch).
 CC
 CC EMBL; U62529; AAB05774.1; -;
 CC PDB; 1L9I; Model; A=100-267.
 CC MEROPS; M10.005; -;
 CC InterPro; IPR000585; Hemopexin.
 CC InterPro; IPR006026; Peptidase M.
 CC InterPro; IPR001818; Pept M10A M12B.
 CC InterPro; IPR006025; Pept M.Zn.BS.
 CC InterPro; IPR009070; PGBD-like.
 CC Pfam; PF00045; Hemopexin_4.
 CC Pfam; PF00413; Peptidase M10; 1.
 CC Pfam; PF03933; Peptidase M10_N; 1.
 CC PRINTS; PR00138; MATRIXIN.
 CC SMART; SM00120; HX; 4.
 CC SMART; SM00235; ZmC; 1.
 CC PROSITE; PS00546; CYSTEINE_SWITCH; FALSE_NEG.
 CC PROSITE; PS00024; HEMOPEXIN; 1.
 CC PROSITE; PS00142; ZINC_PROTEASE; 1.
 CC 3D-structure; Calcium-binding; Collagen degradation;
 CC Extracellular matrix; Glycoprotein; Hydrolase; Metal-binding;

KW	Metalloprotease; Signal; Zinc; Zymogen.	1	17	Potential.	84	GTCCGGATGACGGAATAAGAA---AATATGCAACTGGCTCAGGCATATCTCAACCA	140
FT	SIGNAL	18	99	Activation peptide.	21	AspArgSerAlaArgAspGluAspSerAsnMetAspLeuLeuGlnAspTyrLeuGluLys	40
FT	PROPEP	100	477	Stromelysin-1.	141	TTCTACTCTCTTGAATAGAAAGGAATCATCTTGTCAAAGCAAGAAATAGGAGTCTCAT	200
FT	CHAIN	287	477	Hemopexin-like.	41	TyrTyrAspLeuGlyLysGluMetArgGlnTyrValArgArgLysAspSerGlyProIle	60
FT	SITE	92	92	Cysteine switch (Potential).	201	GATGACAAATTCGGGAAATCAAGCATTTTGGATTGACAGTGCAGTGGAAATCGAC	260
FT	METAL	124	124	Calcium 1 (By similarity).	61	VallLysIleGlnGluMetGlnLysPheLeuGlyLeuValThrGlyLysLeuAsp	80
FT	METAL	158	158	Calcium 2 (By similarity).	261	TCRAACACCTTGAGATCATGACACACCCAGGTGGGTGCTGATGTCGGCCAGTAT	320
FT	METAL	168	168	Zinc 1 (By similarity).	81	SerAspThrValGluValMetHisLysSerArgCysGlyValProAspValGlyHisPhe	100
FT	METAL	170	170	Calcium 3 (By similarity).	321	GGCTACACCTCCCTCGG-----TGGAGAAATACACACCTCACCATAGATAATA	371
FT	METAL	175	175	Calcium 3 (via carbonyl oxygen) (By similarity).	101	--ThrThrPheProGlyMetProLysTrpSerLysThrHisLeuThrTyrArgIleVal	119
FT	METAL	176	176	Calcium 3 (via carbonyl oxygen) (By similarity).	372	AACTATCTCCGGATATGGACAGCTGCTGTGGATGAGGCTATCCAAAGAGTTTGA	431
FT	METAL	178	178	Calcium 3 (via carbonyl oxygen) (By similarity).	120	AsnTyrThrGlnAspLeuProArgAlaValAspSerAspValGluLysAlaLeuLys	139
FT	METAL	180	180	Calcium 3 (via carbonyl oxygen) (By similarity).	432	GTGTGGAGCAAGTCACCTCCACTAAATTCACCAAGATTTCAAAGGGATTCGACATC	491
FT	METAL	183	183	Calcium 1 (By similarity).	140	IleTrpGluGluValThrProLeuThrPheSerArgIleTyrGluGlyGluAlaAspIle	159
FT	METAL	190	190	Calcium 1 and 3 (By similarity).	492	ATGATTGCCTTTAGGACTCGAGTCCATGTCGG---TGTCCTGCTATTTTGATGGTCCC	548
FT	METAL	201	201	Calcium 2 (catalytic) (By similarity).	160	MetIleThrPheAlaValArgGluHisGlyAspPhePro-----PheAspGlyPro	177
FT	METAL	218	218	Zinc 2 (catalytic) (By similarity).	549	TTGGGAGTGTGGCCATGCTTTCCTCCCTGGTCCGGTCTGGGTGTGGTGCATCATTTT	608
FT	METAL	219	219	By similarity.	178	GlyLysValLeuAlaHisAlaTyrProGlyProGlyProGlyMetAsnGlyAspAlaHisPhe	197
FT	METAL	222	222	Zinc 2 (catalytic) (By similarity).	609	GATCAGATGAAACTCGACCAAGATGGAGCAGATTCAACTGTTTCTTGTGGTGGTCT	668
FT	METAL	228	228	Zinc 2 (catalytic) (By similarity).	198	AspAspAspGluHisTrpThrLysAspAlaSerGlyIleAsnPheLeuValAlaAla	217
FT	METAL	297	297	Calcium 4 (via carbonyl oxygen) (By similarity).	669	CATGAATTTGGTCATGCACCTGGGCTCTCTCAATCAATCAATCAACAGCCCTTGATGTC	728
FT	METAL	389	389	Calcium 4 (via carbonyl oxygen) (By similarity).	218	HisGluLeuGlyHisSerLeuGlyLeuTyrHisSerThrAsnThrGluAlaLeuMetTyr	237
FT	METAL	438	438	Calcium 4 (via carbonyl oxygen) (By similarity).	729	CCAAATTTATGTCCTCCCTG---GATCCAGAAATACCCATCTTCTCAGGATGATCAAT	785
FT	METAL	477	477	Calcium 4 (via carbonyl oxygen) (By similarity).	238	ProLeuTyrAsnThrLeuLysGlyProAlaArgValArgLeuSerGlnAspValThr	257
FT	METAL	541	541	Calcium 4 (via carbonyl oxygen) (By similarity).	786	GGAATCCAGTCCATCTATGGAGTCTGCCTAAGGTACTCTGAAGCCAAAGGACCCACT	845
FT	METAL	550	550	Calcium 4 (via carbonyl oxygen) (By similarity).	258	GlyIleGlnSerLeuTyrGlyProProAlaSerProAspSerProValGluProSer	277
FT	METAL	551	551	Calcium 4 (via carbonyl oxygen) (By similarity).	846	ATACCCCAT-----GCCTGTGACCTGACTTGTGACTTTTGAC	881
FT	METAL	552	552	Calcium 4 (via carbonyl oxygen) (By similarity).	278	GluProGluProProAlaProGlyThrLeuAlaMetCysAspProAlaLeuSerPheAsp	297
FT	METAL	553	553	Calcium 4 (via carbonyl oxygen) (By similarity).	882	GCTATCACACTTTCGCAGAGAAATATGTTCTTTAAAGCGCAGCCACCTATGGAGATC	941
FT	METAL	554	554	Calcium 4 (via carbonyl oxygen) (By similarity).	298	AlaIleSerThrLeuArgGlyGluIleLeuPhePheLysAspArgTyrPheTrpArgLys	317
FT	METAL	555	555	Calcium 4 (via carbonyl oxygen) (By similarity).	942	TATTATGATATACGGATGTTGAGTTTGAATTAATGCTTCATCTGGCCATCTCTGCCA	1001
FT	METAL	556	556	Calcium 4 (via carbonyl oxygen) (By similarity).	318	ThrPheArgThrLeuValProGluPheHisProIleSerSerPheTrpProSerLeuPro	337
FT	METAL	557	557	Calcium 4 (via carbonyl oxygen) (By similarity).	1002	GCTGATCTGCACTGCATACAGAG---AACCCAGAGATAAGATTTGTTTAAAGAT	1058
FT	METAL	558	558	Calcium 4 (via carbonyl oxygen) (By similarity).	338	SerGlyIleAspAlaAlaTyrGluValThrSerArgAspSerValPheIlePheLysGly	357
FT	METAL	559	559	Calcium 4 (via carbonyl oxygen) (By similarity).	1059	GAATACTTCGGATGATCAGAGATGCTGCTTGCACATATTCATCAATCCATCCAT	1118
FT	METAL	560	560	Calcium 4 (via carbonyl oxygen) (By similarity).	358	AsnLysPheTrpAlaIleArgGlyAsnGluGlnAlaGlyTyrProArgGlyIleHis	377
FT	METAL	561	561	Calcium 4 (via carbonyl oxygen) (By similarity).	1119	ACATTAGTTTCCAGGACGTGTGAAGAAATAGATGTCAGCCGCTCTGTGATAAGACCACA	1178

Alignment Scores:
 Pred. No.: 1.59e-101 Length: 477
 Score: 1244.00 Matches: 244
 Percent Similarity: 66.04% Conservative: 73
 Best Local Similarity: 50.83% Mismatches: 145
 Query Match: 42.46% Indels: 18
 DB: 1 Gaps: 8

US-10-729-807-28 (1-1627) x MM03_HORSE (1-477)

QY 24 ATGAAGCGCTCTGCTTCTGTGTTCTTCTTATACATTTTCTTCTGATTTCCCTTA 83
 Db 1 MetLysAsnLeuProIleLeuLeuLeuLeuCysValAlaAlaCysSerAlaTyrProLeu 20

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Db 378 ThrLeuGlyPheProThrValArgLysIleAspAlaIlePheAspLysGluLys 397
QY 1179 AGAAAAACCTACTCTTTGTGGCATTTGTGCTGGAGTTTGTATGAATACCCAAACC 1238
Db 398 GlnLysThrTyrPhePheValGluAspLysTyrTipArgPheAspGluLysArgGlnSer 417
QY 1239 ATGGACAAAGGATCCCGCAGAGAGTGGTAAACACTTTCCTGGATCAGTATCCGTGTT 1298
Db 418 MetGluProGlyTyrProLysGlnIleAlaGluAspPheProGlyIleAspSerLysLeu 437
QY 1299 GATGCTGCTTTCAGATACAAAGGATCTCTTTTTCAGCGGTGATCAAGCAATTTGAA 1358
Db 438 AspAlaAlaPheGluSerPheGlyPheTyrPhePheSerGlySerGlnPheGlu 457
QY 1359 TACAACATTAAGACAAGAATAATTACCGAATCATGAGAACTAATACTTGGTTTCAATGC 1418
Db 458 PheAspProAsnAlaLysValThrHisValLeuLysSerAsnSerTrpPheAsnCys 477

RESULT 14
MM10_MOUSE
ID AC MM10_MOUSE STANDARD; PRT; 476 AA.
AC 055123;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Stromelysin-2 precursor (EC 3.4.24.22) (Matrix metalloproteinase-10)
DE (MMP-10) (Transin-2) (SL-2).
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBT_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=BALB/c;
RC MEDLINE=98087420; PubMed=9427548;
RA Madlener M., Warner S.;
RT "CDNA cloning and expression of the gene encoding murine Stromelysin-2
RL (MMP-10).";
RL Gene 202:75-81 (1997).
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Cecum;
RX MEDLINE=22354683; PubMed=12456851; DOI=10.1038/nature01266;
RA Okazaki Y., Furuno M., Kasukawa T., Adachi J., Bono H., Kondo S.,
RA Nikaide I., Osato N., Saito R., Suzuki H., Yamanaka I., Kiyosawa H.,
RA Yagi K., Tomaru Y., Hasegawa Y., Nogami A., Schorbach C., Gojobori T.,
RA Baldarelli R., Hill D.P., Bult C., Hume D.A., Quackenbush J.,
RA Schriml L.M., Kanapin A., Matsuda H., Batalov S., Beisel K.W.,
RA Blake J.A., Bradt D., Brusic V., Chothia C., Corbani L.E., Cousins S.,
RA Daila E., Dragani T.A., Fletcher C.F., Forrest A., Frazer K.S.,
RA Gaasterland T., Gariboldi M., Glissi C., Godzik A., Gough J.,
RA Grimmond S., Gustincich S., Hirokawa N., Jackson I.J., Jarvis E.D.,
RA Kanai A., Kawai H., Kawasawa Y., Kedzierski R.M., King B.L.,
RA Konagaya A., Kurochkin I.V., Lee Y., Lenhard B., Lyons P.A.,
RA Maglott D.R., Maltais L., Marchionni L., McKenzie L., Miki H.,
RA Nagahima T., Numata K., Okido T., Pavan W.J., Perte G., Pesole G.,
RA Petrovsky N., Pillai R., Pontius J.U., Qi D., Ramachandran S.,
RA Ravasi T., Reed J.C., Reed D.J., Reid J., Ring B.Z., Ringwald M.,
RA Sadelin A., Schneider C., Semple C.A., Setou M., Shimada K.,
RA Sultana R., Takenaka Y., Taylor M.S., Teasdale R.D., Tomita M.,
RA Verardo R., Wagner L., Wahlestedt C., Wang Y., Watanabe Y., Wells C.,
RA Wilming L.G., Wynshaw-Boris A., Yanagisawa M., Yang I., Yang L.,
RA Yuan Z., Zavalan M., Zhu Y., Zimmer A., Carninci P., Hayatsu N.,
RA Hirozane-Kishikawa T., Konno H., Nakamura M., Sakazume N., Sato K.,
RA Shiraki T., Waki K., Kawai J., Aizawa K., Arakawa T., Fukuda S.,
RA Hara A., Hashizume M., Imotani K., Ishii Y., Itoh M., Kagawa I.,
RA Miyazaki A., Sakai K., Sasaki D., Shibata K., Shinagawa A.,
RA Yasunishi A., Yoshino M., Waterston R., Lander E.S., Rogers J.,
RA Birney E., Hayashizaki Y.;
RT "Analysis of the mouse transcriptome based on functional annotation of
60,770 full-length cDNAs.";
```

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RL Nature 420:563-573 (2002).
CC -!- FUNCTION: Can degrade fibronectin, gelatins of type I, III, IV,
CC and V; weakly collagens III, IV, and V. Activates procollagenase.
CC -!- CATALYTIC ACTIVITY: Similar to Stromelysin 1, but action on
CC collagen types III, IV and V is weak.
CC -!- COFACTOR: Binds 2 zinc ions per subunit, calcium (By similarity).
CC -!- TISSUE SPECIFICITY: Expressed in small intestine. Weak levels in
CC heart and lung.
CC -!- INDUCTION: By wounding.
CC -!- SIMILARITY: Belongs to peptidase family M10A.
CC -!- SIMILARITY: Contains 1 hemopexin-like domain.
CC
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CC
CC EMBL; Y13185; CAAT3641.1; -.
CC EMBL; AK020292; BAB32058.1; -.
CC F1R; JC6505; JC6505.
CC HSP; P08254; IG05.
CC MEROPS; M10.006; -.
CC MGD; MGI:97007; Mmp10.
CC InterPro; IPR000585; Hemopexin.
CC InterPro; IPR006026; Peptidase M.
CC InterPro; IPR001843; Pept M10A_M10C.
CC InterPro; IPR001818; Pept M10A_M12B.
CC InterPro; IPR006025; Pept M_Zn_BS.
CC InterPro; IPR009070; PGSD_like.
CC Pfam; PF02051; Fragilysin; 1.
CC Pfam; PF00445; Hemopexin; 4.
CC Pfam; PF00413; Peptidase M10; 1.
CC Pfam; PF03933; Peptidase M10_N; 1.
CC PRINTS; PR00138; MATRIXIN.
CC SMART; SM00120; HX; 4.
CC SMART; SM00235; ZNMC; 1.
CC PROSITE; PS00546; CYSTEINE_SWITCH; 1.
CC PROSITE; PS00024; HEMOPEXIN; 1.
CC PROSITE; PS00142; ZINC_PROTEASE; 1.
CC Calcium; Collagen degradation; Extracellular matrix; Hydrolase;
KW Metalloprotease; Signal; Zinc; Zymogen.
FT SIGNAL 1 17 Probable.
FT PROPEP 18 99 Activation peptide (By similarity).
FT CHAIN 100 476 Stromelysin-2.
FT DOMAIN 286 476 Hemopexin-like.
FT SITE 92 92 Cysteine switch (By similarity).
FT METAL 218 218 Zinc (catalytic) (By similarity).
FT ACT_SITE 219 219 By similarity.
FT METAL 222 222 Zinc (catalytic) (By similarity).
FT METAL 228 228 Zinc (catalytic) (By similarity).
FT DISULFID 289 476 By similarity.
SQ SEQUENCE 476 AA; 53911 MW; 2EB1CC41468F0AC6 CRC64;

Alignment Scores:
Pred. No.: 1,76e-101 Length: 476
Score: 1243.50 Matches: 244
Percent Similarity: 66.88% Conservative: 77
Best Local Similarity: 50.83% Mismatches: 140
Query Match: 42.44% Indels: 19
DB: 1 Gaps: 9

US-10-729-807-28 (1-1627) x MM10_MOUSE (1-476)
QY 24 ATGACGGCTTCTGCTCTGTTGTTTATAACATTTTCTTCGATTCCTTA 83
Db 1 MetGluProLeuAlaIleLeuAlaLeuSerLeuProIleCysSerAlaTrpProLeu 20
QY 84 --GTCCGGATGACGGAATAATGAAGAAAATATGCAACTGGCTCAGCATATCTCAACAG 140
Db 21 HisGlyAlaValThrGlnGlyHisProSerMetAspLeuAlaGlnGlnTrpLeuGluLys 40
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[illegible]

Search completed: November 15, 2004, 20:31:08
Job time : 204.5 secs

QY	12	AGAAAGAGAGGAATGAAGCGCCTTCGTCTTCGTGTTTGTTCCTTTATAACATTTCTCTCT	71
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QY	72	GCATTTCCCTTACTCGGATGACGGAAATGAAGAA---AATATGCACTGCCTCAGGCA	128
Db	19	SerTyrProLeuHisAspSerAlaArgAspAspAlaGlyMetGluLeuLeuGlnLys	38
QY	129	TATCTCAACACGAGTTCTACTCTCTGAAATAGAAGGGAATCATCTTGTTTAAAGCAAGAA	188
Db	39	TyrLeuGluAsnTyrTyrGlyLeuAlaLysAspValLysGlnPheIleLysLysAsp	58
QY	189	AGGAGTCTCATGATGACAAAATTCGGGAATGCAAGCATTTTTTGGATTGACAGTGA	248
Db	59	SerSerLeuIleValLysLysIleGlnMetGlnLysPheLeuGlyLeuGluMetThr	78
QY	249	GGAAAACTGCACTCAAAACACCCTTCAGATCATGAAGACACACCGAGTGTGGGGTGCC	308
Db	79	GlyLysLeuAspSerAsnThrMetGluLeuMetHisLysProArgCysGlyValProAsp	98
QY	309	GTGGGGCAGTATGGCTACACCCTCCCTGGG-----TGGAGAAAATCAACCTCA	359
Db	99	ValGlyGlyPheSer---ThrPheProGlySerProLysTrpArgLysSerHisIleThr	117
QY	360	TACAGATAATAATAACTATCTCCGATATGGCAGCAGCTGCTGTGGATGAGGCTATCCAA	419
Db	118	TyrArgIleValAsnTyrThrProAspLeuProArgGlnSerValAspSerAlaIleGlu	137
QY	420	GAAGGTTTGAAGTGTGGAGCAAACTCACTCCACTAAATTCACCAAGATTCACAAAGGG	479
Db	138	LysAlaLeuLysValTrpGluGluValThrProLeuThrPheSerArgIleSerGluGly	157
QY	480	ATTGACAGATCATGATTCCTTTAGGACTCGAGTCCATGCTCGG---TGTCTCTCGCTAT	536
Db	158	GluAlaAspIleMetIleSerPheAlaValGlyGluHisGlyAspPheValPro-----	175
QY	537	TTTGATGTGTCCTTGGGAGTGTTCGGCCATGCCTTTCTCTGCTCGCGGTCTGGGTGGT	596
Db	176	PheAspGlyProGlyThrValLeuAlaHisAlaTyrAlaProGlyProGlyIleAsnGly	195
QY	597	GACACTCATTTGATGAGATGAAACTGAGCAACCAAGATGGAGCAGGATTCACCTGTTT	656
Db	196	AspAlaHisPheAspAspGluArgTrpThrGluAspValThrGlyTyrAsnLeuPhe	215

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OM nucleic - nucleic search, using sw model

Run on: November 15, 2004, 13:11:00 ; Search time 7040 Seconds

(without alignments)
10929.026 Million cell updates/sec

Title: US-10-729-807-28

Perfect score: 1627

Sequence: 1 gcttcagctgaagaaga.....aattctgttcaaatagaa 1627

Scoring table: IDENTITY NUC

Gapop 10.0 , Gapext 1.0

Searched: 4526729 seqs, 23644849745 residues

Total number of hits satisfying chosen parameters: 9053458

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

GenEmbl.*

1: gb_ba.*

2: gb_htg.*

3: gb_in.*

4: gb_om.*

5: gb_ov.*

6: gb_pat.*

7: gb_ph.*

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9: gb_pr.*

10: gb_ro.*

11: gb_sts.*

12: gb_sy.*

13: gb_un.*

14: gb_vi.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	1627	100.0	1845	6	AX358475	Sequence
2	1625.4	99.9	1647	6	AX464058	Sequence
3	1625.4	99.9	1647	9	AY358752	Homo sapi
4	1600.6	98.4	1841	6	AX249969	Sequence
5	1580.8	97.2	1655	9	AF195192	Homo sapi
6	1548	95.1	1583	6	AX089610	Sequence
7	1417.8	87.1	1687	6	AR263900	Sequence
8	1293.4	79.5	1488	6	AX249967	Sequence
9	1257	77.3	1667	4	AF281673	Tupaia be
10	826.6	50.8	833	6	AX249965	Sequence
11	621.8	38.2	1587	5	AF062392	Gallus ga
12	456	28.0	1923	3	AF148882	Equus cab
13	455	28.0	1336	4	SSMNP1	Porcine mmp
14	450.4	27.7	1804	6	ECU62529	Equus cabal
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21	447.6	27.5	1970	6	AX336645	Sequence
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ALIGNMENTS

RESULT 1
AX358475
LOCUS AX358475
DEFINITION Sequence 1 from Patent WO0190326.
ACCESSION AX358475
VERSION AX358475.1 GI:18675086
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens

REFERENCE 1
AUTHORS Holmgren E., Kihlen, M., Wood, T. and Ekblom, J.
TITLE Novel matrix metalloproteinases
JOURNAL Patent: WO 0190326-A 1 29-NOV-2001;
PHARMACIA & UPJOHN COMPANY (US)
FEATURES
source
1. 1845
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ORIGIN
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Best Local Similarity 100.0%; Pred No. 0;
Matches 1627; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy 61 CATTTTCTTGTGATTTCCCTTAGTCGGATGACGGAATGAGAAAATGCAACTGG 120

Db 61 CATTTTCTTGTGATTTCCCTTAGTCGGATGACGGAATGAGAAAATGCAACTGG 120

Qy 121 CTCAGGCAATCTCAACCCAGTCTCTCTTGAATAAGAGGAATCATCTTGTTCAAA 180

Db 121 CTCAGGCAATCTCAACCCAGTCTCTCTTGAATAAGAGGAATCATCTTGTTCAAA 180

Qy 181 GCAAGAAATAGAGTCTCATAGATGACAAAATTCGGGAAATCAAGCAATTTTGGATTGA 240

Db 181 GCAAGAAATAGAGTCTCATAGATGACAAAATTCGGGAAATCAAGCAATTTTGGATTGA 240

Qy	241	CAGTGA	CTGGAAA	CTGGACTCAAA	CAACCCCTTGAGATCATGAAGACACCCAGGTGTGGG	300
Db	241	CAGTGA	CTGGAAA	CTGGAATCAAA	CAACCCCTTGAGATCATGAAGACACCCAGGTGTGGG	300
Qy	301	TGCCTGAT	TGGGCACGAT	TGGCTACAC	CTCCTCGGTGGAGAAATACAACCTCACCT	360
Db	301	TGCCTGAT	TGGGCACGAT	TGGCTACAC	CTCCTCGGTGGAGAAATACAACCTCACCT	360
Qy	361	ACAGAA	TAAATAA	CTATACT	CCGGATATGGCAGAGCTGCTGTGGATGAGGCTATCCAAG	420
Db	361	ACAGAA	TAAATAA	CTATACT	CCGGATATGGCAGAGCTGCTGTGGATGAGGCTATCCAAG	420
Qy	421	AAGGTT	TAGAGTGTGGAGCAAA	AGTCTCACT	CCATAAATAATCACCAAGATTTCAAAGGGGA	480
Db	421	AAGGTT	TAGAGTGTGGAGCAAA	AGTCTCACT	CCATAAATAATCACCAAGATTTCAAAGGGGA	480
Qy	481	TTGCAGACAT	CATGATTGCCTTTTAGGACTCGAGT	CCATGGTCCGCTCGCTGCTATTTTG	540	
Db	481	TTGCAGACAT	CATGATTGCCTTTTAGGACTCGAGT	CCATGGTCCGCTCGCTGCTATTTTG	540	
Qy	541	ATGGTCCCT	TGGGAGTGTGGCCATGCCTTTTCCCTCGGTCCGGGTCTCGGTGGTGACA	600		
Db	541	ATGGTCCCT	TGGGAGTGTGGCCATGCCTTTTCCCTCGGTCCGGGTCTCGGTGGTGACA	600		
Qy	601	CTCAATTTTGAT	TGAGGATGA	AAATCTGGAACCAAGGATGGAGCAGGATCAACTTGTGTTCTTG	660	
Db	601	CTCAATTTTGAT	TGAGGATGA	AAATCTGGAACCAAGGATGGAGCAGGATCAACTTGTGTTCTTG	660	
Qy	661	TGGCTGCTCAT	GAAATTTGGTCA	TGCGACTGGGCTCTCTCACTCCAAATGATCAAAACAGCT	720	
Db	661	TGGCTGCTCAT	GAAATTTGGTCA	TGCGACTGGGCTCTCTCACTCCAAATGATCAAAACAGCT	720	
Qy	721	TGATGTT	CCCCAAATATGTCCTCCCTGGATCCAGAAAATACCCACTTTCTCAGGATGATA	780		
Db	721	TGATGTT	CCCCAAATATGTCCTCCCTGGATCCAGAAAATACCCACTTTCTCAGGATGATA	780		
Qy	781	TCAATGGAAT	CCAGTCCATCTATGGAGGTCTGCCTAAGGTACCTGTAAAGCAAGCAAC	840		
Db	781	TCAATGGAAT	CCAGTCCATCTATGGAGGTCTGCCTAAGGTACCTGTAAAGCAAGCAAC	840		
Qy	841	CCACTATAC	CCCCATGCTGTGACCCCTGACTTTGACTTTTGTAGCGCTATCACAACTTTTCGCA	900		
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Qy	901	GAGAGTAA	TGTTCTTTTAAAGGACAGGCACCTATGAGGATCTAATATGATATACCGATG	960		
Db	901	GAGAGTAA	TGTTCTTTTAAAGGACAGGCACCTATGAGGATCTAATATGATATACCGATG	960		
Qy	961	TTGAGTTTGAA	TAAATTTGCTTCATCTGGCCATCTCTGCCAGCTGATCTGCAAGCTGCAT	1020		
Db	961	TTGAGTTTGAA	TAAATTTGCTTCATCTGGCCATCTCTGCCAGCTGATCTGCAAGCTGCAT	1020		
Qy	1021	ACGAGAAC	CCCAGAGATAAGATTCTGGTTTTTAAAGATGAAAATCTCTGGATGATCAGAG	1080		
Db	1021	ACGAGAAC	CCCAGAGATAAGATTCTGGTTTTTAAAGATGAAAATCTCTGGATGATCAGAG	1080		
Qy	1081	GATATGCTGT	CTTGCCAGATTATCCCAAAATCCATCCATACATTAAGTTTTCCAGGACGTG	1140		
Db	1081	GATATGCTGT	CTTGCCAGATTATCCCAAAATCCATCCATACATTAAGTTTTCCAGGACGTG	1140		
Qy	1141	TGAGRAAAT	TAGATGACCGCTGTGCTATAGACCAAGAAAAACCTACTCTTTCTGTGG	1200		
Db	1141	TGAGRAAAT	TAGATGACCGCTGTGCTATAGACCAAGAAAAACCTACTCTTTCTGTGG	1200		
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Db	1261	GAGTGGTAA	AAACATCTTCTCGGAATCAGTATCCGTGTGTGATGCTGTGCTTCCAGTACAAG	1320		

Qy	1321	GATTCCTCTTTTTCAGCCGTGGATCAAGCAATTTGAAATCAACATTTAAGACAAGAAATA	1381					
Db	1321	GATTCCTCTTTTTCAGCCGTGGATCAAGCAATTTGAAATCAACATTTAAGACAAGAAATA	1380					
Qy	1381	TTACCCGAATCATGAGAACTAAATACTTTGGTTTCAATGCAAAAGAACCAAAAGAACTCCCTCAT	1440					
Db	1381	TTACCCGAATCATGAGAACTAAATACTTTGGTTTCAATGCAAAAGAACCAAAAGAACTCCCTCAT	1440					
Qy	1441	TTGGTTTGTATATCAACACAGGAAAAAGACACATTCAGGAGGCATAAAGATATTTGATCATTA	1500					
Db	1441	TTGGTTTGTATATCAACACAGGAAAAAGACACATTCAGGAGGCATAAAGATATTTGATCATTA	1500					
Qy	1501	AGAGTTTAAAGCTGTTTATTTTGGTATTTGCTTCATTTGCTGAAATAACACATTCATTTATTC	1560					
Db	1501	AGAGTTTAAAGCTGTTTATTTTGGTATTTGCTTCATTTGCTGAAATAACACATTCATTTATTC	1560					
Qy	1561	AATAAAATTCATAGACCTTAAATAATAAACCTCAACAGGCTCTTTTAATATAAAATTCGCTTCAA	1620					
Db	1561	AATAAAATTCATAGACCTTAAATAATAAACCTCAACAGGCTCTTTTAATATAAAATTCGCTTCAA	1620					
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Db	1621	AATAGAA 1627						
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LOCUS	AX464058	1647 bp	DNA linear PAT 16-JUL-2002					
DEFINITION	Sequence 191 from Patent WO0140466.							
ACCESSION	AX464058							
VERSION	AX464058.1	GI:218999046						
KEYWORDS	Homo sapiens (human)							
SOURCE	Homo sapiens							
ORGANISM	Homo sapiens							
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Eureleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.							
AUTHORS	Baker,K.P., Beresini,M., Deforge,L., Desnoyers,L., Filvaroff,E., Gao,W.Q., Gerritsen,M.E., Goddard,A., Godowski,P.J., Gurney,A.L., Sherwood,S., Smith,V., Stewart,T.A., Tumas,D., Watanabe,C.K., Wood,W.L. and Zhang,Z.							
TITLE	Secreted and transmembrane polypeptides and nucleic acids encoding same							
JOURNAL	Patent: WO 0140466-A 191 07-JUN-2001;							
FEATURES	Genentech Inc. (US)							
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ORIGIN								
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Best Local Similarity 99.9%; Pred. No. 0;								
Matches 1626; Conservative 0; Mismatches 1; Indels 0; Gaps 0;								
Qy	1	GCTTCAGCTGAAGAAAGAGAGGAATGAAGCGCCCTCTGCTCTGTGTGTTCTTTATATAA	60					
Db	1	GCTTCAGCTGAAGAAAGAGAGGAATGAAGCGCCCTCTGCTCTGTGTGTTCTTTATATAA	60					
Qy	61	CATTTTCTCTGCATTTCCCTTAGTCCGGATGACGGAATATGAAGAAATATCAACTGG	120					
Db	61	CATTTTCTCTGCATTTCCCTTAGTCCGGATGACGGAATATGAAGAAATATCAACTGG	120					
Qy	121	CTCAGGCATATCTCAACAGCTTCTACTCTCTTGAAATAGAGGAATCATCTGTTCCAA	180					
Db	121	CTCAGGCATATCTCAACAGCTTCTACTCTCTTGAAATAGAGGAATCATCTGTTCCAA	180					
Qy	181	GCAAGATAGAGTCTCATAGATGACAAATTCGGGAATCGCAGCATTTTGGATTGA	240					
Db	181	GCAAGAAATAGAGTCTCATAGATGACAAATTCGGGAATCGCAGCATTTTGGATTGA	240					
Qy	241	CAGTGACTGAAAACCTGGATCTCAAAACCCCTTGAGATCATGAAGACACCCAGGTGTGGG	300					

ORIGIN

Query Match 98.4%; Score 1600.6; DB 6; Length 1841;
 Best Local Similarity 99.4%; Pred. No. 0;
 Matches 1606; Conservative 0; Mismatches 9; Indels 0; Gaps 0;

QY 13 GAAAGAGAGGAAATGAAGCGCTTCTGCTTCTGTTGTTGTTTATTAACATTTTCTTCTG 72
 DB 1 GAAAGAGAGGAAATGAAGCGCTTCTGCTTCTGTTGTTGTTTATTAACATTTTCTTCTG 60

QY 73 CATTTCCCTTATGTCGGATGACGGAATGAAGAAATATGCAACTGCTCAGGCAATC 132
 DB CATTTCCCTTATGTCGGATGACGGAATGAAGAAATATGCAACTGCTCAGGCAATC 120

QY 133 TCACCAAGTTCTACTCTTCTGAAATGAGAGGAATCATCTGTTTCAAAGCAAGATAGGA 192
 DB TCACCAAGTTCTACTCTTCTGAAATGAGAGGAATCATCTGTTTCAAAGCAAGATAGGA 180

QY 193 GTCTCATAGATGACAAAATTCGGGAAATGCAAGCAATTTTGGATTTGACAGTGAAGTGGAA 252
 DB GTCTCATAGATGACAAAATTCGGGAAATGCAAGCAATTTTGGATTTGACAGTGAAGTGGAA 240

QY 253 AACTGGACTCAAAACACCTTGATGATCATGAAGACACCCAGGTGTGGGTGCTGATGTGG 312
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QY 313 GCCAGTATGGCTACACCTCCCTGGGTGGAGAAATACAACTCAGTGAAGTGAAG 372
 DB GCCAGTATGGCTACACCTCCCTGGGTGGAGAAATACAACTCAGTGAAGTGAAG 360

QY 373 ACTATACCTCCGATATGCAAGCTGCTGTGGATGAGGCTATCCAAGAGGTTTGAAG 432
 DB ACTATACCTCCGATATGCAAGCTGCTGTGGATGAGGCTATCCAAGAGGTTTGAAG 420

QY 433 TGTGAGCAAAAGTCACTCCATCAAAATTCACAAAGATTTCAAAGGGATTCGAGACATCA 492
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QY 493 TGATTTGCTTTAGGACTCGAGTCCAGTCCGTTGCTGCTATTTTATGATGCTCCCTTGG 552
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QY 553 GAGTGTCTGGCATGCTCTTCTCTGCTGCTGGGTCTGGGTGTCACACTCATTTTGTGATG 612
 DB GAGTGTCTGGCATGCTCTTCTCTGCTGCTGGGTCTGGGTGTCACACTCATTTTGTGATG 600

QY 613 AGGATGAAATCGGACCAAGGATGAGCAGGATTCAACTGTTTCTTGTGGCTGCTCATG 672
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QY 673 AATTGGTTCATGCACTGGGCTCTCTCACTCCATGATCAACAGCCTTGATGTTCCCAA 732
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QY 733 ATTATGCTCCCTGGATCCCAAGAAATACCACTTTCTCAGGATGATATCAATGGAATCC 792
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QY 1393 TGAGAACTAATACTTGTGTTTCAATGCAAGAACCAAGAACTCCCTCATTTGGTTTGATA 1452
 DB 1381 TGAGAACTAATACTTGTGTTTCAATGCAAGAACCAAGAACTCCCTCATTTGGTTTGATA 1440

QY 1453 TCAACAGGAAAAGACACATTCAGGAGCATAAAGATATTGTATCATAGAGTTTAAAGT 1512
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QY 1573 GACCTAAATAAACCCTCAACAGGCTTTTATATAAATCTGCTTCAAAATAGAA 1627
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RESULT 5
 AF195192
 LOCUS Homo sapiens matrix metalloprotease MMP-27 mRNA linear PRI 29-NOV-2000
 DEFINITION Homo sapiens matrix metalloprotease MMP-27 mRNA, complete cds.
 ACCESSION AF195192
 VERSION AF195192.1 GI:11066089
 KEYWORDS
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 REFERENCE 1 (bases 1 to 1655)
 AUTHORS Benoit de Coignac, A., Elson, G., Magistrelli, G., Jeannin, P.,
 Delneste, Y., Aubry, J.P., Berthier, O., Bonnefoy, J.Y. and
 Gauchat, J.F.
 TITLE Cloning of a Novel Matrix Metalloproteinase Homologous to
 Stromelysins
 JOURNAL Unpublished
 REFERENCE 2 (bases 1 to 1655)
 AUTHORS Benoit de Coignac, A., Elson, G., Magistrelli, G., Jeannin, P.,
 Delneste, Y., Aubry, J.P., Berthier, O., Bonnefoy, J.Y. and
 Gauchat, J.F.
 TITLE Direct Submission
 JOURNAL Submitted (15-OCT-1999) Molecular Biology, Pierre-Fabre, 5, Avenue
 Napoleon III, Saint Julien en Genevois, 74 74164, France
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ORIGIN			
Query Match		97.2%; Score 1580.8; DB 9; Length 1655;	
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QY	24	ATGAAGCGCCTCTGCTCTGTGTTGTTCTTTATACCAFTTTCTCTGCAATTCCTCTTA	83
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DB	187	GACAAATTCGGAAATGCAAGCATTTTTTGGATTGACAGTGACTGCGAAATCGGACTCA	246
QY	264	AACACCTTCAGATCATGAACACCCAGTGTGGGTGCTGATGTGGCCAGTATGCG	323
DB	247	AACACCTTCAGATCATGAACACCCAGTGTGGGTGCTGATGTGGCCAGTATGCG	306
QY	324	TACACCTTCCTGGTGGAGAAATCAACCTCACCTACAGATAATAAATACTATCTCCG	383
DB	307	TACACCTTCCTGGTGGAGAAATCAACCTCACCTACAGATAATAAATACTATCTCCG	366
QY	384	GATATGCGACGAGCTGCTGTGATGAGGCTATCCAAAGAGGTTTGAAGTGTGGAGCAA	443
DB	367	GATATGCGACGAGCTGCTGTGATGAGGCTATCCAAAGAGGTTTGAAGTGTGGAGCAA	426
QY	444	GTCACTCCACTAAATTCACCAAGATTTCAGAGGGATTCAGACATCATGATTCCTTT	503
DB	427	GTCACTCCACTAAATTCACCAAGATTTCAGAGGGATTCAGACATCATGATTCCTTT	486
QY	504	AGGACTCGAGTCATGTCGGTGCCTGCTATTTTGTATGCTCCCTTGGAGTGTGGC	563
DB	487	AGGACTCGAGTCATGTCGGTGCCTGCTATTTTGTATGCTCCCTTGGAGTGTGGC	546
QY	564	CATGCTCTTCTCTGTCGGGTCTGGGTGGTGAACATCATTTTGTATGAGGATGAAAC	623
DB	547	CATGCTCTTCTCTGTCGGGTCTGGGTGGTGAACATCATTTTGTATGAGGATGAAAC	606
QY	624	TGACCAAGATGAGGAGGATTCACCTGCTTCTGTTGCTGCTCATGAAATTTGTCAT	683
DB	607	TGACCAAGATGAGGAGGATTCACCTGCTTCTGTTGCTGCTCATGAAATTTGTCAT	666
QY	684	GCACTGGGGCTCTCTCACTCCAATGATCAAAACAGCCTTGATGTTCCCAATTTATGTCCT	743
DB	667	GCACTGGGGCTCTCTCACTCCAATGATCAAAACAGCCTTGATGTTCCCAATTTATGTCCT	726
QY	744	CTGGATCCCAAGAAATACCACTTTCTCAGATGATATCAATGAATCCAGTCCATCTAT	803
DB	727	CTGGATCCCAAGAAATACCACTTTCTCAGATGATATCAATGAATCCAGTCCATCTAT	786

QY	804	GGAGGTCTGCTTAAGGTACTCTGTAAGCCAAAGAACCCACTATATACCCCATGCTGTGAC	863
DB	787	GGAGGTCTGCTTAAGGAACCTGCTAAGCCAAAGAACCCACTATATACCCCATGCTGTGAC	846
QY	864	CCTGACTTCACTTTTCCAGCGTATCAAACTTTCCGAGAGAGTAATGTTCTTTAAAGGC	923
DB	847	CCTGACTTCACTTTTCCAGCGTATCAAACTTTCCGAGAGAGTAATGTTCTTTAAAGGC	906
QY	924	AGGCACTTGAAGGATCTATTATGATATCACGGATGTTGAGTTGAAATTAATGCTTCA	983
DB	907	AGGCACTTGAAGGATCTATTATGATATCACGGATGTTGAGTTGAAATTAATGCTTCA	966
QY	984	TTCTGGCCATCTCTGCGAGTGTGCAAGCTGATACGAGACCCAGAGATAAGATT	1043
DB	967	TTCTGGCCATCTCTGCGAGTGTGCAAGCTGATACGAGACCCAGAGATAAGATT	1026
QY	1044	CTGGTTTTTAAAGATGAAACCTTCTGGATGATCAGAGGATATGCTCTTTCGCAGATTAT	1103
DB	1027	CTGGTTTTTAAAGATGAAACCTTCTGGATGATCAGAGGATATGCTCTTTCGCAGATTAT	1086
QY	1104	CCCAATTCATCATACATTAGGTTTTTCCAGGACGTGTGAAGAAATAGATGACGCGTC	1163
DB	1087	CCCAATTCATCATACATTAGGTTTTTCCAGGACGTGTGAAGAAATAGATGACGCGTC	1146
QY	1164	TGTGATAAGACCAACCAAGAAACCTACTTCTTGTGGCATTTGCTGGAGTTTGAT	1223
DB	1147	TGTGATAAGACCAACCAAGAAACCTACTTCTTGTGGCATTTGCTGGAGTTTGAT	1206
QY	1224	GAAATGACCAACCAACCAAGAAATTCCTGAGAGAGTGTGTAACCACTTTCCTGGA	1283
DB	1207	GAAATGACCAACCAACCAAGAGGTTCCCGCAGAGAGTGTGTAACCACTTTCCTGGA	1266
QY	1284	ATCAGTATCGGTGTTGATGCTGCTTTCAGTACAAAGGATTTCTTTTTCAGCCGTGA	1343
DB	1267	ATCAGTATCGGTGTTGATGCTGCTTTCAGTACAAAGGATTTCTTTTTCAGCCGTGA	1326
QY	1344	TCAAAGCAATTTGAATACCAACATTAAAGACAAAGATATTACCCGAATCATGAGAACTAAT	1403
DB	1327	TCAAAGCAATTTGAATACCAACATTAAAGACAAAGATATTACCCGAATCATGAGAACTAAT	1386
QY	1404	ACTTGGTTTTCAATGCAAGAACCAAGAACTCTCTATTTTGGTTTTGATATCAACAGAA	1463
DB	1387	ACTTGGTTTTCAATGCAAGAACCAAGAACTCTCTATTTTGGTTTTGATATCAACAGAA	1446
QY	1464	AAAGCACTTCAGGAGGCATAAAGATTTGTATCATAGAGTTTAACTTTTATTTT	1523
DB	1447	AAAGCACTTCAGGAGGCATAAAGATTTGTATCATAGAGTTTAACTTTTATTTT	1506
QY	1524	GGTATTGTTTCATTTGTGAAACACCTCTATTATTAATAAATTCATGACCTAAATA	1583
DB	1507	GGTATTGTTTCATTTGTGAAACACCTCTATTATTAATAAATTCATGACCTAAATA	1565
QY	1584	AACCTCAACAGGCTTTTAAATAATAAATTCCTGTTCAAAATAGAA	1627
DB	1566	AACCTCAACAGGCTTTTAAATAATAAATTCCTGTTCAAAATAGAA	1609

RESULT 6			
AX089610	1583 bp	DNA	linear
LOCUS	Sequence 1 from Patent WO0116335.		
DEFINITION			
ACCESSION	AX089610		
VERSION	AX089610.1	GI:13443799	
KEYWORDS			
SOURCE			
ORGANISM	Homo sapiens (human)		
REFERENCE			
AUTHORS	Homo sapiens		
TITLE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
JOURNAL	Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.		
	1 benoit de Coignac, A., Elson, G. and Gauchat, J.F.		
	Stromelysin-homologous novel mmp-27 matrix metalloproteinase		
	Patent: WO 0116335-A 1 08-MAR-2001;		

PIERRE FABRE MEDICAMENT (FR)
Location/Qualifiers
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/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"
/note="Gene codant pour MMP-24"

ORIGIN

Query Match 95.1%; Score 1548; DB 6; Length 1583;
Best Local Similarity 99.0%; Pred. No. 0;
Matches 1568; Conservative 0; Mismatches 15; Indels 1; Gaps 1;

QY 10 GAAGAAAGAGAGGATGAAGCGCTTCCTGCTCTGCTGTTGTTCTTTTATACATTTCTT 69
Db 1 GAAGAAAGAGAGGATGAAGCGCTTCCTGCTCTGCTGTTGTTCTTTTATACATTTCTT 60

QY 70 CTGCAATTTCCCTTAGTCCGGATGACGGAAATGAAGAAATATGCAACTGGCTCAGGCAT 129
Db 61 CTGCAATTTCCCTTAGTCCGGATGACGGAAATGAAGAAATATGCAACTGGCTCAGGCAT 120

QY 130 ATCTCAACAGCTTCTCTCTTGAATAGAGGAATCACTTGTTCAAAGCAAGAATA 189
Db 121 ATCTCAACAGCTTCTCTCTTGAATAGAGGAATCACTTGTTCAAAGCAAGAATA 180

QY 190 GGAGTCTCATAGATCACAATAATCGGAAATGCAAGCAATTTTGGATTGACAGTGACTG 249
Db 181 GGAGTCTCATAGATCACAATAATCGGAAATGCAAGCAATTTTGGATTGACAGTGACTG 240

QY 250 GAAAACTGGAATCAAAACCCCTTCAGATCATGAACACACCCAGGTGGGGTGCCTGATG 309
Db 241 GAAAACTGGAATCAAAACCCCTTCAGATCATGAACACACCCAGGTGGGGTGCCTGATG 300

QY 310 TGGGCCAGTATGGCTACACCTCCCTGGGTGAGAAATACACCTCCTACAGAAATA 369
Db 301 TGGGCCAGTATGGCTACACCTCCCTGGGTGAGAAATACACCTCCTACAGAAATA 360

QY 370 TAAACTATACCTCCGATATGCAGAGCTGCTGTGGATGAGGCTATCCAAAGGTTTAG 429
Db 361 TAAACTATACCTCCGATATGCAGAGCTGCTGTGTGGATGAGGCTATCCAAAGGTTTAG 419

QY 430 AAGTGTGAGCAAAAGTCACTCCACTAAATTCACCAAGATTTCAAAGGGGATTCAGACA 489
Db 420 AAGTGTGAGCAAAAGTCACTCCACTAAATTCACCAAGATTTCAAAGGGGATTCAGACA 479

QY 490 TCATGATTCCTTTAGGATCGAGTCATGTCGTCGTCCTATTTGATGTCCTC 549
Db 480 TCATGATTCCTTTAGGATCGAGTCATGTCGTCGTCCTATTTGATGTCCTC 539

QY 550 TGGGAGTCTTGGCCATGCTCTTCTCTGTCGCTGTCGCTGTCGCTGTCACACTCATTTTG 609
Db 540 TGGGAGTCTTGGCCATGCTCTTCTCTGTCGCTGTCGCTGTCGCTGTCACACTCATTTTG 599

QY 610 ATGAGGATGAAATCTGGACCAAGATGAGCAGGATTCACACTTGTTCCTGCTGCTGCTC 669
Db 600 ATGAGGATGAAATCTGGACCAAGATGAGCAGGATTCACACTTGTTCCTGCTGCTGCTC 659

QY 670 ATGAATTTGGTCATGCACTGGGGCTCTCTCACTCCAAATGATCAAAACAGCTTGTATTC 729
Db 660 ATGAATTTGGTCATGCACTGGGGCTCTCTCACTCCAAATGATCAAAACAGCTTGTATTC 719

QY 730 CAAATATGCTCCCTGGATCCAGAAATACCACTTCTCAGGATGATCAATGAA 789
Db 720 CAAATATGCTCCCTGGATCCAGAAATACCACTTCTCAGGATGATCAATGAA 779

QY 790 TCCAGTCCATCTATGAGGCTCTGCTTAAGGATGCTGTAAGCAAGCAAGCAATATAC 849
Db 780 TCAAGTCCATCTATGAGGCTCTGCTTAAGGATGCTGTAAGCAAGCAAGCAATATAC 839

QY 850 CCCATGCTGTGACCTGACTTGAATTTTGAGGCTATCACAACTTTCGCGAGAGATGAA 909
Db 840 CCCATGCTGTGACCTGACTTGAATTTTGAGGCTATCACAACTTTCGCGAGAGATGAA 899

QY 910 TGTTCTTTAAAGCAGGCACCTATGGAGATCTATTATGATATCACGATGTTGAGTTTG 969
Db 900 TGTTCTTTAAAGCAGGCACCTATGGAGATCTATTATGATATCACGATGTTGAGTTTG 959

QY 970 AATTAATTTGCTTCAATCTGGCCATCTCTGCCAGCTGATCTGCAAGCTCATACGAGAACC 1029
Db 960 AATTAATTTGCTTCAATCTGGCCATCTCTGCCAGCTGATCTGCAAGCTCATACGAGAACC 1019

QY 1030 CCAGAGATAAGATTTCTGGTTTTTAAAGATGAAAACCTCTGGATGATCAGAGATGCTG 1089
Db 1020 CCAGAGATAAGATTTCTGGTTTTTAAAGATGAAAACCTCTGGATGATCAGAGATGCTG 1079

QY 1090 TCTTGCAGATTTATCCCAATCCATACATTAAGTGTTCAGAGAGCTGGAAGAAA 1149
Db 1080 TCTTGCAGATTTATCCCAATCCATACATTAAGTGTTCAGAGAGCTGGAAGAAA 1139

QY 1150 TAGATGCAAGCCGCTGTGTATGAAGCAACCAAGAAAACCTACTTCTTGTGGGCATTTGGT 1209
Db 1140 TAGATGCAAGCCGCTGTGTATGAAGCAACCAAGAAAACCTACTTCTTGTGGGCATTTGGT 1199

QY 1210 GCTGAGGTTTGATGAATGACCCAAACCATGGACAAAGGATTCCTGCGAGAGTGTAA 1269
Db 1200 GCTGAGGTTTGATGAATGACCCAAACCATGGACAAAGGATTCCTGCGAGAGTGTAA 1259

QY 1270 AACACTTTCTCGAATCAGTATCCGTGTGTGCTGCTTCCAGTACAAAGATTTCTCT 1329
Db 1260 AACACTTTCTCGAATCAGTATCCGTGTGTGCTGCTTCCAGTACAAAGATTTCTCT 1319

QY 1330 TTTTCAGCCGTGGATCAAGCAATTTGAATACAAATTAAGACAAAGAAATATTACCCGAA 1389
Db 1320 TTTTCAGCCGTGGATCAAGCAATTTGAATACAAATTAAGACAAAGAAATATTACCCGAA 1379

QY 1390 TCATGAGAACTAATACTTGGTTTCAATGCAAGAACCAAGAACTCTCATTTGGTTTG 1449
Db 1380 TCATGAGAACTAATACTTGGTTTCAATGCAAGAACCAAGAACTCTCATTTGGTTTG 1439

QY 1450 ATATCAACAGGAAAGAACCAATTCAGGAGCATTAAGATATTGTATCAAGAGTTTAA 1509
Db 1440 ATATCAACAGGAAAGAACCAATTCAGGAGCATTAAGATATTGTATCAAGAGTTTAA 1499

QY 1510 GCTTGTATTTTGGTATTTGTTTCAATTTGCTGAAACACCTTCTATTTATCAATAATTC 1569
Db 1500 GCTTGTATTTTGGTATTTGTTTCAATTTGCTGAAACACCTTCTATTTATCAATAATTC 1559

QY 1570 ATAGACCTAAATTAACCTCAACA 1593
Db 1560 ATAGACCTAAATTAACCTCAACA 1583

RESULT 7
AR263900/c
LOCUS AR263900 1687 bp DNA linear PAT 29-JAN-2003
DEFINITION Sequence 78 from patent US 6331427.
ACCESSION AR263900
VERSION AR263900.1 GI:28075904
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 1687)
AUTHORS Robison,K.E.
TITLE Protease homologs
JOURNAL Patent: US 6331427-A 78 18-DEC-2001;
FEATURES Location/Qualifiers
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ORIGIN

Query Match 87.1%; Score 1417.8; DB 6; Length 1687;
Best Local Similarity 99.8%; Pred. No. 0;
Matches 1430; Conservative 0; Mismatches 2; Indels 1; Gaps 1;

QY	196	TCATAGATGACAAAATTTCGGGAAATCAAGCAATTTTTTGTGATTGACAGTGCATCGGAAAAC	255
Db	1680	TCCGAGATGACAAAATTTCGGGAAATCAAGCAATTTTTTGTGATTGACAGTGCATCGGAAAAC	1621
QY	256	TGGACTCAAAACACCCCTTGAGATCATGAAAGACACCCAGGTCTGGGGTGCCTGTGATGTGGGCC	315
Db	1620	TGGACTCAAAACACCCCTTGAGATCATGAAAGACACCCAGGTCTGGGGTGCCTGTGATGTGGGCC	1561
QY	316	AGTATGGCTACACCCCTCCCTGGGTGGAGAAAATACAACCTCACCTACAGAAATAATAAAT	375
Db	1560	AGTATGGCTACACCCCTCCCTGGGTGGAGAAAATACAACCTCACCTACAGAAATAATAAAT	1501
QY	376	ATACTCCGATATGGCACGAGCTGCTGTGATGAGGCTATCCAAGAGGTTTGAAGAAGTGT	435
Db	1500	ATACTCCGATATGGCACGAGCTGCTGTGATGAGGCTATCCAAGAGGTTTGAAGAAGTGT	1441
QY	436	GGAGCAAGTCACTCCACTAAATTCACCAAGATTTCAAAGGGATTCAGACATCATGA	495
Db	1440	GGAGCAAGTCACTCCACTAAATTCACCAAGATTTCAAAGGGATTCAGACATCATGA	1381
QY	496	TTGCTTTTAGGACTTCGAGTCCATGGTCCGTGTCTCTCGCTATTTTGTATGGTCCCTTGGGAG	555
Db	1380	TTGCTTTTAGGACTTCGAGTCCATGGTCCGTGTCTCTCGCTATTTTGTATGGTCCCTTGGGAG	1321
QY	556	TGCTTGGCCATGCTTTCTCTCGGTCCGGTCTGGGTGTGTGACATCATATTTGTATGAGG	615
Db	1320	TGCTTGGCCATGCTTTCTCTCGGTCCGGTCTGGGTGTGTGACATCATATTTGTATGAGG	1261
QY	616	ATGAAACTGGACCAAGGATGGACAGGATCAACTTGTGTTTCTGTGGCTGCTCATGAAT	675
Db	1260	ATGAAACTGGACCAAGGATGGACAGGATCAACTTGTGTTTCTGTGGCTGCTCATGAAT	1201
QY	676	TTGCTCATGCACTGGGGCTCTCTCACTCCAATGATCAAAAGCCTTGATGTTTCCCAAAT	735
Db	1200	TTGCTCATGCACTGGGGCTCTCTCACTCCAATGATCAAAAGCCTTGATGTTTCCCAAAT	1141
QY	736	ATGTCCTCCCTGGATCCAGAAAATACCCACTTTCTCAGGATGATCAATGGAAATCCAGT	795
Db	1140	ATGTCCTCCCTGGATCCAGAAAATACCCACTTTCTCAGGATGATCAATGGAAATCCAGT	1081
QY	796	CCATCATGAGGCTTCGCTTAAGTACCTGCTAAGCCAAAGGACCCACATATACCCCATG	855
Db	1080	CCATCATGAGGCTTCGCTTAAGTACCTGCTAAGCCAAAGGACCCACATATACCCCATG	1021
QY	856	CCGTGTGACCTGACTTGACTTTTTCAGCGCTATACAACTTTCCGACAGAAAGTATGTTCT	915
Db	1020	CCGTGTGACCTGACTTGACTTTTTCAGCGCTATACAACTTTCCGACAGAAAGTATGTTCT	961
QY	916	TTAAAGCAGGCACTATGAGGATCTATTATGATATCACGGATGTTTGAATTTGAATTA	975
Db	960	TTAAAGCAGGCACTATGAGGATCTATTATGATATCACGGATGTTTGAATTTGAATTA	901
QY	976	TTGCTTCAATTCTGGCCATCTCTGCCAGCTGATCTGCAAGCTGCATACAGAAACCCAGAG	1035
Db	900	TTGCTTCAATTCTGGCCATCTCTGCCAGCTGATCTGCAAGCTGCATACAGAAACCCAGAG	841
QY	1036	ATAAGATTCTGGTTTTTAAAGATGAAAACCTTCTGGATGATCAGAGGATATGCTGTCTTGC	1095
Db	840	ATAAGATTCTGGTTTTTAAAGATGAAAACCTTCTGGATGATCAGAGGATATGCTGTCTTGC	781
QY	1096	CAGATTATCCAAATCCATCCATATAGTTTTTCCAGA-CGTGTGAAGAAAATAGAT	1154
Db	780	CAGATTATCCAAATCCATCCATATAGTTTTTCCAGA-CGTGTGAAGAAAATAGAT	721
QY	1155	GCAGCCGTCTGTGATAGACACCAAGAAACCTACTCTTTCTGTGGGCATTTGGTGCTGG	1214
Db	720	GCAGCCGTCTGTGATAGACACCAAGAAACCTACTCTTTCTGTGGGCATTTGGTGCTGG	661
QY	1215	AGGTTTGTATGAAATGACCCAAACCATGGACAAAGGATTCGCGACAGAGTGGTAAACAC	1274
Db	660	AGGTTTGTATGAAATGACCCAAACCATGGACAAAGGATTCGCGACAGAGTGGTAAACAC	601
QY	1275	TTTCTCCGGAATCAGTATCCGGTTGTGCTGCTTTCCAGTACAAGGATTTCTTTTTTC	1334

Db	600	TTTTCTTGGAAATCAGTATCCCGTGTGTGATGCTGCTTCCAGTACAAGGATTTCTTCTTTTC	541
Qy	1335	AGCGTGGATCAAGCAATTTGAATCAACATTAAGACAAAGAATATTACCCGAATCATG	1394
Db	540	AGCGTGGATCAAGCAATTTGAATCAACATTAAGACAAAGAATATTACCCGAATCATG	481
Qy	1395	AGAACTAATATCTGGTTTCAATGCAAGAACCAAGAACTCTCTCATTTGGTTTGTATC	1454
Db	480	AGAACTAATATCTGGTTTCAATGCAAGAACCAAGAACTCTCTCATTTGGTTTGTATC	421
Qy	1455	AACAGGAAAAAGCACAATTCAGAGGCAATAAGATATTGTATCATATAGAGTTTAAAGCTTG	1514
Db	420	AACAGGAAAAAGCACAATTCAGAGGCAATAAGATATTGTATCATATAGAGTTTAAAGCTTG	361
Qy	1515	TTTATTTTTCGTTATGTTTCATTTGCTGAAAAACACTTCTATTTATCAATAAATTCATAGA	1574
Db	360	TTTATTTTTCGTTATGTTTCATTTGCTGAAAAACACTTCTATTTATCAATAAATTCATAGA	301
Qy	1575	CCTAAAATAAACCTCAACAGCTCTTTTAAATATAAAATTCCTGCTCAAAATAGAA	1627
Db	300	CCTAAAATAAACCTCAACAGCTCTTTTAAATATAAAATTCCTGCTCAAAATAGAA	248
<p>RESULT 8</p> <p>LOCUS AX249967 1488 bp DNA linear PAT 28-SEP-2001</p> <p>DEFINITION Sequence 3 from Patent WO0166766.</p> <p>ACCESSION AX249967</p> <p>VERSION AX249967.1 GI:15864453</p> <p>KEYWORDS</p> <p>SOURCE Homo sapiens (human)</p> <p>ORGANISM Homo sapiens</p> <p>REFERENCE 1 Fajardo,M.D., Smith,R. and Moss,P.</p> <p>AUTHORS A matrix metalloproteinase (mmp-25)</p> <p>TITLE Patent: WO 0166766-A 3 13-SEP-2001;</p> <p>JOURNAL DARWIN MOLECULAR CORPORATION (US)</p> <p>FEATURES</p> <p>source Location/Qualifiers</p> <p>1..1488</p> <p>/organism="Homo sapiens"</p> <p>/mol_type="unassigned DNA"</p> <p>/db_xref="taxon:9606"</p>			
ORIGIN			
<p>Query Match 79.5%; Score 1293.4; DB 6; Length 1488;</p> <p>Best Local Similarity 91.1; Pred. No. 3.1e-308;</p> <p>Matches 1439; Conservative 0; Mismatches 11; Indels 129; Gaps 1;</p>			
Qy	7	GCTGAAGAAAGAGAGGAATCAAGCGCTTCTGCTTCTGTGTTGTTCTTTTATAACATTTT	66
Db	36	GCAGTGAAAGAGAGGAATCAAGCGCTTCTGCTTCTGTGTTGTTCTTTTATAACATTTT	95
Qy	67	CTTCTGCATTTCCCTTAGTCGGGATGCGAAATGAAGAAATATCAACTGGCTCAGG	126
Db	96	CTTCTGCATTTCCCTTAGTCGGGATGCGAAATGAAGAAATATCAACTGGCTCAGG	155
Qy	127	CATATCTCAACCAAGTTCTACTCTCTTGAATAGAGGAATCATCTTGTTCGAAGCAAGA	186
Db	156	CATATCTCAACCAAGTTCTACTCTCTTGAATAGAGGAATCATCTTGTTCGAAGCAAGA	215
Qy	187	ATAGGAGTCTCATAGATGACAAATTCGGGAATGCAAGCATTTTGGATTCGACGTGA	246
Db	216	ATAGGAGTCTCATAGATGACAAATTCGGGAATGCAAGCATTTTGGATTCGACGTGA	275
Qy	247	CTGGAATACTGGACTCAAAACCCCTTGAGATCATGAAGACCCAGGTGTGGGTGCGCTG	306
Db	276	CTGGAATACTGGACTCAAAACCCCTTGAGATCATGAAGACCCAGGTGTGGGTGCGCTG	335
Qy	307	ATGTGGGCCAGTATGGCTACACCTCCCTGGGTGGAGAAATACAACTCACCTACAGAA	366

Db 336 ATGTGGCCAGTATGGCTACACCCCTCCCTGGTGGAGAAAATAACAACTCACACAGAA 395
 QY 367 TAATAAACTATACCTCCGATATGGACAGAGCTGCTGGATGAGGCTATCCAGAGGTT 426
 Db 396 TAATAAACTATACCTCCGATATGGACAGAGCTGCTGGATGAGGCTATCCAGAGGTT 455
 QY 427 TAGAAGTGTGGAGCAAGTCACTCCACTAAATTCACCAAGATTTCAAAGGGATTCGAG 486
 Db 456 TAGAAGTGTGGAGCAAGTCACTCCACTAAATTCACCAAGATTTCAAAGGGATTCGAG 515
 QY 487 ACATCATGATTGCCCTTTAGGACTCGAGTCCAGTCCAGTCCGCTCGCTATTTTGTATGTC 546
 Db 516 ACATCATGATTGCCCTTTAGGACTCG----- 540
 QY 547 CTTGGGAGTGTGGCCATGCCCTTCCTCTGCTCGGTCCGGTCTGGGTGGACACTCAT 606
 Db 541 ----- 540
 QY 607 TTGATGAGGATGAATACTGGACCAAGGATGGAGCAGGATTCAACTTGTTCCTTGTGGCTG 666
 Db 541 -----AGGATTCAACTTGTTCCTTGTGGCTG 566
 QY 667 CTCATGAATTTGGTCATGCACTGGGCTCTCTCACTCCAAATGATCAAAACAGCCTTGATG 726
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 QY 727 TCCCAAAATTTGCTCCCTGGATCCAGAAATACCCACTTCTCAGGATGATCAATG 786
 Db 627 TCCCAAAATTTGCTCCCTGGATCCAGAAATACCCACTTCTCAGGATGATCAATG 686
 QY 787 GAATCCAGTCCATCATGAGGCTCTGCCCTTAAGTACCTGCTAAAGCAAGCAACCACTA 846
 Db 687 GAATCCAGTCCATCATGAGGCTCTGCCCTTAAGTACCTGCTAAAGCAAGCAACCACTA 746
 QY 847 TACCCATGCTGTCGACCTGACTGCTTTGAGCGCTATCACAACTTTCCGACAGAGAG 906
 Db 747 TACCCATGCTGTCGACCTGACTGCTTTGAGCGCTATCACAACTTTCCGACAGAGAG 806
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 QY 967 TTGAATTAATGCTTCACTTCTGGCCATCTCTGCCAGCTGATCGCAAGCTGCATACGAGA 1026
 Db 867 TTGAATTAATGCTTCACTTCTGGCCATCTCTGCCAGCTGATCGCAAGCTGCATACGAGA 926
 QY 1027 ACCCAGAGATAAGATTCTGGTTTTTAAAGATGAATACTTCTGGATGATCAGAGATATG 1086
 Db 927 ACCCAGAGATAAGATTCTGGTTTTTAAAGATGAATACTTCTGGATGATCAGAGATATG 986
 QY 1087 CTGCTTCCGAGATATCCCAATCCATCCATACATAGTATAGTCTTCCAGAGCTGTGAAGA 1146
 Db 987 CTGCTTCCGAGATATCCCAATCCATCCATACATAGTATAGTCTTCCAGAGCTGTGAAGA 1046
 QY 1147 AAATAGATGCAAGCTCTGTGATAGAGACCAAGAAAAACCTACTCTTTTGGGCACTTT 1206
 Db 1047 AAATAGATGCAAGCTCTGTGATAGAGACCAAGAAAAACCTACTCTTTTGGGCACTTT 1106
 QY 1207 GGTGCTGAGGTTTGATGAATGACCCAAACCATGGAACAAAGGATTCCTCCGACAGAGTGG 1266
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 QY 1267 TAAACACTTTCCTCGAATCAGTATCCGTTGATGCTCTTCCAGTACAAAGGATTCCT 1326
 Db 1167 TAAACACTTTCCTCGAATCAGTATCCGTTGATGCTCTTCCAGTACAAAGGATTCCT 1226
 QY 1327 TCTTTTTCAGCGCTGGATCAAGCAATTTGAATACAAATTAAGCAAAAGATATATACC 1386
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 QY 1387 GAATCATGAGAACTAATACTTGGTTTCAATGCAAAAGAACCAAGAACTCCTCATTTGGTT 1446
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QY 1447 TTGATATCAACAGAAAAAGCACATTCCAGGAGCATAAAGATATTGTATCATAGAGTT 1506
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 QY 1507 TAAGCTTCTTTTATTTTGGTATTGTTTCATTTGCTGAAAAACACCTTCTATTTATCAATAA 1566
 Db 1407 TAAGCTTCTTTTATTTTGGTATTGTTTCATTTGCTGAAAAACACCTTCTATTTATCAATAA 1466
 QY 1567 TTCATAGACCTTAAATAAA 1585
 Db 1467 TTCATAGACCTTAAATAAA 1485
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 LOCUS Tupaia belangeri matrix metalloproteinase-27 mRNA, complete cds.
 DEFINITION AF281673
 ACCESSION AF281673.1 GI:12006363
 VERSION
 KEYWORDS
 SOURCE Tupaia belangeri (northern tree shrew)
 ORGANISM Tupaia belangeri
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Scandentia; Tupaiidae; Tupaiia.
 REFERENCE 1 (bases 1 to 1667)
 AUTHORS Guggenheim, J.A., To, C.H. and Frost, M.R.
 TITLE Molecular cloning of a novel matrix metalloproteinase (MMP-27) from
 JOURNAL sciera
 REFERENCE 2 (bases 1 to 1667)
 AUTHORS Guggenheim, J.A. and Frost, M.R.
 TITLE Direct Submission
 JOURNAL Submitted (23-JUN-2000) Department of Optometry & Vision Sciences,
 Cardiff University, King Edward VII Avenue, Cardiff, Wales CF10
 3NB, UK
 FEATURES
 source Location/Qualifiers
 1..1667
 /organism="Tupaia belangeri"
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LOCUS Sequence 1 from Patent WO0166766.
DEFINITION AX249965
ACCESSION AX249965
VERSION AX249965.1 GI:15864451
KEYWORDS Homo sapiens (human)
SOURCE Homo sapiens
ORGANISM Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1
AUTHORS Fajardo,M.D., Smith,R. and Moss,P.
TITLE A matrix metalloproteinase (mmp-25) expressed in skin cells
JOURNAL Patent: WO 016766-A 1 13-SEP-2001;
DARWIN MOLECULAR CORPORATION (US)
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CDS
Query Match 50.8%; Score 826.6; DB 6; Length 833;
Best Local Similarity 99.5%; Pred. No. 5.2e-193;
Matches 829; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

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RESULT 11
AF062392 1587 bp mRNA linear VRT 02-SEP-1998
LOCUS
DEFINITION Gallus gallus matrix metalloproteinase mRNA, complete cds.
ACCESSION AF062392
VERSION AF062392.1 GI:3511148
KEYWORDS
SOURCE Gallus gallus (chicken)
ORGANISM Gallus gallus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Archosauria; Aves; Neognathae; Galliformes; Phasianidae;
Phasianinae; Gallus.
1 (bases 1 to 1587)
Yang, M. and Kurkinen, M.
Cloning of a novel matrix metalloproteinase (CIMP) from chicken
embryo fibroblasts
J. Biol. Chem. (1998) In press
2 (bases 1 to 1587)
Yang, M. and Kurkinen, M.
Direct Submission
Submitted (29-APR-1998) Center for Molecular Medicine and Genetics,
Wayne State University School of Medicine, 5047 Gullen Mall,
Detroit, MI 48202, USA
FEATURES
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ECU62529
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DEFINITION Equus caballus matrix metalloproteinase 3 mRNA, complete cds.
ACCESSION U62529
VERSION U62529.1 GI:1480745
KEYWORDS
SOURCE Equus caballus (horse)
ORGANISM Equus caballus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Perissodactyla; Equidae; Equus.
REFERENCE 1 (bases 1 to 1804)
AUTHORS Richardson,D.W. and Dodge,G.R.
TITLE Molecular characteristics of equine stromelysin and the tissue
inhibitor of metalloproteinase 1
JOURNAL Am. J. Vet. Res. 59 (12), 1557-1562 (1998)
MEDLINE 99074117
PUBMED 9858406
REFERENCE 2 (bases 1 to 1804)
AUTHORS Richardson,D.W. and Dodge,G.R.
TITLE Direct Submission
JOURNAL Submitted (28-JUN-1996) Clinical Studies, New Bolton Center, School
of Veterinary Medicine, University of Pennsylvania, 382 West Street
Road, Kennett Square, PA 19348-1692, USA
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Best Local Similarity 60.4%; Pred. No. 3.8e-100;
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RESULT 15
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LOCUS AX393848 1804 bp DNA linear PAT 23-MAR-2002
DEFINITION Sequence 237 from Patent WO0212329.
ACCESSION AX393848
VERSION AX393848.1 GI:19701814
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE
1. Wang, T. and Fan, L.
Compositions and methods for the therapy and diagnosis of head and neck cancer
Patent: WO 0212329-A 237 14-FEB-2002;
CORIXA CORPORATION (US)
FEATURES
Location/Qualifiers
1..1804
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"

ORIGIN
Query Match 27.7%; Score 450.4; DB 6; Length 1804;
Best Local Similarity 60.4%; Pred. No. 3.8e-100;
Matches 868; Conservative 0; Mismatches 526; Indels 42; Gaps 6;

Qy 21 GGAATGAAGCCCTTCTGCTTCTGTTGTTTCTTTTAAATTTTCTGTCATTTCC 80
Db 50 GAAATGAAGATTTTCCAAATTTCTGCTGTACTATGCTGGCAGCGTGTCAACCTATCG 109
Qy 81 TTAGTCCG---GATGACGGAATAACAGAAATATGCAATGCACTGGCTCAGCATATCTCAAC 137
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Qy 138 CAGTTTCTACTCTCTTGAATAAGAGGAATCATCTTGTTCAAAGCAAGAAATAGGAGTCTC 197
Db 170 AAATACTACGACCTTGGAAAGAAATGAGACAATATGTTAGNAGAAAGACAGTGTCT 229
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Db 230 ATTGTTAAAAAATTCAGAAATTCAGAAATTCCTGGGTTTCAAGGTTCAGAGTGAAGAACTG 289
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Qy 318 T-----ATGGCTACACCTCCCTGGGTGGAGAAATACAACTCACCTACAGATATA 371
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QY 1122 TTAGGTTTTCCAGGACGTGTGAAGAAATAGATGACGCGTCTGTGATAGACCAAGA 1181
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QY 1362 AACATTAGACAAAGATATTTACCGAATCATGAGAACTAATCTCGTTTCAATG 1417
Db 1427 GACCCAAATGCAAGAAAGTGACACATGTTCTCAAGAGTAATAGTGTGTTTAATTG 1482

Search completed: November 15, 2004, 15:22:40
Job time : 7051 secs

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: November 15, 2004, 13:11:00 ; Search time 833 Seconds

(without alignments)
10253.071 Million cell updates/sec

Title: US-10-729-807-28

Perfect score: 1627

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Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 4134886 seqs, 2624710521 residues

Total number of hits satisfying chosen parameters: 8269772

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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1: Geneseqn1980s:*

2: Geneseqn1990s:*

3: Geneseqn2000s:*

4: Geneseqn2001as:*

5: Geneseqn2001bs:*

6: Geneseqn2002as:*

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8: Geneseqn2003as:*

9: Geneseqn2003bs:*

10: Geneseqn2003cs:*

11: Geneseqn2003ds:*

12: Geneseqn2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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24	1625.4	99.9	1647	9	ADA91616	Novel hum
25	1625.4	99.9	1647	9	ADB14679	Human PRO
26	1625.4	99.9	1647	9	ADB18640	Novel hum
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28	1625.4	99.9	1647	9	ADB19751	Novel hum
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34	1625.4	99.9	1647	9	ADA75037	Human PRO
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ALIGNMENTS

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ID AAA37666 standard; DNA; 1627 BP.

XX

AC AAA37666;

XX

DT 24-OCT-2000 (first entry)

XX

DE Human peptidase, HPEP-10 coding sequence.

XX

KW Human; peptidase; cell proliferative disorder; arteriosclerosis;

KW psoriasis; myelofibrosis; cancer; autoimmune disorder; Crohn's disease;

KW inflammatory disorder; AIDS; anaemia; allergy; asthma; atherosclerosis;

KW Grave's disease; multiple sclerosis; scleroderma; infection; diabetes;

KW metabolic disorder; Addison's disease; cystic fibrosis; diagnosis;

KW glycogen storage disease; obesity; therapy; HPEP-10; ds.

XX

OS Homo sapiens.

XX

PH Key

Location/Qualifiers

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/product= "HPEP-10"

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WO200042201-A2.

XX

PD 20-JUL-2000.

XX

PF 11-JAN-2000; 2000WO-US000641.

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PR 11-JAN-1999; 99US-0172247P.

PR

03-MAY-1999; 99US-0132253P.

PR

27-MAY-1999; 99US-0136653P.

XX

(INCY-) INCYTE PHARM INC.

PA

Bandman O, Hillman JL, Tang YT, Azimzai Y, Baughn MR, Lal P;

PI

Yue H, Lu DM;

XX

WPI; 2000-482832/42.

DR

P-PSDB; AAY90293.

XX

An isolated polypeptide for diagnosis, prevention and treatment of cell proliferative, autoimmune/ inflammatory and metabolic disorders comprises

KW Matrix metalloproteinase; MMP; extracellular matrix; ECM;
 KW embryonic development; morphogenesis; reproduction; tissue repair;
 KW mental disorder; Alzheimer's disease; multiple sclerosis; obesity;
 KW Parkinson's disease; motor neuron disease; metabolic disease; retinopathy;
 KW type 2 diabetes; cardiovascular; dyslipidaemia; adipogenesis; neuropathy;
 KW nephropathy; proliferative disease; cancer; psoriasis;
 KW prostate hyperplasia; hormonal disorder; alopecia; Crohn's disease;
 KW central nervous system disorder; CNS; inflammatory condition; arthritis;
 KW periodontal disease; wound healing; human; MMP1; ss.
 OS Homo sapiens.
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 FT /product= "Matrix metalloproteinase MMP1"
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 PN WO200190326-A2.
 XX
 PD 29-NOV-2001.
 XX
 PF 22-MAY-2001; 2001WO-US016563.
 XX
 PR 22-MAY-2000; 2000US-0206119P.
 XX
 PA (PHRA) PHARMACIA & UPJOHN CO.
 XX
 PI Holmgren E, Kihlen M, Wood T, Ekblom J;
 XX
 DR WPI; 2002-083105/11.
 DR P-PSDB; AAE14392.
 XX
 XX New matrix metalloproteinases (MMP) genes and polypeptides, useful for
 PT treating diseases or for screening modulators of MMP to treat such
 PT diseases, e.g. mental disorders, Parkinson's disease, cancers or
 PT inflammatory conditions.
 XX
 PS Claim 4; Page 59; 94pp; English.
 XX
 CC The invention relates to genes encoding matrix metalloproteinases (MMP).
 CC The MMP genes are useful for producing MMP polypeptides and for screening
 CC modulators of MMP. The MMPs are useful for breaking down extracellular
 CC matrix (ECM), which is essential for processes including embryonic
 CC development, morphogenesis, reproduction, or tissue repair and
 CC remodelling. The MMPs are particularly useful for identifying compounds
 CC that modulate the activity of genes to treat pathologies, e.g. mental
 CC disorders, Alzheimer's disease, multiple sclerosis, Parkinson's disease
 CC or motor neuron disease. The MMP polypeptides and genes, as well as their
 CC modulators, are useful for treating metabolic diseases and disorders
 CC (e.g. type 2 diabetes, obesity, cardiovascular, dyslipidaemias,
 CC adipogenesis, retinopathies, neuropathies or nephropathies),
 CC proliferative diseases and cancers (e.g. breast, colon or lung cancer,
 CC tumour growth, tumour invasion, psoriasis or prostate hyperplasia),
 CC hormonal disorders (e.g. male/female hormonal replacement, polycystic
 CC ovarian syndrome or alopecia), central nervous system (CNS) disorders,
 CC inflammatory conditions (e.g. Crohn's disease or arthritis), periodontal
 CC diseases or wound healing. The present sequence is human matrix
 CC metalloproteinase MMP1 cDNA
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 DB 481 TTGCAGACATCATGATTTGCTTTAGGACTCGAGTCCATGCTCGGTGCTCCTCGCTATTG 540
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 DB 541 ATGGTCCCTTGGGAGTGTGGCCATGCTTTCCCTCCTGGTCCGGGTCTGGGTGTGACA 600
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 DB 661 TGGCTGCTCATGAATTTGGTCAATGCACTGGGCTCTCTCACTCCAATGATCAACAGCCT 720
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 DB 721 TGATGTTCCCAAAATATGTCTCCCTGGATCCCAAGAAATACCCACTTTCTCAGGATGATA 780
 QY 781 TCAATGGAAATCAGTCCATATATGAGGTCTGCTTAAGTACTCTGAAGCAAAAGGAAC 840
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QY      1561 AATAAAATTCATAGACCTTAAATAAACCTCAACAGCTCTTTTAAATATAAATTCGTTCAA 1620
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RESULT 3

AA521339
ID AA521339 standard; cDNA; 1647 BP.

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XX      DT      24-OCT-2001 (first entry)
XX      DE      Human cDNA sequence encoding for PR05992 polypeptide.
XX      KW      Human secretory and transmembrane; PRO; mammalian; cancer; lung; breast;
KW      prostate; cervical; tumour necrosis factor-alpha; TNF-alpha; cartilage;
KW      ear; proliferation; glucose; free fatty acid; skeletal muscle; adipocyte;
KW      A-peptide; factor VIIA; gene therapy; ss.
XX      OS      Homo sapiens.
XX      PN      WO200140466-A2.
XX      PD      07-JUN-2001.
XX      PF      01-DEC-2000; 2000WO-US032678.
XX      PR      01-DEC-1999; 99WO-US028301.
PR      01-DEC-1999; 99WO-US028634.
PR      02-DEC-1999; 99WO-US028551.
PR      02-DEC-1999; 99WO-US028564.
PR      02-DEC-1999; 99WO-US028565.
PR      09-DEC-1999; 99US-0170262P.
PR      16-DEC-1999; 99WO-US030095.
PR      20-DEC-1999; 99WO-US030911.
PR      20-DEC-1999; 99WO-US030999.
PR      30-DEC-1999; 99WO-US031243.
PR      30-DEC-1999; 99WO-US031274.
PR      05-JAN-2000; 2000WO-US000219.
PR      06-JAN-2000; 2000WO-US000277.
PR      06-JAN-2000; 2000WO-US000376.
PR      11-FEB-2000; 2000WO-US003565.
PR      18-FEB-2000; 2000WO-US004341.
PR      18-FEB-2000; 2000WO-US004342.
PR      22-FEB-2000; 2000WO-US004414.

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PR      24-FEB-2000; 2000WO-US004914.
PR      24-FEB-2000; 2000WO-US005004.
PR      01-MAR-2000; 2000WO-US005601.
PR      02-MAR-2000; 2000WO-US005841.
PR      03-MAR-2000; 2000US-0187202P.
PR      10-MAR-2000; 2000WO-US006319.
PR      15-MAR-2000; 2000WO-US006884.
PR      20-MAR-2000; 2000WO-US007377.
PR      21-MAR-2000; 2000WO-US007532.
PR      30-MAR-2000; 2000WO-US008439.
PR      17-MAY-2000; 2000WO-US013705.
PR      22-MAY-2000; 2000WO-US014042.
PR      30-MAY-2000; 2000WO-US014941.
PR      02-JUN-2000; 2000WO-US015264.
PR      05-JUN-2000; 2000US-0209832P.
PR      28-JUL-2000; 2000WO-US020710.
PR      11-AUG-2000; 2000WO-US022031.
PR      23-AUG-2000; 2000WO-US023522.
PR      24-AUG-2000; 2000WO-US023328.
PR      08-NOV-2000; 2000WO-US030952.
PR      10-NOV-2000; 2000WO-US030873.
XX
PA      (GETH ) GENENTECH INC.
XX      Baker KP, Beresini M, Deforge L, Desnoyers L, Filvaroff E, Gao W;
PI      Gerritsen ME, Goddard A, Godowski PJ, Gurney AL, Sherwood S;
PI      Smith V, Stewart TA, Tumas D, Watanabe CK, Wood WI, Zhang Z;
XX      WPI; 2001-408281/43.
DR      P-PSDB; AAU12267.
XX
XX      Isolated , secretory and transmembrane PRO polypeptide used to detect
PT      other PRO polypeptides, link bioactive molecules to cells expressing PRO
PT      polypeptides, and detect the presence of mammalian tumors e.g. lung,
PT      breast, prostate, cervical.
XX
XX      Claim 3; Fig 191; 813pp; English.
XX
XX      AA521244-AA521518 encode for novel human secretory and transmembrane PRO
CC      polypeptides. The PRO polypeptides are useful to detect other PRO
CC      polypeptides, to link bioactive molecules to cells expressing PRO
CC      polypeptides, to modulate biological activities of cells expressing PRO
CC      polypeptides, and to detect the presence of mammalian lung, colon,
CC      breast, prostate, rectal, cervical or liver tumours by comparing PRO
CC      polypeptide expression in a cell sample to that in a control sample. Some
CC      of the 275 sequences are also useful to stimulate the release of tumour
CC      necrosis factor-alpha (TNF-alpha) from human blood, the proliferation or
CC      differentiation of chondrocytes, the proliferation or gene expression in
CC      pericyte cells, the release of proteoglycans from cartilage, the
CC      proliferation of inner ear utricular supporting cells or of T-
CC      lymphocytes, the release of a cytokine from peripheral blood monocytes
CC      (PBMCs), or the proliferation of endothelial cells. Some of the PRO
CC      polypeptides may modulate glucose or free fatty acid uptake by skeletal
CC      muscle cells or by adipocytes; or inhibit binding of A-peptide to factor
CC      VIIA. The PRO polypeptides can be used in assays to identify molecules
CC      involved in binding interactions. The polynucleotides encoding PRO
CC      polypeptides can be used to generate probes, antisense RNA/DNA,
CC      transgenic or knock out animals and can be used in gene therapy
XX
XX      Sequence 1647 BP; 492 A; 341 C; 347 G; 467 T; 0 U; 0 Other;
SQ

```

```

Query Match      99.9%; Score 1625.4; DB 4; Length 1647;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 1626; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      1 GCTTCAGCTCAAGAAAGAGAGGAATGAAGCGCTTCGCTTCGTGTTGTTCTTTATAA 60
Db      1 GCTTCAGCTCAAGAAAGAGAGGAATGAAGCGCTTCGCTTCGTGTTGTTCTTTATAA 60
QY      61 CATTTTCTTCTGCATTTCCCTTACTCGGATGACGGAATGAAGAAAATATGCACTGG 120
Db      61 CATTTTCTTCTGCATTTCCCTTACTCGGATGACGGAATGAAGAAAATATGCACTGG 120

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QY	121	CTCAGGCATATCTCAACCCAGTCTCTACTCTCTTGAAATAGAGGGAATCACTTTGTTCAA	180
Db	121	CTCAGGCATATCTCAACCCAGTCTCTACTCTCTTGAAATAGAGGGAATCACTTTGTTCAA	180
QY	181	GCAAGAATAGGAGTCTCATAGATGACAAAATTCGGGAATGCAAGCATTTTTTGGATTTGA	240
Db	181	GCAAGAATAGGAGTCTCATAGATGACAAAATTCGGGAATGCAAGCATTTTTTGGATTTGA	240
QY	241	CAGTGACTGGAAACTGGACTCAAAACACCTTCAGAGATCATGAAGACACCCAGAGTGTGGG	300
Db	241	CAGTGACTGGAAACTGGACTCAAAACACCTTCAGAGATCATGAAGACACCCAGAGTGTGGG	300
QY	301	TGCCTGATGTGGCCACGATATGGCTACACCTCCCTGGGTGGAGAAAATCAACCTCACCT	360
Db	301	TGCCTGATGTGGCCACGATATGGCTACACCTCCCTGGGTGGAGAAAATCAACCTCACCT	360
QY	361	ACAGAATAATAACTATACTCCGGATATGSCACGAGCTGCTGGATGAGGCTATCCAAG	420
Db	361	ACAGAATAATAACTATACTCCGGATATGSCACGAGCTGCTGGATGAGGCTATCCAAG	420
QY	421	AAGGTTTAGAAGTGTGGAGCAAAAGTCACTCCACTAAAAATTCACCAAGATTTCAAGGGGA	480
Db	421	AAGGTTTAGAAGTGTGGAGCAAAAGTCACTCCACTAAAAATTCACCAAGATTTCAAGGGGA	480
QY	481	TTGCAGACATCATGATTCCTTTTAGGACTCGAGTCCATGGTCGGTCTCGCTATTTTG	540
Db	481	TTGCAGACATCATGATTCCTTTTAGGACTCGAGTCCATGGTCGGTCTCGCTATTTTG	540
QY	541	ATGGTCCCTTTGGAGTGTCTTGGCCATGCTTTTCTCTCTGTCGGGTCTGGGTGGTGACA	600
Db	541	ATGGTCCCTTTGGAGTGTCTTGGCCATGCTTTTCTCTCTGTCGGGTCTGGGTGGTGACA	600
QY	601	CTCAATTTTGATGAGGATGAAAATCGGACCAAGGATGGAGCAGGATTCAACTGTTCTTG	660
Db	601	CTCAATTTTGATGAGGATGAAAATCGGACCAAGGATGGAGCAGGATTCAACTGTTCTTG	660
QY	661	TGGCTGCTCATGAATTTGGTCATGCTACGCTGGGGCTCTCTCACTCCAATGATCAAAACGCT	720
Db	661	TGGCTGCTCATGAATTTGGTCATGCTACGCTGGGGCTCTCTCACTCCAATGATCAAAACGCT	720
QY	721	TGATGTTCCAAATATATGTCTCCCTGATCCGAGAAAATACCACTTTCTCAGGATGATA	780
Db	721	TGATGTTCCAAATATATGTCTCCCTGATCCGAGAAAATACCACTTTCTCAGGATGATA	780
QY	781	TCAATGAATCCAGTCCATCTATGGAGGTCTGCTTAAGGTACCTGCTAAAGGCAAGCAAC	840
Db	781	TCAATGAATCCAGTCCATCTATGGAGGTCTGCTTAAGGTACCTGCTTAAGGCAAGCAAC	840
QY	841	CCACTATACCCCATGCTGTCGACCTGACTTGACTTTTGACGCTATCACAACTTTCCGCA	900
Db	841	CCACTATACCCCATGCTGTCGACCTGACTTGACTTTTGACGCTATCACAACTTTCCGCA	900
QY	901	GAGAAGTAATGTTCTTTAAAGGAGGCACTTATGGAGGATCTATATGATATCACGGATG	960
Db	901	GAGAAGTAATGTTCTTTAAAGGAGGCACTTATGGAGGATCTATATGATATCACGGATG	960
QY	961	TTGAGTTTGAAATTAATTTGCTTCACTTCGCGCATCTGTCAGCTGATCTGCAAGCTGCAT	1020
Db	961	TTGAGTTTGAAATTAATTTGCTTCACTTCGCGCATCTGTCAGCTGATCTGCAAGCTGCAT	1020
QY	1021	ACGAGAACCCAGAGATAAGATTTCTGGTTTTTAAAGATGAAAATCTCTGGATGATCAGAG	1080
Db	1021	ACGAGAACCCAGAGATAAGATTTCTGGTTTTTAAAGATGAAAATCTCTGGATGATCAGAG	1080
QY	1081	GATATGCTGCTTGCCAGATATATCCCAAATCCATCCATACATTAAGTGTTTCCAGGAGCTG	1140
Db	1081	GATATGCTGCTTGCCAGATATATCCCAAATCCATCCATACATTAAGTGTTTCCAGGAGCTG	1140
QY	1141	TGAGAAAATAGATGCGCGCTGCTGATATAGACCAAGGAAAACCTACTCTTTCTGTGG	1200
Db	1141	TGAGAAAATAGATGCGCGCTGCTGATATAGACCAAGGAAAACCTACTCTTTCTGTGG	1200
QY	1201	GCATTTGGTGTCTGGAGGTTTGATGAATGACCCAAAACATGCGACAAAGGATTTCCCGCAGA	1260

Db	1201	GCATTTGGTCTGGAGGTTTGGATGAAATGATGCCAAACCATGGACAAAGGATTTCCCGCAGA	1261
Qy	1261	GAGTGGTAAACACATTTCTCGGAATCAGTATCCGTGTTGATGCTGCTTTCCAGTACAAAG	1320
Db	1261	GAGTGGTAAACACATTTCTCGGAATCAGTATCCGTGTTGATGCTGCTTTCCAGTACAAAG	1320
Qy	1321	GATTCTTTCTTTTTCAGCCGTGGATCAAGCAATTTGGAATCAACATTTAAGACAAAGAATA	1380
Db	1321	GATTCTTTCTTTTTCAGCCGTGGATCAAGCAATTTGGAATCAACATTTAAGACAAAGAATA	1380
Qy	1381	TTACCCGAATCATGAGAACTAATCTTTGGTTTCAATGCAAGGACCAAGAACTCCCTCAT	1440
Db	1381	TTACCCGAATCATGAGAACTAATCTTTGGTTTCAATGCAAGGACCAAGAACTCCCTCAT	1440
Qy	1441	TTGGTTTGGATATCAACAGGAAAGACACATTCAGGAGGCATAAAGATATTTGATCATATA	1500
Db	1441	TTGGTTTGGATATCAACAGGAAAGACACATTCAGGAGGCATAAAGATATTTGATCATATA	1500
Qy	1501	AGAGTTTAAGCTTGTTTATTTTGGTATTTGTTCAATTTGCTGGAACACATTTCTATTTATC	1560
Db	1501	AGAGTTTAAGCTTGTTTATTTTGGTATTTGTTCAATTTGCTGGAACACATTTCTATTTATC	1560
Qy	1561	AATTAATTCATAGACCTTAATAATAAACCTCAACAGGTCCTTTTAATATAAATTCGCTTCAA	1620
Db	1561	AATTAATTCATAGACCTTAATAATAAACCTCAACAGGTCCTTTTAATATAAATTCGCTTCAA	1620
Qy	1621	AATAGAA 1627	
Db	1621	AATAGAA 1627	

RESULT 4
ACA03698
ID ACA03698 standard; cDNA; 1647 BP.
XX AC ACA03698;
XX DT
XX DE 23-MAY-2003 (first entry)
XX DE cDNA encoding human PRO polypeptide #96.
XX KW Human; PRO polypeptide; secreted and transmembrane protein;
XX KW tumour necrosis factor-alpha; TNF-alpha; blood; proliferation;
XX KW differentiation; chondrocyte; tumour; genetic disorder; cytostatic; gene;
XX KW ss.
XX OS Homo sapiens.
XX PN
XX PN US2003036180-A1.
XX PD 20-FEB-2003.
XX PF 09-MAY-2002; 2002US-00143114.
XX PF 31-MAR-1997; 97WO-US005230.
XX PR 12-JUN-1998; 98WO-US012456.
XX PR 14-JUL-1998; 98WO-US014552.
XX PR 28-AUG-1998; 98WO-US017888.
XX PR 10-SEP-1998; 98WO-US018824.
XX PR 14-SEP-1998; 98WO-US019093.
XX PR 14-SEP-1998; 98WO-US019094.
XX PR 16-SEP-1998; 98WO-US019177.
XX PR 17-SEP-1998; 98WO-US019330.
XX PR 07-OCT-1998; 98WO-US019437.
XX PR 29-OCT-1998; 98WO-US021141.
XX PR 29-OCT-1998; 98WO-US022991.
XX PR 29-OCT-1998; 98WO-US022992.
XX PR 01-NOV-1998; 98WO-US024855.
XX PR 01-DEC-1998; 98WO-US025108.
XX PR 05-JAN-1999; 99WO-US0000106.
XX PR 08-MAR-1999; 99WO-US005028.
XX PR 10-MAR-1999; 99WO-US005190.

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PR 20-APR-1999; 99WO-US0008615.
PR 14-MAY-1999; 99WO-US010733.
PR 02-JUN-1999; 99WO-US012252.
PR 01-SEP-1999; 99WO-US020111.
PR 08-SEP-1999; 99WO-US020594.
PR 13-SEP-1999; 99WO-US020944.
PR 15-SEP-1999; 99WO-US021090.
PR 18-SEP-1999; 99WO-US021547.
PR 03-OCT-1999; 99WO-US023089.
PR 23-NOV-1999; 99WO-US028214.
PR 30-NOV-1999; 99WO-US028313.
PR 30-NOV-1999; 99WO-US028409.
PR 01-DEC-1999; 99WO-US028301.
PR 01-DEC-1999; 99WO-US028634.
PR 02-DEC-1999; 99WO-US028551.
PR 02-DEC-1999; 99WO-US028564.
PR 16-DEC-1999; 99WO-US028565.
PR 20-DEC-1999; 99WO-US030095.
PR 20-DEC-1999; 99WO-US030911.
PR 22-DEC-1999; 99WO-US030999.
PR 22-DEC-1999; 99WO-US030720.
PR 30-DEC-1999; 99WO-US031243.
PR 30-DEC-1999; 99WO-US031274.
PR 05-JAN-2000; 2000WO-US0000219.
PR 06-JAN-2000; 2000WO-US000277.
PR 06-JAN-2000; 2000WO-US000376.
PR 11-FEB-2000; 2000WO-US003565.
PR 18-FEB-2000; 2000WO-US004341.
PR 18-FEB-2000; 2000WO-US004342.
PR 22-FEB-2000; 2000WO-US004414.
PR 24-FEB-2000; 2000WO-US004914.
PR 24-FEB-2000; 2000WO-US005004.
PR 01-MAR-2000; 2000WO-US005061.
PR 02-MAR-2000; 2000WO-US005746.
PR 02-MAR-2000; 2000WO-US005841.
PR 10-MAR-2000; 2000WO-US006319.
PR 15-MAR-2000; 2000WO-US006884.
PR 20-MAR-2000; 2000WO-US007377.
PR 21-MAR-2000; 2000WO-US007532.
PR 30-MAR-2000; 2000WO-US008439.
PR 17-MAY-2000; 2000WO-US013705.
PR 22-MAY-2000; 2000WO-US014042.
PR 30-MAY-2000; 2000WO-US014941.
PR 02-JUN-2000; 2000WO-US015264.
PR 28-JUL-2000; 2000WO-US020710.
PR 11-AUG-2000; 2000WO-US022031.
PR 23-AUG-2000; 2000WO-US023522.
PR 24-AUG-2000; 2000WO-US023328.
PR 08-NOV-2000; 2000WO-US030952.
PR 10-NOV-2000; 2000WO-US030873.
PR 01-DEC-2000; 2000WO-US032678.
PR 20-DEC-2000; 2000US-00747259.
PR 20-DEC-2000; 2000WO-US034956.
PR 28-FEB-2001; 2001US-00796498.
PR 28-FEB-2001; 2001WO-US006520.
PR 01-MAR-2001; 2001WO-US006666.
PR 09-MAR-2001; 2001US-00802706.
PR 14-MAR-2001; 2001US-00808689.
PR 22-MAR-2001; 2001US-00815744.
PR 05-APR-2001; 2001US-00828366.
PR 10-MAY-2001; 2001US-00854208.
PR 10-MAY-2001; 2001US-00854280.
PR 18-MAY-2001; 2001US-00860216.
PR 25-MAY-2001; 2001US-00866028.
PR 25-MAY-2001; 2001US-00866034.
PR 25-MAY-2001; 2001WO-US017092.
PR 01-JUN-2001; 2001US-00872035.
PR 01-JUN-2001; 2001WO-US017800.
PR 05-JUN-2001; 2001US-00874503.
PR 14-JUN-2001; 2001US-00882636.
PR 19-JUN-2001; 2001US-00886342.
PR 20-JUN-2001; 2001WO-US019692.
PR 21-JUN-2001; 2001US-00887879.

PR 22-JUN-2001; 2001WO-US020116.
PR 29-JUN-2001; 2001WO-US021066.
PR 03-JUL-2001; 2001WO-US021735.
PR 18-JUL-2001; 2001US-00908827.
PR 06-AUG-2001; 2001US-00924419.
PR 09-AUG-2001; 2001US-00927796.
PR 16-AUG-2001; 2001US-00931836.
PR 19-DEC-2001; 2001US-00028072.
XX
XX (GETH ) GENENTECH INC.
XX
XX Baker KP, Beresini M, Deforge L, Desnoyers L, Filvaroff E, Gao W;
XX Gerritsen ME, Goddard A, Godowski PJ, Gurney AL, Sherwood S;
XX Smith V, Stewart TA, Tumas D, Watanabe CK, Wood WI, Zhang Z;
XX
XX WPI; 2003-332040/31.
XX P-PSDB; ABU66665.
XX
XX New secreted and transmembrane PRO nucleic acids, useful for gene
XX therapy, in chromosome and gene mapping, as chromosome markers, in tissue
XX typing, and in chromosome identification.
XX
XX Claim 2; Fig 191; 660pp; English.
XX
XX The present invention relates to the isolation of novel human PRO
XX polypeptides, and the polynucleotide sequences encoding them. The PRO
XX polypeptides are secreted and transmembrane proteins. The PRO
XX polypeptides are useful for detecting other PRO polypeptides, for linking
XX bioactive molecules to cells expressing PRO polypeptides, for modulating
XX biological activities of cells expressing PRO polypeptides, and for
XX identifying agonists or antagonists. The PRO polypeptides are useful for
XX for stimulating the release of tumour necrosis factor (TNF)-alpha from
XX human blood, for stimulating the proliferation or differentiation of
XX chondrocytes, and detecting the presence of tumours. The polynucleotide
XX sequences encoding PRO polypeptides are useful as hybridisation probes,
XX in chromosome and gene mapping, in the generation of antisense RNA and
XX DNA, in the preparation of PRO polypeptides, for generating transgenic
XX animals or knockout animals, for the genetic analysis of individuals with
XX genetic disorders, and in gene therapy. ACA03603-ACA03877 represent cDNAs
XX encoding the human PRO polypeptides of the invention. Note: the sequence
XX data for this patent was obtained in electronic format directly from the
XX USPTO web site at seqdata.uspto.gov/psipdentry.html
XX
XX Sequence 1647 BP; 492 A; 341 C; 347 G; 467 T; 0 U; 0 Other;

Query Match 99.9%; Score 1625.4; DB 8; Length 1647;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 1626; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GCTTCAGCTGAGAAAGAGAGGAATGAAGCGCTTCTGCTTCTGCTGTTGTTCTTTTATAA 60
DB 1 GCTTCAGCTGAGAAAGAGAGGAATGAAGCGCTTCTGCTTCTGCTGTTGTTCTTTTATAA 60

QY 61 CATTTTCTTCTGCAATTCCTTAGTCGGATGACGAAATGAAGAAATATGCAACTGG 120
DB 61 CATTTTCTTCTGCAATTCCTTAGTCGGATGACGAAATGAAGAAATATGCAACTGG 120

QY 121 CTCAGGCATATCTCAACCAAGTCTACTCTTGAATAGAGGAATCATCTGTTCAA 180
DB 121 CTCAGGCATATCTCAACCAAGTCTACTCTTGAATAGAGGAATCATCTGTTCAA 180

QY 181 GCAAGAATAGGAGTCTCATAGATGACAAAATTCGGGAATTCGAGCATTTTGGATTGA 240
DB 181 GCAAGAATAGGAGTCTCATAGATGACAAAATTCGGGAATTCGAGCATTTTGGATTGA 240

QY 241 CAGTGACTGGAATACTGGACTCAACACCCCTTGAGATCATGAGACACCCAGTGTGGGG 300
DB 241 CAGTGACTGGAATACTGGACTCAACACCCCTTGAGATCATGAGACACCCAGTGTGGGG 300

QY 301 TGCCTGATGTGGGCCAGTATGGCTACACCTCCCTGGGTGGAGAAATACCACTCACCT 360
DB 301 TGCCTGATGTGGGCCAGTATGGCTACACCTCCCTGGGTGGAGAAATACCACTCACCT 360
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QY	361	ACAGAAATAA	AAAC	CTATATA	CTCCGGATAT	GGCAGAGCT	GCTGTG	AGATG	AGGCTAT	CCCAAG	420										
Db	361	ACAGAATAA	AAACTATA	CTCCGGATAT	GGCAGAGCT	GCTGTG	AGATG	AGGCTAT	CCCAAG	420											
QY	421	AAGGTTT	TAGAGTGT	GGAGCAAGT	CAC	TCCCA	TAAATTT	CACCA	AGATTT	CAAAAGGGA	480										
Db	421	AAGGTTT	TAGAGTGT	GGAGCAAGT	CAC	TCCCA	TAAATTT	CACCA	AGATTT	CAAAAGGGA	480										
QY	481	TTGCAGACAT	CA	TGAT	TGCCTTT	PAGGACT	CGAGT	CCAT	GGT	CGGTCT	CGCTATTTTG	540									
Db	481	TTGCAGACAT	CA	TGAT	TGCCTTT	PAGGACT	CGAGT	CCAT	GGT	CGGTCT	CGCTATTTTG	540									
QY	541	ATGGT	CCCTGG	AGTGT	CTTGG	CCAT	GCCTTT	CTCT	CGT	CCGGT	CTGGGTGGTGACA	600									
Db	541	ATGGT	CCCTGG	AGTGT	CTTGG	CCAT	GCCTTT	CTCT	CGT	CCGGT	CTGGGTGGTGACA	600									
QY	601	CTCAT	TTTGN	TAGGAT	GA	AACTG	CAGCA	AGAT	GGAGC	AGATTT	CAACTTTGTTCTTG	660									
Db	601	CTCAT	TTTGN	TAGGAT	GA	AACTG	CAGCA	AGAT	GGAGC	AGATTT	CAACTTTGTTCTTG	660									
QY	661	TGGCT	GCTCAT	GAA	TTTGGT	CA	TGCA	CTGGG	CTCT	CACT	CCAA	TGATCAAA	AGCCT	720							
Db	661	TGGCT	GCTCAT	GAA	TTTGGT	CA	TGCA	CTGGG	CTCT	CACT	CCAA	TGATCAAA	AGCCT	720							
QY	721	TGAT	GTTC	CCAA	ATTA	TG	CTCC	TGGAT	CC	CA	AGAA	ATA	CCCA	CTTTCT	CAGGATGATA	780					
Db	721	TGAT	GTTC	CCAA	ATTA	TG	CTCC	TGGAT	CC	CA	AGAA	ATA	CCCA	CTTTCT	CAGGATGATA	780					
QY	781	TCAAT	GGAT	CCAGT	CCAT	CTAT	G	AGG	CTG	CTTA	AGT	CACT	GTCT	TA	AGC	CAAAAGGAAC	840				
Db	781	TCAAT	GGAT	CCAGT	CCAT	CTAT	G	AGG	CTG	CTTA	AGT	CACT	GTCT	TA	AGC	CAAAAGGAAC	840				
QY	841	CCA	CTAT	AC	CC	CA	TG	CC	TG	CA	CTTG	CA	CTTTTG	AC	CG	CTATCA	CAAACTTTCCGGA	900			
Db	841	CCA	CTAT	AC	CC	CA	TG	CC	TG	CA	CTTG	CA	CTTTTG	AC	CG	CTATCA	CAAACTTTCCGGA	900			
QY	901	GAGA	AGTAA	TG	TTCTTT	AA	AG	CA	GG	CA	GG	CA	CTTA	TG	AG	GA	TATCA	CCGGATG	960		
Db	901	GAGA	AGTAA	TG	TTCTTT	AA	AG	CA	GG	CA	GG	CA	CTTA	TG	AG	GA	TATCA	CCGGATG	960		
QY	961	TTGAG	TTTGA	TTAA	TTG	CTTCA	TTCTGG	CCAT	CTCTG	CCAG	CTGAT	CTCTG	CAAG	CTG	CA	AGCTG	CGAT	1020			
Db	961	TTGAG	TTTGA	TTAA	TTG	CTTCA	TTCTGG	CCAT	CTCTG	CCAG	CTGAT	CTCTG	CAAG	CTG	CA	AGCTG	CGAT	1020			
QY	1021	ACGAGA	ACCC	CAGAG	ATA	GA	AGTTCT	GGTTTT	AAAA	GATG	AAAA	CTCT	CTGG	ATGAT	CAG	AG	1080				
Db	1021	ACGAGA	ACCC	CAGAG	ATA	GA	AGTTCT	GGTTTT	AAAA	GATG	AAAA	CTCT	CTGG	ATGAT	CAG	AG	1080				
QY	1081	GATAT	G	CTGT	CTTG	CCAG	ATTAT	CC	CAAA	TCC	CA	TCA	AT	PAG	GT	TTTCC	AGG	CGTG	1140		
Db	1081	GATAT	G	CTGT	CTTG	CCAG	ATTAT	CC	CAAA	TCC	CA	TCA	AT	PAG	GT	TTTCC	AGG	CGTG	1140		
QY	1141	TGA	AAAA	ATAG	ATG	CAG	CGT	CTGT	GAT	TA	AG	CA	CA	AG	AAAA	CC	TACT	CTTTG	1200		
Db	1141	TGA	AAAA	ATAG	ATG	CAG	CGT	CTGT	GAT	TA	AG	CA	CA	AG	AAAA	CC	TACT	CTTTG	1200		
QY	1201	GCAT	TTG	G	TG	CTG	AG	G	TTT	GAT	G	AAAT	TG	AC	CC	AAAA	CCAT	GG	CA	1260	
Db	1201	GCAT	TTG	G	TG	CTG	AG	G	TTT	GAT	G	AAAT	TG	AC	CC	AAAA	CCAT	GG	CA	1260	
QY	1261	GAGT	G	G	T	A	A	A	A	A	A	A	A	A	A	A	A	A	A	1320	
Db	1261	GAGT	G	G	T	A	A	A	A	A	A	A	A	A	A	A	A	A	A	1320	
QY	1321	GAT	T	CT	CT	TTT	T	CAG	CG	TG	GG	AT	T	G	A	T					

Db	1441	TTGGTTTGTATATCAACAGGAAAAAGACATTCAGGAGGCATTAAGATATTGTATCATTA	1500
Qy	1501	AGAGTTTAAAGCTTGGTTTATTTTGGTATTTGTTTCATTTGCTGAAAAACACTTCTATTATTC	1560
Db	1501	AGAGTTTAAAGCTTGGTTTATTTTGGTATTTGTTTCATTTGCTGAAAAACACTTCTATTATTC	1560
Qy	1561	AATAAATTCATAGACCTTAATAAATAAAGCTCAACAGGCTCTTTTAATATAAATTCGCTTCAA	1620
Db	1561	AATAAATTCATAGACCTTAATAAATAAAGCTCAACAGGCTCTTTTAATATAAATTCGCTTCAA	1620
Qy	1621	AATAGAA 1627	
Db	1621	AATAGAA 1627	
RESULT 5			
ABX89236			
ID	ABX89236 standard; cDNA; 1647 BP.		
XX			
AC	ABX89236;		
XX			
DT	13-MAY-2003 (first entry)		
XX			
DE	DNA encoding novel secreted and transmembrane protein PRO5992.		
XX			
KW	Human; PRO; hypertrophy of neonatal heart; angiogenesis; wound healing;		
KW	cardiac insufficiency disorder; cancer; tumour; immune response;		
KW	adrenal cortical capillary endothelial growth; c-fos induction;		
KW	vascular endothelial growth factor inhibition; VEGF inhibition;		
KW	endothelial cell growth inhibitor; T-lymphocytes stimulation;		
KW	retinal neurons cell survival; rod photoreceptor cell survival;		
KW	retinal disorder; retinitis pigmentosa; kidney disorder;		
KW	mammalian kidney mesangial cell proliferation; Berger disease;		
KW	dermatitis; herpeticiformis; Crohn's disease; chondrocyte proliferation;		
XX	chondrocyte redifferentiation; sports injury; arthritis; gene; ss.		
OS	Homo sapiens.		
XX			
PN	US2003017563-A1.		
XX			
PD	23-JAN-2003.		
XX			
PF	07-MAY-2002; 2002US-00140808.		
XX			
PR	31-MAR-1997; 97WO-US005230.		
PR	12-JUN-1998; 98WO-US012456.		
PR	14-JUL-1998; 98WO-US014552.		
PR	28-AUG-1998; 98WO-US017888.		
PR	10-SEP-1998; 98WO-US018824.		
PR	14-SEP-1998; 98WO-US019093.		
PR	14-SEP-1998; 98WO-US019094.		
PR	14-SEP-1998; 98WO-US019177.		
PR	16-SEP-1998; 98WO-US019330.		
PR	17-SEP-1998; 98WO-US019437.		
PR	07-OCT-1998; 98WO-US021141.		
PR	29-OCT-1998; 98WO-US022991.		
PR	29-OCT-1998; 98WO-US022992.		
PR	20-NOV-1998; 98WO-US024855.		
PR	01-DEC-1998; 98WO-US025108.		
PR	05-JAN-1999; 99WO-US000106.		
PR	08-MAR-1999; 99WO-US005028.		
PR	10-MAR-1999; 99WO-US005190.		
PR	20-APR-1999; 99WO-US008615.		
PR	14-MAY-1999; 99WO-US010733.		
PR	02-JUN-1999; 99WO-US012252.		
PR	01-SEP-1999; 99WO-US020111.		
PR	08-SEP-1999; 99WO-US020594.		
PR	13-SEP-1999; 99WO-US020944.		
PR	15-SEP-1999; 99WO-US021090.		
PR	05-OCT-1999; 99WO-US021547.		
PR	15-SEP-1999; 99WO-US023089.		
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PR 06-JAN-2000; 2000WO-US000376.
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PR 18-FEB-2000; 2000WO-US000432.
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PR 24-FEB-2000; 2000WO-US000491.
PR 24-FEB-2000; 2000WO-US000504.
PR 01-MAR-2000; 2000WO-US000501.
PR 02-MAR-2000; 2000WO-US005746.
PR 02-MAR-2000; 2000WO-US000581.
PR 10-MAR-2000; 2000WO-US006319.
PR 15-MAR-2000; 2000WO-US006884.
PR 21-MAR-2000; 2000WO-US007377.
PR 21-MAR-2000; 2000WO-US007332.
PR 30-MAR-2000; 2000WO-US008439.
PR 17-MAY-2000; 2000WO-US013705.
PR 22-MAY-2000; 2000WO-US014042.
PR 30-MAY-2000; 2000WO-US014941.
PR 02-JUN-2000; 2000WO-US015264.
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PR 11-AUG-2000; 2000WO-US022031.
PR 23-AUG-2000; 2000WO-US023522.
PR 24-AUG-2000; 2000WO-US023328.
PR 08-NOV-2000; 2000WO-US030952.
PR 10-NOV-2000; 2000WO-US030873.
PR 01-DEC-2000; 2000WO-US032578.
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PR 20-DEC-2000; 2000WO-US034956.
PR 28-FEB-2001; 2001US-00796498.
PR 28-FEB-2001; 2001WO-US0006520.
PR 01-MAR-2001; 2001WO-US0006666.
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PR 22-MAR-2001; 2001US-00816744.
PR 05-APR-2001; 2001US-00828366.
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PR 10-MAY-2001; 2001US-00854280.
PR 18-MAY-2001; 2001US-00860216.
PR 25-MAY-2001; 2001US-00866028.
PR 25-MAY-2001; 2001US-00866034.
PR 25-MAY-2001; 2001WO-US017092.
PR 01-JUN-2001; 2001US-00872035.
PR 01-JUN-2001; 2001WO-US017800.
PR 05-JUN-2001; 2001US-00874503.
PR 14-JUN-2001; 2001US-00882636.
PR 19-JUN-2001; 2001US-00886342.
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PR 21-JUN-2001; 2001US-00887879.
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PR 09-AUG-2001; 2001US-00927796.
PR 16-AUG-2001; 2001US-00931836.
PR 19-DEC-2001; 2001US-00028072.
XX
PA (GETH) GENENTECH INC.
XX
PI Baker KP, Beresini M, Deforge L, Desnoyers L, Filvaroff E, Gao W;

PI Gerritsen ME, Goddard A, Godowski PJ, Gurney AL, Sherwood S;
PI Smith V, Stewart TA, Tumas D, Watanabe CK, Wood WI, Zhang Z;
XX
DR WPI; 2003-466355/44.
DR P-PSDE; ABO24936.
XX
PT New isolated nucleic acid encoding a PRO polypeptide, e.g. PRO1114 or
PT PRO4978, useful in molecular biology, chromosome and gene mapping, in
PT generating antisense RNA and DNA, and in gene therapy.
XX
XX Claim 2; Fig 191; 659pp; English.
XX
XX The invention relates to an isolated nucleic acid comprising at least 80%
CC sequence identity to a PRO (secreted and transmembrane protein) cDNA
CC comprising a nucleic acid (a) encoding a PRO polypeptide, or its
CC extracellular domain (with or without its associated signal peptide),
CC which comprises any of the 275 120-850 residue amino acid sequences,
CC given in the specification; (b) comprising any of the 275 300-3500
CC nucleotide sequences, given in the specification; or (c) comprising the
CC full-length coding sequence of the nucleotide sequences given in the
CC specification, or of the DNA deposited under any of the American Type
CC Culture Collection (ATCC) Accession Numbers listed in the specification.
CC Also included are a vector comprising the novel nucleic acid, a host cell
CC comprising the vector, producing a PRO polypeptide, the isolated PRO
CC polypeptides detailed above, a chimaeric molecule comprising the PRO
CC polypeptide of fused to a heterologous amino acid sequence, an anti-PRO
CC antibody, detecting a PRO polypeptide in a sample suspected of containing
CC the PRO polypeptide, linking a bioactive molecule to a cell expressing a
CC PRO polypeptide, modulating at least one biological activity of a cell
CC expressing a PRO polypeptide, stimulating the release of tumour necrosis
CC factor-alpha (TNF-alpha) from human blood, (or proteoglycans from
CC cartilage or cytokine from peripheral blood mononuclear cells (PBMC)),
CC modulating the uptake of glucose or FFA by skeletal muscle cells or
CC adipocyte cells, stimulating the proliferation or differentiation of
CC chondrocyte cells (or proliferation of or gene expression in pericyte
CC cells), stimulating the proliferation of inner ear utricular supporting
CC cells (or of T-lymphocyte cells, or of endothelial cells), inhibiting the
CC binding of A-peptide to factor VIIA, or differentiation of adipocyte
CC cells, detecting the presence of a tumour in a mammal and an
CC oligonucleotide probe derived from any of the nucleotide sequences given
CC in the specification. The polynucleotide is useful in molecular biology,
CC including uses as hybridisation probes, in chromosome and gene mapping,
CC in generating antisense RNA and DNA, and in gene therapy. The
CC polynucleotide may also be used in preparing PRO polypeptides by
CC recombinant techniques, and in generating either transgenic animals or
CC knock-out animals which, in turn, are useful in the development and
CC screening of therapeutically useful reagents. The PRO polypeptide or the
CC antibody is used in preparing a medicament for treating a condition
CC responsive to the polypeptide or antibody, such as tumours, and in
CC various diagnostic assays. The present sequence encodes a PRO polypeptide
XX
SQ Sequence 1647 BP; 492 A; 341 C; 347 G; 467 T; 0 U; 0 Other;

Query Match 99.9%; Score 1625.4; DB 8; Length 1647;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 1626; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1 GCTTCAGCTCAAGAAAGAGAGGAGGATGAGCGCTTCTGCTTCTGTTGTTCTTTATAA 60
DB 1 GCTTCAGCTCAAGAAAGAGAGGAGGATGAGCGCTTCTGCTTCTGTTGTTCTTTATAA 60
QY 61 CATTTTCTCTGATTTCCCTTAGTCGGATGACGGAATAATGAAGAAATATGCAACTGG 120
DB 61 CATTTTCTCTGATTTCCCTTAGTCGGATGACGGAATAATGAAGAAATATGCAACTGG 120
QY 121 CTCAGGCATATCTCAACAGTCTTACTCTCTTGAATAGAGGGAATCATCTGTTTCAAA 180
DB 121 CTCAGGCATATCTCAACAGTCTTACTCTCTTGAATAGAGGGAATCATCTGTTTCAAA 180
QY 181 GCAAGATAGGAGTCTCATAGATGACAAATTCGGGAATTCGGAATTTTTCGATTGA 240
DB 181 GCAAGATAGGAGTCTCATAGATGACAAATTCGGGAATTCGGAATTTTTCGATTGA 240

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Db 241 CAGTGACTGGAACACTGGACTCAAAACACCCCTTGAGATCATGAAGACACCCAGGTGTGGG 300
QY 301 TGCCTGATGTGGGCGAGTATGCTACACCCCTCCCTGGGTGGAGAAAATACAACTCCACT 360
Db 301 TGCCTGATGTGGGCGAGTATGCTACACCCCTCCCTGGGTGGAGAAAATACAACTCCACT 360
QY 361 ACAGATAATAACTATCTACTCCGGATATGGACGAGCTGCTGTGATGAGGCTATCCAAAG 420
Db 361 ACAGATAATAACTATCTACTCCGGATATGGACGAGCTGCTGTGATGAGGCTATCCAAAG 420
QY 421 AAGGTTTGAAGTGTGGAGCAAGTCACTCCACTAAAATTCACCAAGATTTCAAAGGGGA 480
Db 421 AAGGTTTGAAGTGTGGAGCAAGTCACTCCACTAAAATTCACCAAGATTTCAAAGGGGA 480
QY 481 TTGCAGACATCATGATGCTTTAGGACTTCAGACTCGAGTCCATGGTCCGCTGCTGCTATTTTG 540
Db 481 TTGCAGACATCATGATGCTTTAGGACTTCAGACTCGAGTCCATGGTCCGCTGCTGCTATTTTG 540
QY 541 ATGGTCCCTTGGAGTGTCTGGCCATGCTTTCCTCTGCTGGTCCGGTCTGGGTGGTGACA 600
Db 541 ATGGTCCCTTGGAGTGTCTGGCCATGCTTTCCTCTGCTGGTCCGGTCTGGGTGGTGACA 600
QY 601 CTCATTTTGTGATGAGATGAAAACTGGACCAAGATGGAGCAGATTCAACTTGTTCCTTG 660
Db 601 CTCATTTTGTGATGAGATGAAAACTGGACCAAGATGGAGCAGATTCAACTTGTTCCTTG 660
QY 661 TGGCTGCTCATGAATTTGGTTCATGCACTGGGCTCTCTCACTCCAATGATCAAAACAGCCT 720
Db 661 TGGCTGCTCATGAATTTGGTTCATGCACTGGGCTCTCTCACTCCAATGATCAAAACAGCCT 720
QY 721 TGATGTTCCCAATATGCTCCCTGGATCCCGAATAATACCACTTCTCAGGATGATA 780
Db 721 TGATGTTCCCAATATGCTCCCTGGATCCCGAATAATACCACTTCTCAGGATGATA 780
QY 781 TCAATGGAATCCAGTCCATCTATGAGGTCTGCTTAAGTACTCTTAAGCCAAAGGAAC 840
Db 781 TCAATGGAATCCAGTCCATCTATGAGGTCTGCTTAAGTACTCTTAAGCCAAAGGAAC 840
QY 841 CCACATATACCCCATGCTGTGACCCCTGACTTGTGACGCTATCAAACTTTCCGCA 900
Db 841 CCACATATACCCCATGCTGTGACCCCTGACTTGTGACGCTATCAAACTTTCCGCA 900
QY 901 GAGAGTATGTTCTTTAAAGCAGGCACCTATGAGGATCTATTATGATATCAGGATG 960
Db 901 GAGAGTATGTTCTTTAAAGCAGGCACCTATGAGGATCTATTATGATATCAGGATG 960
QY 961 TTGAGTTTGAATTAATTTGCTTCATTTCTGGCCATCTCTGCCAGTCTATGCAAGCTGCAT 1020
Db 961 TTGAGTTTGAATTAATTTGCTTCATTTCTGGCCATCTCTGCCAGTCTATGCAAGCTGCAT 1020
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Db 1021 ACGAGAACCCAGAGATAGATCTTGGTTTTTAAAGATGAAAACCTTGGATGATCAGAG 1080
QY 1081 GATATGCTGTCTTGCCAGATATCCCAATCCATCCATACATTTAGTGTTCAGGACGCTG 1140
Db 1081 GATATGCTGTCTTGCCAGATATCCCAATCCATCCATACATTTAGTGTTCAGGACGCTG 1140
QY 1141 TGAAGAAAATAGATGAGCGCTGCTGTGATAAGACCAAGAAAACCTACTTCTTTGTGG 1200
Db 1141 TGAAGAAAATAGATGAGCGCTGCTGTGATAAGACCAAGAAAACCTACTTCTTTGTGG 1200
QY 1201 GCATTTGGTGTGGAGTTTGTATGAATGACCCAAACCATGACAAAGGATTTCCCGCAGA 1260
Db 1201 GCATTTGGTGTGGAGTTTGTATGAATGACCCAAACCATGACAAAGGATTTCCCGCAGA 1260
QY 1261 GAGTGTGTAACACATTTCTCGAATCAGTATCCGTTGATGCTGCTTCCAGTACAAG 1320
Db 1261 GAGTGTGTAACACATTTCTCGAATCAGTATCCGTTGATGCTGCTTCCAGTACAAG 1320
QY 1321 GATTCCTCTTTTTCAGCCGCTGGATCAAGCAATTTTGAATACAACTTAAGACAAAGAATA 1380
Db 1321 GATTCCTCTTTTTCAGCCGCTGGATCAAGCAATTTTGAATACAACTTAAGACAAAGAATA 1380
QY 1381 TTACCCGAATCATGAGAACTAATACTTGGTTTCAATGCAAAAGAACCAAGAACTCTCTCAT 1440
Db 1381 TTACCCGAATCATGAGAACTAATACTTGGTTTCAATGCAAAAGAACCAAGAACTCTCTCAT 1440
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Db 1441 TTGGTTTGTATATCAACAGGAAAGCACATTCAGGAGGCATAAGATATTGTATCATA 1500
QY 1501 AGAGTTTAAAGCTTGTATTTTGGTATTGTTTCAATTTGCTGAAAAACACTTCTATTATTC 1560
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QY 1561 AATAAATTCATAGACCTAAAATAAACCTCAACAGTCTTTTAAATATAAATTCGTCTCAA 1620
Db 1561 AATAAATTCATAGACCTAAAATAAACCTCAACAGTCTTTTAAATATAAATTCGTCTCAA 1620
QY 1621 AATAGAA 1627
Db 1621 AATAGAA 1627
RESULT 7
ACA04119
ID ACA04119 standard; cDNA; 1647 BP.
XX
AC ACA04119;
XX
DT 27-MAY-2003 (first entry)
XX
DE Human cDNA encoding a secreted/transmembrane protein, SEQ ID 191.
XX
KW Human; ss; gene; secreted protein; transmembrane protein; PRO; inflammatory disease; organ failure; atherosclerosis; cardiac injury;
KW infertility; birth defects; premature aging; AIDS; biosensor;
KW acquired immunodeficiency syndrome; cancer; diabetic complication;
KW bio reactor; tumour.
XX
OS Homo sapiens.
XX
PN US2003032155-A1.
XX
PD 13-FEB-2003.
XX
PF 03-MAY-2002; 2002US-00137865.
XX
PR 31-MAR-1997; 97WO-US005230.
PR 12-JUN-1998; 98WO-US012456.
PR 14-JUL-1998; 98WO-US014552.
PR 28-AUG-1998; 98WO-US017888.
PR 10-SEP-1998; 98WO-US018824.
PR 14-SEP-1998; 98WO-US019093.
PR 14-SEP-1998; 98WO-US019094.
PR 16-SEP-1998; 98WO-US019177.
PR 16-SEP-1998; 98WO-US019330.
PR 17-SEP-1998; 98WO-US019437.
PR 07-OCT-1998; 98WO-US021141.
PR 29-OCT-1998; 98WO-US022991.
PR 29-OCT-1998; 98WO-US022992.
PR 20-NOV-1998; 98WO-US024855.
PR 01-DEC-1998; 98WO-US025108.
PR 05-JAN-1999; 99WO-US000106.
PR 08-MAR-1999; 99WO-US005028.
PR 10-MAR-1999; 99WO-US005190.
PR 20-APR-1999; 99WO-US008615.
PR 14-MAY-1999; 99WO-US010733.
PR 02-JUN-1999; 99WO-US012252.
PR 01-SEP-1999; 99WO-US020111.
PR 08-SEP-1999; 99WO-US020594.
PR 13-SEP-1999; 99WO-US020944.
PR 15-SEP-1999; 99WO-US021090.
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PR 05-OCT-1999; 99WO-US023089.
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PR 01-DEC-1999; 99WO-US028634.
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PR 02-DEC-1999; 99WO-US028564.
PR 02-DEC-1999; 99WO-US028565.
PR 16-DEC-1999; 99WO-US030095.
PR 20-DEC-1999; 99WO-US030911.
PR 20-DEC-1999; 99WO-US030999.
PR 22-DEC-1999; 99WO-US030720.
PR 30-DEC-1999; 99WO-US031243.
PR 30-DEC-1999; 99WO-US031274.
PR 05-JAN-2000; 2000WO-US000219.
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PR 06-JAN-2000; 2000WO-US000376.
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PR 18-FEB-2000; 2000WO-US004342.
PR 22-FEB-2000; 2000WO-US004414.
PR 24-FEB-2000; 2000WO-US004914.
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PR 02-MAR-2000; 2000WO-US005501.
PR 02-MAR-2000; 2000WO-US005746.
PR 02-MAR-2000; 2000WO-US005841.
PR 10-MAR-2000; 2000WO-US006319.
PR 15-MAR-2000; 2000WO-US006884.
PR 20-MAR-2000; 2000WO-US007377.
PR 21-MAR-2000; 2000WO-US007532.
PR 30-MAR-2000; 2000WO-US008439.
PR 17-MAY-2000; 2000WO-US013705.
PR 22-MAY-2000; 2000WO-US014042.
PR 30-MAY-2000; 2000WO-US014941.
PR 02-JUN-2000; 2000WO-US015264.
PR 28-JUL-2000; 2000WO-US020710.
PR 11-AUG-2000; 2000WO-US022031.
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PR 24-AUG-2000; 2000WO-US023328.
PR 08-NOV-2000; 2000WO-US030952.
PR 10-NOV-2000; 2000WO-US030873.
PR 01-DEC-2000; 2000WO-US032678.
PR 20-DEC-2000; 2000WO-US032678.
PR 20-DEC-2000; 2000WO-US0747259.
PR 28-FEB-2001; 2001US-00796498.
PR 01-MAR-2001; 2001WO-US006666.
PR 09-MAR-2001; 2001US-00802706.
PR 14-MAR-2001; 2001US-00806889.
PR 22-MAR-2001; 2001US-00816744.
PR 05-APR-2001; 2001US-00828366.
PR 10-MAY-2001; 2001US-00854208.
PR 18-MAY-2001; 2001US-00860216.
PR 25-MAY-2001; 2001US-00866028.
PR 25-MAY-2001; 2001US-00866034.
PR 25-MAY-2001; 2001WO-US017092.
PR 01-JUN-2001; 2001US-00872035.
PR 01-JUN-2001; 2001WO-US017800.
PR 05-JUN-2001; 2001US-00874503.
PR 14-JUN-2001; 2001US-00886342.
PR 19-JUN-2001; 2001US-00886342.
PR 20-JUN-2001; 2001WO-US019692.
PR 21-JUN-2001; 2001US-00887879.
PR 22-JUN-2001; 2001WO-US020116.
PR 29-JUN-2001; 2001US-0021066.
PR 09-JUL-2001; 2001WO-US021735.
PR 18-JUL-2001; 2001US-00908827.
PR 06-AUG-2001; 2001US-00924419.
PR 09-AUG-2001; 2001US-00927796.

PR 16-AUG-2001; 2001US-00931836.
PR 19-DEC-2001; 2001US-00028072.
PR XX (GETH ) GENENTECH INC.
PR PI Baker KP, Beresini M, Deforge L, Desnoyers L, Filvaroff E, Gao W;
PR PI Gerritsen ME, Goddard A, Godowski PJ, Gurney AL, Sherwood S;
PR PI Smith V, Stewart TA, Tumas D, Watanabe CK, Wood WI, Zhang Z;
PR XX WPI; 2003-584997/55.
PR DR P-PSDB; ADA45711.
PR XX
PR PT Novel secreted and transmembrane polypeptide for modulating biological
PR PT activity of cell expressing the polypeptide, identifying agonists or
PR PT antagonists of polypeptide, and as molecular weight markers.
PR XX
PR PS Claim 2; Fig 191; 659pp; English.
PR XX
PR CC The invention describes 305 nucleic acids encoding PRO (secreted and
PR CC transmembrane) polypeptides (I). (I) is useful for stimulating the
PR CC release of TNF-alpha from human blood, for modulating the uptake of
PR CC glucose or FFA by skeletal muscle cells or adipocyte cells, for
PR CC stimulating the proliferation or differentiation of chondrocyte cells,
PR CC for stimulating the proliferation of or gene expression in pericyte
PR CC cells, for stimulating the release of proteoglycans from cartilage, for
PR CC stimulating the proliferation of inner ear utricular supporting cells,
PR CC for stimulating the proliferation of T-lymphocyte cells, for stimulating
PR CC the release of a cytokine from BMC cells, for inhibiting the binding of
PR CC A-peptide to factor VIIA, for inhibiting the differentiation of adipocyte
PR CC cells, for stimulating proliferation of endothelial cells, for detecting
PR CC the presence of tumour in a mammal. The tumour is lung, colon, breast,
PR CC prostate, rectal, cervical or liver tumour. The oligonucleotide probes
PR CC are useful for isolating genomic and cDNA nucleotide sequences or
PR CC antisense probes. (I) is also useful as therapeutic agent. PRO is useful
PR CC in assays to identify other proteins or molecules involved in binding
PR CC interaction. A polynucleotide (II) encoding (I) is useful in chromosome
PR CC and gene mapping, in generation of antisense RNA and DNA, in the
PR CC preparation of PRO polypeptide, for generating transgenic animals or
PR CC knockout animals which in turn are useful in the development and
PR CC screening of therapeutically useful reagents, in gene therapy, for
PR CC chromosome identification, as chromosome marker, and for generating
PR CC probes. An anti-(I)-antibody is useful in diagnostic assays for PRO, e.g.
PR CC detecting its expression in specific cells, tissues or serum, and for
PR CC affinity purification of PRO from recombinant cell culture or natural
PR CC sources. (I) and (II) are useful for tissue typing. This sequence encodes
PR CC a novel human secreted and transmembrane PRO polypeptide.
PR XX
PR SQ Sequence 1647 BP; 492 A; 341 C; 347 G; 467 T; 0 U; 0 Other;

Query Match 99.9%; Score 1625.4; DB 9; Length 1647;
Best Local Similarity 99.9%; Pred No. 0;
Matches 1626; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 GCTTCAGCTGAAGAAAGAGAGGAATGAAGCGCCCTTCTGCTTCTGTGTGTTCTTTATAA 60
Db 1 GCTTCAGCTGAAGAAAGAGAGGAATGAAGCGCCCTTCTGCTTCTGTGTGTTCTTTATAA 60
Qy 61 CATTTTCTTCGATTTCCCTTAGTCCGGATGACGGAAATGAGAAATATGCAACTGG 120
Db 61 CATTTTCTTCGATTTCCCTTAGTCCGGATGACGGAAATGAGAAATATGCAACTGG 120
Qy 121 CTCAGGCATATCTCAACCACTTCTACTCTCTTGAATAGAGAGGAATCATCTTGTTCAAA 180
Db 121 CTCAGGCATATCTCAACCACTTCTACTCTCTTGAATAGAGAGGAATCATCTTGTTCAAA 180
Qy 181 GCAAGAATAGAGTCTCATAGATGACAAAATTCGGGAAATGCAAGCATTTTGTGATGA 240
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Qy 241 CAGTGACTGAAAACCTGGACTCAACACCCCTTCAGATCATGAGACACCCAGGTCGGG 300
Db 241 CAGTGACTGAAAACCTGGACTCAACACCCCTTCAGATCATGAGACACCCAGGTCGGG 300
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QY 301 TGCCTGATGTGGCCAGTAGTGGCTACACCTCCCTGGTGGAGAAATACAACTCACCT 360
Db 301 TGCCTGATGTGGCCAGTAGTGGCTACACCTCCCTGGTGGAGAAATACAACTCACCT 360
QY 361 ACAGAAATAAATATATATCCGGATATGCGAGAGCTCTGTGGATGAGGCTATCCAAAG 420
Db 361 ACAGAAATAAATATATATCCGGATATGCGAGAGCTCTGTGGATGAGGCTATCCAAAG 420
QY 421 AAGGTTTAAAGTGTGGAGCAAGTCACTCCACTAAATTCACCAAGATTTCAAAGGGA 480
Db 421 AAGGTTTAAAGTGTGGAGCAAGTCACTCCACTAAATTCACCAAGATTTCAAAGGGA 480
QY 481 TTGCAGACATCATGATTCGCTTTAGGACTCGAGTCCATGGTCCGCTCGCTATTTTG 540
Db 481 TTGCAGACATCATGATTCGCTTTAGGACTCGAGTCCATGGTCCGCTCGCTATTTTG 540
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QY 661 TGGCTGCTCATGAATTTGGTCTATGCTACCTGGGCTCTCTCACTCCAATGATCAACAGCCT 720
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Db 721 TGATGTTCCAAATATATGTTCCCTGGATCCCGAGAAATACCCACTTTCTCAGGATGATA 780
QY 781 TCAATGGATCAGTCCATCTATGAGGCTCGCTTAAGTACTCTGTAAGTCCCAAGGAAC 840
Db 781 TCAATGGATCAGTCCATCTATGAGGCTCGCTTAAGTACTCTGTAAGTCCCAAGGAAC 840
QY 841 CCACATATACCCATGCTGTGACCTGACTTTCAGCTATTCACCACTTTCCCGCA 900
Db 841 CCACATATACCCATGCTGTGACCTGACTTTCAGCTATTCACCACTTTCCCGCA 900
QY 901 GAGAAGTAAATGTTCTTTAAAGCAGGACCTATGAGGATCTATTATGATATCAAGGATG 960
Db 901 GAGAAGTAAATGTTCTTTAAAGCAGGACCTATGAGGATCTATTATGATATCAAGGATG 960
QY 961 TTGAGTTTGAATTAATGCTTCAATCTGCCATCTCTGCCATCTCTGCAAGCTGAT 1020
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Db 1021 ACGAGAACCCAGAGATAGATTTCTGGTTTAAAGATGAAACTTCTGGATGATCAGAG 1080
QY 1081 GATATGCTGTCTTGGCAGATTAATCCCAATCCATCCATATAGTGTTCAGAGCTG 1140
Db 1081 GATATGCTGTCTTGGCAGATTAATCCCAATCCATCCATATAGTGTTCAGAGCTG 1140
QY 1141 TGAAGAAATAGATCAGCGCTGTGTATGATGACCAAGAAACCTTCTTTTGG 1200
Db 1141 TGAAGAAATAGATCAGCGCTGTGTATGATGACCAAGAAACCTTCTTTTGG 1200
QY 1201 GCATTTGGTGTGGAGGTTTGTATGAAATGACCAACCAAGATTCCTGGCAGAG 1260
Db 1201 GCATTTGGTGTGGAGGTTTGTATGAAATGACCAACCAAGATTCCTGGCAGAG 1260
QY 1261 GAGTGGTAAACACTTTCTCGAATCAGTATCCGTTGATGCTGTTTCCAGTACAAG 1320
Db 1261 GAGTGGTAAACACTTTCTCGAATCAGTATCCGTTGATGCTGTTTCCAGTACAAG 1320
QY 1321 GATTTCTTTTTCAGCGTGTGATCAAGCAATTTGAATACAACTTAAGACAAAGATA 1380
Db 1321 GATTTCTTTTTCAGCGTGTGATCAAGCAATTTGAATACAACTTAAGACAAAGATA 1380
QY 1381 TTACCCGAATCATGAGAACTAATACTTGGTTTCAATGCAAGAACCAAGAACTCCTCAT 1440
Db 1381 TTACCCGAATCATGAGAACTAATACTTGGTTTCAATGCAAGAACCAAGAACTCCTCAT 1440

1381 TTACCCGAATCATGAGAACTAATACTTGGTTTCAATGCAAGAACCAAGAACTCCTCAT 1440
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1501 AAGGTTTAAAGCTGTTTATTTTGGTATTTGTTTCAATTTGCTGTAACACCTTCTATTATC 1560
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1621 AATAGAA 1627
1621 AATAGAA 1627

RESULT 9
ADA76141
ID ADA76141 standard; cDNA; 1647 BP.
XX
AC ADA76141;
XX
DT 20-NOV-2003 (first entry)
XX
DE Human PRO polynucleotide #96.
XX
Human; gene; ss; PRO; secreted polypeptide; TNF-alpha; chondrocyte cell; tumour;
tumour necrosis factor-alpha; TNF-alpha; chondrocyte cell; tumour;
cancer; adrenal; lung; colon; breast; prostate; rectum; kidney; cervix;
liver; microvascular endothelial cell; glucose; FFA;
skeletal muscle cell; adipocyte cell; pericyte cell;
inner ear utricular supporting cell; T-lymphocyte cell;
endothelial cell tube formation; bone disorder; cartilage disorder;
sports injury; proteoglycan; articular cartilage defect; osteoarthritis;
rheumatoid arthritis; haemoglobin-associated disorder thalassemia;
immune system cell infiltration.
XX
OS Homo sapiens.
XX
PN US2003073212-A1.
XX
PD 17-APR-2003.
XX
PF 16-APR-2002; 2002US-00123903.
XX
PR 31-MAR-1997; 97WO-US005230.
PR 12-JUN-1998; 98WO-US012456.
PR 14-JUL-1998; 98WO-US014552.
PR 28-AUG-1998; 98WO-US017888.
PR 10-SEP-1998; 98WO-US018824.
PR 14-SEP-1998; 98WO-US019093.
PR 14-SEP-1998; 98WO-US019094.
PR 14-SEP-1998; 98WO-US019177.
PR 16-SEP-1998; 98WO-US019330.
PR 17-SEP-1998; 98WO-US019437.
PR 07-OCT-1998; 98WO-US021141.
PR 29-OCT-1998; 98WO-US022991.
PR 29-OCT-1998; 98WO-US022992.
PR 20-NOV-1998; 98WO-US024855.
PR 01-DEC-1998; 98WO-US025108.
PR 05-JAN-1999; 99WO-US000106.
PR 08-MAR-1999; 99WO-US005028.
PR 10-MAR-1999; 99WO-US005190.
PR 20-APR-1999; 99WO-US008615.
PR 14-MAY-1999; 99WO-US010733.
PR 02-JUN-1999; 99WO-US012252.
PR 01-SEP-1999; 99WO-US020111.
PR 08-SEP-1999; 99WO-US020594.
PR 13-SEP-1999; 99WO-US020944.
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PR 15-SEP-1999; 99WO-US021090.
PR 15-SEP-1999; 99WO-US021547.
PR 05-OCT-1999; 99WO-US023089.
PR 29-NOV-1999; 99WO-US028214.
PR 30-NOV-1999; 99WO-US028313.
PR 30-NOV-1999; 99WO-US028409.
PR 01-DEC-1999; 99WO-US028301.
PR 01-DEC-1999; 99WO-US028634.
PR 02-DEC-1999; 99WO-US028551.
PR 02-DEC-1999; 99WO-US028564.
PR 02-DEC-1999; 99WO-US028565.
PR 16-DEC-1999; 99WO-US030095.
PR 20-DEC-1999; 99WO-US030311.
PR 20-DEC-1999; 99WO-US030399.
PR 22-DEC-1999; 99WO-US030720.
PR 30-DEC-1999; 99WO-US031243.
PR 30-DEC-1999; 99WO-US031274.
PR 05-JAN-2000; 2000WO-US000219.
PR 06-JAN-2000; 2000WO-US000277.
PR 06-JAN-2000; 2000WO-US000376.
PR 11-FEB-2000; 2000WO-US003365.
PR 18-FEB-2000; 2000WO-US004341.
PR 18-FEB-2000; 2000WO-US004342.
PR 22-FEB-2000; 2000WO-US004414.
PR 24-FEB-2000; 2000WO-US004914.
PR 24-FEB-2000; 2000WO-US005004.
PR 01-MAR-2000; 2000WO-US005601.
PR 02-MAR-2000; 2000WO-US005746.
PR 02-MAR-2000; 2000WO-US005841.
PR 10-MAR-2000; 2000WO-US006319.
PR 15-MAR-2000; 2000WO-US006884.
PR 20-MAR-2000; 2000WO-US007377.
PR 21-MAR-2000; 2000WO-US007532.
PR 30-MAR-2000; 2000WO-US008439.
PR 17-MAY-2000; 2000WO-US013705.
PR 22-MAY-2000; 2000WO-US014042.
PR 30-MAY-2000; 2000WO-US014941.
PR 02-JUN-2000; 2000WO-US015264.
PR 28-JUL-2000; 2000WO-US020710.
PR 11-AUG-2000; 2000WO-US022031.
PR 23-AUG-2000; 2000WO-US023522.
PR 24-AUG-2000; 2000WO-US023328.
PR 08-NOV-2000; 2000WO-US030952.
PR 10-NOV-2000; 2000WO-US030873.
PR 01-DEC-2000; 2000WO-US032878.
PR 20-DEC-2000; 2000US-00747259.
PR 20-DEC-2000; 2000WO-US034956.
PR 28-FEB-2001; 2001US-00796498.
PR 28-FEB-2001; 2001WO-US006520.
PR 01-MAR-2001; 2001WO-US006666.
PR 09-MAR-2001; 2001US-00802706.
PR 14-MAR-2001; 2001US-00808689.
PR 22-MAR-2001; 2001US-00816744.
PR 05-APR-2001; 2001US-00828366.
PR 10-MAY-2001; 2001US-00854208.
PR 10-MAY-2001; 2001US-00854280.
PR 18-MAY-2001; 2001US-00860216.
PR 25-MAY-2001; 2001US-00866028.
PR 25-MAY-2001; 2001US-00866034.
PR 01-JUN-2001; 2001WO-US017092.
PR 01-JUN-2001; 2001US-00872035.
PR 01-JUN-2001; 2001WO-US017800.
PR 05-JUN-2001; 2001US-00874503.
PR 14-JUN-2001; 2001US-00882636.
PR 19-JUN-2001; 2001US-00886342.
PR 20-JUN-2001; 2001WO-US019692.
PR 21-JUN-2001; 2001US-00887879.
PR 22-JUN-2001; 2001WO-US020116.
PR 29-JUN-2001; 2001WO-US021066.
PR 09-JUL-2001; 2001WO-US021735.
PR 18-JUL-2001; 2001US-00908827.
PR 06-AUG-2001; 2001US-00924419.
PR 09-AUG-2001; 2001US-00927796.

PR 16-AUG-2001; 2001US-00931836.
PR 19-DEC-2001; 2001US-00028072.
PR XX (GETH ) GENENTECH INC.
PR Baker KP, Beresini M, Deforge L, Desnoyers L, Filvaroff E, Gao W;
PR Gerritsen ME, Goddard A, Godowski PJ, Gurney AL, Sherwood S;
PR Smith V, Stewart TA, Tumas D, Watanabe CK, Wood WI, Zhang Z;
PR WPI; 2003-687639/65.
PR P-PSDB; ADA76142.
PR New isolated nucleic acid encoding a secreted and transmembrane
PR polypeptide, designated e.g. PRO1114 or PRO4978, useful in chromosome and
PR gene mapping, in generating antisense RNA and DNA, and in gene therapy.
PR Claim 2; Fig 191; 659pp; English.
PR The invention relates to isolated human PRO polypeptides (secreted and
PR transmembrane polypeptides) and the polynucleotides encoding them. The
PR invention also relates to an antibody which specifically binds to a PRO
PR polypeptide, a method for stimulating the release of tumour necrosis
PR factor-alpha (TNF-alpha) from human blood, a method for stimulating the
PR proliferation or differentiation of chondrocyte cells and a method for
PR detecting the presence of a tumour in a mammal (e.g. adrenal, lung,
PR colon, breast, prostate, rectal, kidney, cervical and liver tumours). The
PR polynucleotides are useful in molecular biology, including uses as
PR hybridisation probes, in chromosome and gene mapping, in generating
PR antisense RNA and DNA and in gene therapy. The polynucleotides may also
PR be used in preparing PRO polypeptides by recombinant techniques and in
PR generating either transgenic animals or knock-out animals which are
PR useful in the development and screening of therapeutically useful
PR reagents. The PRO polypeptides or antibodies are used in preparing a
PR medicament for treating a condition responsive to the polypeptides or
PR antibodies, such as tumours, for stimulating and inhibiting proliferation
PR of human microvascular endothelial cells, for modulating the uptake of
PR glucose or FFA by skeletal muscle cells or adipocyte cells, for
PR stimulating differentiation of adipocyte cells, for stimulating
PR proliferation of or gene expression in pericyte cells, for stimulating
PR the proliferation of inner ear utricular supporting cells or T-lymphocyte
PR cells, for inducing endothelial cell tube formation and for treating
PR various bone and/or cartilage disorders such as sports injuries and
PR arthritis. PRO polypeptides which stimulate the release of proteoglycans
PR from cartilage are useful for treating sports-related joint problems,
PR articular cartilage defects, osteoarthritis and rheumatoid arthritis. PRO
PR polypeptides are also useful for treating various mammalian haemoglobin-
PR associated disorders such as various thalassaemias and conditions which
PR may benefit from enhanced local immune system cell infiltration. This
PR sequence represents a human PRO polynucleotide of the invention. Note:
PR The sequence data for this patent is also available in electronic format
PR CC from USPTO at seqdata.uspto.gov/sequence.html.
PR XX
SQ Sequence 1647 BP; 492 A; 341 C; 347 G; 467 T; 0 U; 0 Other;

Query Match          99.9%; Score 1625.4; DB 9; Length 1647;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 1626; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 GCTTCAGCTGAAGAAAGAGAGGAATGAAGCGCCTTCTGCTTCTGTTTGTCTTTATAA 60
Db 1 GCTTCAGCTGAAGAAAGAGAGGAATGAAGCGCCTTCTGCTTCTGTTTGTCTTTATAA 60

Qy 61 CATTTTCTTCGCATTTCCCTTACTCGGATGACGGAATGAAGAAAATATGCAACTGG 120
Db 61 CATTTTCTTCGCATTTCCCTTACTCGGATGACGGAATGAAGAAAATATGCAACTGG 120

Qy 121 CTCAGGCATATCTCAACAGGTTCTACTCTCTTGAATAGAGGGAATCATCTGTTCAA 180
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Qy 181 GCAAGAATAGAGTCTCATAGATGACAAAATTCGGAAATCGAGCAATTTTGGATTGA 240
Db 181 GCAAGAATAGAGTCTCATAGATGACAAAATTCGGAAATCGAGCAATTTTGGATTGA 240
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QY 241 CAGTGACTGGAAAACTGGACTCAACACACCCCTTGAGATCATGAGACACCCAGGTGTGGGG 300
Db 241 CAGTGACTGGAAAACTGGACTCAACACCCCTTGAGATCATGAGACACCCAGGTGTGGGG 300
QY 301 TGCCTGATGTGGGCCAGTAGTGGCTACACCCCTCCCTGGGTGGAGAAAATACAACTCACCT 360
Db 301 TGCCTGATGTGGGCCAGTAGTGGCTACACCCCTCCCTGGGTGGAGAAAATACAACTCACCT 360
QY 361 ACAGAAATAAATATATATCTCCGGATATGCGACGAGCTGCTGGATGAGGCTATCCAAG 420
Db 361 ACAGAAATAAATATATATCTCCGGATATGCGACGAGCTGCTGGATGAGGCTATCCAAG 420
QY 421 AAGGTTTGAAGTGGAGCAAGTCACTCCACTAAATTCACCAAGATTCARAGGGA 480
Db 421 AAGGTTTGAAGTGGAGCAAGTCACTCCACTAAATTCACCAAGATTCARAGGGA 480
QY 481 TTGCAGACATCATGATTGCTCTTTAGGACTCGAGTCCATGGTGGTCTCGCTATTTTG 540
Db 481 TTGCAGACATCATGATTGCTCTTTAGGACTCGAGTCCATGGTGGTCTCGCTATTTTG 540
QY 541 ATGGTCCCTTGGAGTGTGGCCATGCTTCCCTCGTCCGCTCGGCTCGGCTGAGTGTGACA 600
Db 541 ATGGTCCCTTGGAGTGTGGCCATGCTTCCCTCGTCCGCTCGGCTCGGCTGAGTGTGACA 600
QY 601 CTCATTTTGCATGAGGATGAATCTGACCAAGATGGAGCAGGATTCACACTTGTCTCTTG 660
Db 601 CTCATTTTGCATGAGGATGAATCTGACCAAGATGGAGCAGGATTCACACTTGTCTCTTG 660
QY 661 TGGCTGCTCATGAATTTGGTGCATGTCACCTGGGGCTCTCTCACTCCAATGATCAACAGCCT 720
Db 661 TGGCTGCTCATGAATTTGGTGCATGTCACCTGGGGCTCTCTCACTCCAATGATCAACAGCCT 720
QY 721 TGATGTTCCCAATTTATGTTCTCCCTGGATCCAGAAAATACCCACATTTCTCAGGATGATA 780
Db 721 TGATGTTCCCAATTTATGTTCTCCCTGGATCCAGAAAATACCCACATTTCTCAGGATGATA 780
QY 781 TCAATGGATCAGTCCATCTATGAGGCTCGCTTAAGTACTCTAGCTAGCCAGCAAGGAAC 840
Db 781 TCAATGGATCAGTCCATCTATGAGGCTCGCTTAAGTACTCTAGCTAGCCAGCAAGGAAC 840
QY 841 CCACATATACCCATGCTGTGACCCCTGACTTTCAGCTATCAACACTTTCCGCA 900
Db 841 CCACATATACCCATGCTGTGACCCCTGACTTTCAGCTATCAACACTTTCCGCA 900
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Db 961 TTGAGTTTGAATTAATTTGCTTCAATCTGCCATCTCTGCCAGTCTGCAAGCTGCAT 1020
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QY 1321 GATTCTCTCTTTTTCAGCCGTGGATCAAGCAATTTGAATACACATTTAGACAAAGAATA 1380
Db 1321 GATTCTCTCTTTTTCAGCCGTGGATCAAGCAATTTGAATACACATTTAGACAAAGAATA 1380
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Db 1381 TTACCCGGAATCATGAGAACTAATACTTGGTTTCAATGCAAGAAACCAAGAACTCTCTCAT 1440
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Db 1561 AATAAATTCATAGACCTTAAATAAACCTCAACAGGCTCTTTTAATATAAATTCCTGTTCAA 1620
QY 1621 AATAGAA 1627
Db 1621 AATAGAA 1627

RESULT 10
ADAL8791
ID ADAL8791 standard; cDNA; 1647 BP.
XX
AC ADAL8791;
DT 20-NOV-2003 (first entry)
XX
DE Human PRO polynucleotide #96.
XX
KW Human; gene; ss; PRO; secreted polypeptide; transmembrane polypeptide;
tumour necrosis factor-alpha; TNF-alpha; blood; chondrocyte cell; lung;
colon; breast; prostate; rectum; cervix; liver; tumour; cancer;
glucose uptake; FFA; adipocyte cell; pericyte cell; proteoglycan;
cartilage; inner ear utricular supporting cell; cytokine; A-peptide;
factor VIIA; endothelial cell.
XX
OS Homo sapiens.
XX
PN US2003054517-A1.
XX
PD 20-MAR-2003.
XX
PF 08-MAY-2002; 2002US-00141755.
XX
PR 31-MAR-1997; 97WO-US005230.
PR 12-JUN-1998; 98WO-US012456.
PR 14-JUL-1998; 98WO-US014552.
PR 28-AUG-1998; 98WO-US017888.
PR 10-SEP-1998; 98WO-US018824.
PR 14-SEP-1998; 98WO-US019093.
PR 14-SEP-1998; 98WO-US019094.
PR 14-SEP-1998; 98WO-US019177.
PR 16-SEP-1998; 98WO-US019330.
PR 17-SEP-1998; 98WO-US019437.
PR 07-OCT-1998; 98WO-US021141.
PR 29-OCT-1998; 98WO-US022991.
PR 29-OCT-1998; 98WO-US022992.
PR 20-NOV-1998; 98WO-US024855.
PR 01-DEC-1998; 98WO-US025108.
PR 05-JAN-1999; 99WO-US000106.
PR 08-MAR-1999; 99WO-US005028.
PR 10-MAR-1999; 99WO-US005190.
PR 20-APR-1999; 99WO-US008615.
PR 14-MAY-1999; 99WO-US010733.
PR 02-JUN-1999; 99WO-US012252.
PR 01-SEP-1999; 99WO-US020111.
PR 08-SEP-1999; 99WO-US020594.
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PR 13-SEP-1999; 99WO-US020944.
PR 15-SEP-1999; 99WO-US021090.
PR 15-SEP-1999; 99WO-US021547.
PR 05-OCT-1999; 99WO-US023089.
PR 29-NOV-1999; 99WO-US028214.
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PR 30-NOV-1999; 99WO-US028409.
PR 01-DEC-1999; 99WO-US028301.
PR 01-DEC-1999; 99WO-US028634.
PR 02-DEC-1999; 99WO-US028551.
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PR 16-DEC-1999; 99WO-US030095.
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PR 22-DEC-1999; 99WO-US030720.
PR 30-DEC-1999; 99WO-US031243.
PR 30-DEC-1999; 99WO-US031274.
PR 05-JAN-2000; 2000WO-US000219.
PR 06-JAN-2000; 2000WO-US000277.
PR 06-JAN-2000; 2000WO-US000376.
PR 11-FEB-2000; 2000WO-US003565.
PR 18-FEB-2000; 2000WO-US004341.
PR 18-FEB-2000; 2000WO-US004342.
PR 22-FEB-2000; 2000WO-US004414.
PR 24-FEB-2000; 2000WO-US004914.
PR 24-FEB-2000; 2000WO-US005004.
PR 01-MAR-2000; 2000WO-US005601.
PR 02-MAR-2000; 2000WO-US005746.
PR 02-MAR-2000; 2000WO-US005841.
PR 10-MAR-2000; 2000WO-US006319.
PR 15-MAR-2000; 2000WO-US006884.
PR 20-MAR-2000; 2000WO-US007377.
PR 21-MAR-2000; 2000WO-US007532.
PR 30-MAR-2000; 2000WO-US008439.
PR 17-MAY-2000; 2000WO-US013705.
PR 22-MAY-2000; 2000WO-US014042.
PR 30-MAY-2000; 2000WO-US014941.
PR 02-JUN-2000; 2000WO-US015264.
PR 28-JUL-2000; 2000WO-US020710.
PR 11-AUG-2000; 2000WO-US022031.
PR 22-AUG-2000; 2000WO-US023522.
PR 24-AUG-2000; 2000WO-US023328.
PR 08-NOV-2000; 2000WO-US030952.
PR 10-NOV-2000; 2000WO-US030873.
PR 01-DEC-2000; 2000WO-US032678.
PR 20-DEC-2000; 2000US-00747259.
PR 20-DEC-2000; 2000WO-US034956.
PR 28-FEB-2001; 2001US-00796498.
PR 28-FEB-2001; 2001WO-US006520.
PR 01-MAR-2001; 2001WO-US006666.
PR 09-MAR-2001; 2001US-00802706.
PR 14-MAR-2001; 2001US-00808689.
PR 22-MAR-2001; 2001US-00816744.
PR 05-APR-2001; 2001US-00828366.
PR 10-MAY-2001; 2001US-00854208.
PR 18-MAY-2001; 2001US-00860216.
PR 25-MAY-2001; 2001US-00866028.
PR 25-MAY-2001; 2001US-00866034.
PR 25-MAY-2001; 2001WO-US017092.
PR 01-JUN-2001; 2001US-00872035.
PR 01-JUN-2001; 2001WO-US017800.
PR 05-JUN-2001; 2001US-00874503.
PR 14-JUN-2001; 2001US-00882636.
PR 19-JUN-2001; 2001US-00886342.
PR 20-JUN-2001; 2001WO-US019692.
PR 21-JUN-2001; 2001US-00887879.
PR 22-JUN-2001; 2001WO-US020116.
PR 29-JUN-2001; 2001WO-US021066.
PR 09-JUL-2001; 2001WO-US021735.
PR 18-JUL-2001; 2001US-00908827.
PR 06-AUG-2001; 2001US-00924419.

PR 09-AUG-2001; 2001US-00927796.
PR 16-AUG-2001; 2001US-00931836.
PR 19-DEC-2001; 2001US-00028072.
XX
PA (GETH ) GENENTECH INC.
XX
XX Baker KP, Beresini M, Deforge L, Desnoyers L, Filvaroff E, Gao W;
PI Gerritsen ME, Goddard A, Godowski PJ, Gurney AL, Sherwood S;
PI Smith V, Stewart TA, Tumas D, Watanabe CK, Wood WI, Zhang Z;
XX
XX WPI; 2003-521854/49.
DR P-PSDB; ADA18792.
XX
XX New PRO nucleic acid, useful for preparing a composition for treating
PT e.g., tumors.
XX
XX Claim 2; Fig 191; 660pp; English.
XX
XX The invention relates to isolated human PRO polypeptides (secreted and
transmembrane polypeptides) and the polynucleotides encoding them. The
invention also relates to an antibody which specifically binds to a PRO
polypeptide, a method for stimulating the release of tumour necrosis
factor-alpha (TNF-alpha) from human blood, a method for stimulating the
proliferation or differentiation of chondrocyte cells and a method for
detecting the presence of a tumour in a mammal (e.g. lung, colon, breast,
prostate, rectal, cervical and liver tumours). The polynucleotides are
useful in molecular biology, including uses as hybridisation probes, in
chromosome and gene mapping, in generating antisense RNA and DNA and in
gene therapy. The polynucleotides may also be used in preparing PRO
polypeptides by recombinant techniques and in generating either
transgenic animals or knock-out animals which are useful in the
development and screening of therapeutically useful reagents. The PRO
polypeptides or antibodies are used in preparing a medicament for
treating a condition responsive to the polypeptides or antibodies, such
as tumours, for modulating the uptake of glucose or FFA by adipocyte
cells, for stimulating the proliferation of or gene expression in
pericyte cells, for stimulating the release of proteoglycans from
cartilage, for stimulating the proliferation of inner ear utricular
supporting cells, for stimulating the release of cytokines from PSMC
cells, for inhibiting the binding of A-peptide to factor VIIA, for
inhibiting the differentiation of adipocyte cells and for stimulating the
proliferation of endothelial cells. This sequence represents a human PRO
polynucleotide of the invention. Note: The sequence data for this patent
is also available in electronic format from USPTO at
seqdata.uspto.gov/sequence.html.
XX
SQ Sequence 1647 BP; 492 A; 341 C; 347 G; 467 T; 0 U; 0 Other;

Query Match 99.9%; Score 1625.4; DB 9; Length 1647;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 1626; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 GCTTCAGCTGAAGAAGAGAGAGGAATGAAGCGCCTTCGCTTCTGTGTGTTGTTCTTTATAA 60
Db 1 GCTTCAGCTGAAGAAGAGAGAGGAATGAAGCGCCTTCGCTTCTGTGTGTTGTTCTTTATAA 60
Qy 61 CATTTTCTCTCGATTTCCTTCTAGTCGGATGACGGAATGAAGAAAATGCAACTGG 120
Db 61 CATTTTCTCTCGATTTCCTTCTAGTCGGATGACGGAATGAAGAAAATGCAACTGG 120
Qy 121 CTCAGGCATATCTCAACCACTTCTACTCTCTTGAATGAGAGGAATCATCTGTTTCAAA 180
Db 121 CTCAGGCATATCTCAACCACTTCTACTCTCTTGAATGAGAGGAATCATCTGTTTCAAA 180
Qy 181 GCAAGATAGAGTCTCATAGATGACAAAATTCGGGAATTCGGAAGATTTTGGATTGA 240
Db 181 GCAAGATAGAGTCTCATAGATGACAAAATTCGGGAATTCGGAAGATTTTGGATTGA 240
Qy 241 CAGTGACTGGAAAACTGGACTCAACACCTTCAGATCATGACACACCCAGGTTGGGG 300
Db 241 CAGTGACTGGAAAACTGGACTCAACACCTTCAGATCATGACACACCCAGGTTGGGG 300
Qy 301 TGCCTGATGTGGGCCAGTATGGGTACACCTTCCTGGGTGGAGAAAATACAACTCACT 360
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||||| 301 TGCCTGATGGGCGAGTATGGCTACACCTCCCTGGGTGAGAAATACAACTCCACT 360
Db
Qy 361 ACAGATAATAAATATACTCCGATATGGCAGGCTGCTGTGGATGAGGCTATCCAAAG 420
Db
361 ACAGATAATAAATATACTCCGATATGGCAGGCTGCTGTGGATGAGGCTATCCAAAG 420
Qy 421 AAGGTTTAGAAGTGGAGCAAGTCACTCCACTTAAATTCACCAAGATTTCAAGGGGA 480
Db
421 AAGGTTTAGAAGTGGAGCAAGTCACTCCACTTAAATTCACCAAGATTTCAAGGGGA 480
Qy 481 TTGAGACATCATGATTCCTTTAGGACTCCAGTCCATGGTCCGCTGCTCGCTATTTTG 540
Db
481 TTGAGACATCATGATTCCTTTAGGACTCCAGTCCATGGTCCGCTGCTCGCTATTTTG 540
Qy 541 ATGGTCCCTTGGGAGTGTCTGGCCATGCTTTCCCTCTGGTCCGGTCTGGGTGGTGACA 600
Db
541 ATGGTCCCTTGGGAGTGTCTGGCCATGCTTTCCCTCTGGTCCGGTCTGGGTGGTGACA 600
Qy 601 CTCATTTTGATGAGATGAATACTGGACCAAGGATGGAGCAGGATTCAACTGTTCTTG 660
Db
601 CTCATTTTGATGAGATGAATACTGGACCAAGGATGGAGCAGGATTCAACTGTTCTTG 660
Qy 661 TGGCTGCTCATGAATTTGGTCACTGCTGGGCTCTCTCACTCCCAATGATCAACAGCCT 720
Db
661 TGGCTGCTCATGAATTTGGTCACTGCTGGGCTCTCTCACTCCCAATGATCAACAGCCT 720
Qy 721 TGATGTTCCCAATATGTCCTCCCTGGATCCAGAAATACCCACTTTCTCAGGATGATA 780
Db
721 TGATGTTCCCAATATGTCCTCCCTGGATCCAGAAATACCCACTTTCTCAGGATGATA 780
Qy 781 TCAATGGAATCCAGTCCATCATGAGGCTGCTTAAGTACCTCTAAGCCAAAGGAAC 840
Db
781 TCAATGGAATCCAGTCCATCATGAGGCTGCTTAAGTACCTCTAAGCCAAAGGAAC 840
Qy 841 CCACATATACCCATGCTGCTGACCTGCTGACCTTTTGAAGCTATCAAACTTTCCGCA 900
Db
841 CCACATATACCCATGCTGCTGACCTGCTGACCTTTTGAAGCTATCAAACTTTCCGCA 900
Qy 901 GAGAGTAAATGTTTAAAGCAGGACCTATGAGGATCTATTATGATATCAAGGATG 960
Db
901 GAGAGTAAATGTTTAAAGCAGGACCTATGAGGATCTATTATGATATCAAGGATG 960
Qy 961 TTGAGTTTGAATTAATGCTTCAATCTGCGCATCTCTGCCAGTCTGCAAGCTGCAT 1020
Db
961 TTGAGTTTGAATTAATGCTTCAATCTGCGCATCTCTGCCAGTCTGCAAGCTGCAT 1020
Qy 1021 ACGAGAACCCAGAGATAAGATTTCTGGTTTAAAGATGAAACTTCTGGATGATCAGAG 1080
Db
1021 ACGAGAACCCAGAGATAAGATTTCTGGTTTAAAGATGAAACTTCTGGATGATCAGAG 1080
Qy 1081 GATATGCTGTGTCAGATATCCCAATCCATCCATATAGGTTTCCAGACGCTG 1140
Db
1081 GATATGCTGTGTCAGATATCCCAATCCATCCATATAGGTTTCCAGACGCTG 1140
Qy 1141 TGAAGAAATAGATGACGCGCTGTGATGAAACCAATGACCAAGGATTTCCCGCAGA 1200
Db
1141 TGAAGAAATAGATGACGCGCTGTGATGAAACCAATGACCAAGGATTTCCCGCAGA 1200
Qy 1201 GCATTTGGTGTGGAGTTTGTATGAAATGACCAACCAATGACCAAGGATTTCCCGCAGA 1260
Db
1201 GCATTTGGTGTGGAGTTTGTATGAAATGACCAACCAATGACCAAGGATTTCCCGCAGA 1260
Qy 1261 GAGTGGTAAACACTTTCTCGAATCAGTATCCGTTGATGCTGTTTCCAGTACAAG 1320
Db
1261 GAGTGGTAAACACTTTCTCGAATCAGTATCCGTTGATGCTGTTTCCAGTACAAG 1320
Qy 1321 GATTTCTTTTTCAGCCGTGATCAAGCAATTTGAATACAAATTAAGAACAAGATA 1380
Db
1321 GATTTCTTTTTCAGCCGTGATCAAGCAATTTGAATACAAATTAAGAACAAGATA 1380
Qy 1381 TTACCCGAATCATGAGAACTAATCTGTTTCAATGCAAGAACCAAGAACTCTCTCAT 1440
Db
1381 TTACCCGAATCATGAGAACTAATCTGTTTCAATGCAAGAACCAAGAACTCTCTCAT 1440

1381 TTACCCGAATCATGAGAACTAATCTGTTTCAATGCAAGAACCAAGAACTCTCTCAT 1440
Qy 1441 TTGTTTTGATATCAACAGGAAAAAGCACATTCAGGAGGATTAAGATATGTATCAT 1500
Db
1441 TTGTTTTGATATCAACAGGAAAAAGCACATTCAGGAGGATTAAGATATGTATCAT 1500
Qy 1501 AAGTTTTAAGCTGTTTATTTTGGTATTGTTTCTGCTGAAAAACACTTCTATTATC 1560
Db
1501 AAGTTTTAAGCTGTTTATTTTGGTATTGTTTCTGCTGAAAAACACTTCTATTATC 1560
Qy 1561 AATAAATTCATAGACCTAAAAATAAACCTCAACAGCTCTTTTAATAATAAATCTGTTCAA 1620
Db
1561 AATAAATTCATAGACCTAAAAATAAACCTCAACAGCTCTTTTAATAATAAATCTGTTCAA 1620
Qy 1621 AATAGAA 1627
Db
1621 AATAGAA 1627

RESULT 11
ADA61414
ID ADA61414 standard; cDNA; 1647 BP.
XX
AC ADA61414;
XX
DT 20-NOV-2003 (first entry)
XX
DE Homo sapiens.
XX
KW Human; secreted and transmembrane protein; PRO; gene; ss;
KW Tumour necrosis factor alpha release; TNF-alpha release;
KW glucose uptake modulator; PFA uptake modulator;
KW cell proliferation stimulator; cell differentiation stimulator;
KW lung tumour; colon tumour; breast tumour; prostate tumour; rectal tumour;
KW cervical tumour; liver tumour; chromosome mapping; gene mapping;
KW gene therapy; chromosome identification; chromosome marker.
XX
OS Novel.
OS human.
OS secreted.
OS and.
OS transmembrane.
OS protein.
OS PRO5992.
OS cDNA.
XX
US2003049816-A1.
PN
XX
PD 13-MAR-2003.
XX
PF 15-APR-2002; 2002US-00123262.
XX
PR 31-MAR-1997; 97WO-US005230.
PR 12-JUN-1998; 98WO-US012456.
PR 14-JUL-1998; 98WO-US014552.
PR 28-AUG-1998; 98WO-US017888.
PR 10-SEP-1998; 98WO-US018824.
PR 14-SEP-1998; 98WO-US019093.
PR 14-SEP-1998; 98WO-US019094.
PR 14-SEP-1998; 98WO-US019177.
PR 16-SEP-1998; 98WO-US019330.
PR 17-SEP-1998; 98WO-US019437.
PR 07-OCT-1998; 98WO-US021141.
PR 29-OCT-1998; 98WO-US022991.
PR 29-OCT-1998; 98WO-US022992.
PR 20-NOV-1998; 98WO-US024855.
PR 01-DEC-1998; 98WO-US025108.
PR 05-JAN-1999; 98WO-US000106.
PR 08-MAR-1999; 98WO-US000528.
PR 10-MAR-1999; 98WO-US005190.
PR 20-APR-1999; 98WO-US008615.
PR 14-MAY-1999; 98WO-US010733.

Db 241 CAGTGACTGAAAACCTGGATCAAAACCCCTTGATCATGAAGACACCCAGGTGTGGG 300
Qy 301 TGCCCTGATGGGCGAGTATGGCTACACCTCCCTCGGTGGAGAAAATACAACTCACCT 360
Db 301 TGCCCTGATGGGCGAGTATGGCTACACCTCCCTCGGTGGAGAAAATACAACTCACCT 360
Qy 361 ACAGAAATAAATACTACTCCGATATGGACAGCTGCTGTGGATGAGGCTATCCAAG 420
Db 361 ACAGAAATAAATACTACTCCGATATGGACAGCTGCTGTGGATGAGGCTATCCAAG 420
Qy 421 AAGGTTTAGAAGTGTGGAGCAAGTCACTCCACTAAAATTCACCAAGATTTCAAAGGGGA 480
Db 421 AAGGTTTAGAAGTGTGGAGCAAGTCACTCCACTAAAATTCACCAAGATTTCAAAGGGGA 480
Qy 481 TTGCAGACATCATGATTCGCTTTAGGACTCGAGTCCATGGTCCGCTCGCTGATTTTG 540
Db 481 TTGCAGACATCATGATTCGCTTTAGGACTCGAGTCCATGGTCCGCTCGCTGATTTTG 540
Qy 541 ATGGTCCCTTGGAGTGTGGCCATGCTTTCCCTGCTGCTGGTCCGGTCTGGGTGGTACA 600
Db 541 ATGGTCCCTTGGAGTGTGGCCATGCTTTCCCTGCTGCTGGTCCGGTCTGGGTGGTACA 600
Qy 601 CTCATTTTGATGAGGATGAAAACCTGGACCAAGGATGGACAGGATTCAACTTGTTCCTTG 660
Db 601 CTCATTTTGATGAGGATGAAAACCTGGACCAAGGATGGACAGGATTCAACTTGTTCCTTG 660
Qy 661 TGGCTGCTCATGAATTTGGTCATGCACTGGGGCTCTCTCACTCCAAATGATCAAAACGCT 720
Db 661 TGGCTGCTCATGAATTTGGTCATGCACTGGGGCTCTCTCACTCCAAATGATCAAAACGCT 720
Qy 721 TGATGTTCCCAATATGCTCCCTGGATCCAGAAATACCCACTTTCAGAGTATA 780
Db 721 TGATGTTCCCAATATGCTCCCTGGATCCAGAAATACCCACTTTCAGAGTATA 780
Qy 781 TCAATGGAATCCAGTCCATCTATGGAGTCTGCTTAAGTACCTGCTAAGCAAGCAAGAAC 840
Db 781 TCAATGGAATCCAGTCCATCTATGGAGTCTGCTTAAGTACCTGCTAAGCAAGCAAGAAC 840
Qy 841 CCATATACCCCATGCTGACCTGACTTGAATTTTGAAGTATCAAACTTTCCGCA 900
Db 841 CCATATACCCCATGCTGACCTGACTTGAATTTTGAAGTATCAAACTTTCCGCA 900
Qy 901 GAGAGTAAATGTTCTTAAAGGCGAGGACCTATGGAGATCTATATGATATCAGGATG 960
Db 901 GAGAGTAAATGTTCTTAAAGGCGAGGACCTATGGAGATCTATATGATATCAGGATG 960
Qy 961 TTGAGTTTGAATTAATTCCTTCAATTCGCGCATCTCTGCCAGCTGATTCGCAAGTGCAT 1020
Db 961 TTGAGTTTGAATTAATTCCTTCAATTCGCGCATCTCTGCCAGCTGATTCGCAAGTGCAT 1020
Qy 1021 ACAGAAACCCAGAGATAAGATTTCTGGTTTTTAAAGATGAAAACCTTCTGGATGATCAG 1080
Db 1021 ACAGAAACCCAGAGATAAGATTTCTGGTTTTTAAAGATGAAAACCTTCTGGATGATCAG 1080
Qy 1081 GATATGCTGCTGCCAGATTAATCCCAATCCATCCATACATAGTGTTCCTCAGGACCTG 1140
Db 1081 GATATGCTGCTGCCAGATTAATCCCAATCCATCCATACATAGTGTTCCTCAGGACCTG 1140
Qy 1141 TGAAGAAATAGATGACGCGCTGCTGTGATGATGACCAAGAAAACCTTCTTTTGTGG 1200
Db 1141 TGAAGAAATAGATGACGCGCTGCTGTGATGATGACCAAGAAAACCTTCTTTTGTGG 1200
Qy 1201 GCATTTGCTGGAGGTTTGAATGAAATGACCCAAACCATGGACAAAGGATTCGCCGAGA 1260
Db 1201 GCATTTGCTGGAGGTTTGAATGAAATGACCCAAACCATGGACAAAGGATTCGCCGAGA 1260
Qy 1261 GAGTGGTAAACACATTTCTGGAATCAGTATCCGTTGATGCTCTTCCAGTACAAG 1320
Db 1261 GAGTGGTAAACACATTTCTGGAATCAGTATCCGTTGATGCTCTTCCAGTACAAG 1320
Qy 1321 GATTCCTCTTTTTCAGCGGTGATCAAGCAATTTGAATACAACTTAAGACAAAGAATA 1380

Db 1321 GATTCCTCTTTTTCAGCGGTGATCAAGCAATTTGAATACAACTTAAGACAAAGAATA 1380
Qy 1381 TTATCCCAATCATGAGAACTAATACTTTGGTTTCAATGCAAGAACCAAGAACTCCTCAT 1440
Db 1381 TTATCCCAATCATGAGAACTAATACTTTGGTTTCAATGCAAGAACCAAGAACTCCTCAT 1440
Qy 1441 TTGGTTTGTATATCAACAAGGAAAAGCACATTCAGGAGGCATAAAGATATTGTATCATA 1500
Db 1441 TTGGTTTGTATATCAACAAGGAAAAGCACATTCAGGAGGCATAAAGATATTGTATCATA 1500
Qy 1501 AGAGTTTAAAGCTTTTATTTTGGTATGTTCAATTTGCTGAAAAACACTTCTATTATC 1560
Db 1501 AGAGTTTAAAGCTTTTATTTTGGTATGTTCAATTTGCTGAAAAACACTTCTATTATC 1560
Qy 1561 AATAAATTCATAGACCTTAAATTAACCTCAACAGTCTTTTAAATATAATTTCTGCTTCAA 1620
Db 1561 AATAAATTCATAGACCTTAAATTAACCTCAACAGTCTTTTAAATATAATTTCTGCTTCAA 1620
Qy 1621 AATAGAA 1627
Db 1621 AATAGAA 1627

RESULT 12
ADBI9199
ID ADBI9199 standard; cDNA; 1647 BP.
XX ADBI9199;
XX 20-NOV-2003 (first entry)
XX Novel human secreted and transmembrane protein PRO5992 cDNA.
XX Human; secreted and transmembrane protein; PRO; gene; ss;
KW Tumour necrosis factor alpha release; TNF-alpha release;
KW glucose uptake modulator; FFA uptake modulator;
KW cell proliferation stimulator; cell differentiation stimulator;
KW cell differentiation inhibitor; cytokin.
XX Homo sapiens.
XX US2003068796-A1.
XX 10-APR-2003.
XX 15-APR-2002; 2002US-00123261.
XX 31-MAR-1997; 97WO-US005230.
PR 12-JUN-1998; 98WO-US012456.
PR 14-JUL-1998; 98WO-US014552.
PR 28-AUG-1998; 98WO-US017888.
PR 10-SEP-1998; 98WO-US018824.
PR 14-SEP-1998; 98WO-US019093.
PR 14-SEP-1998; 98WO-US019094.
PR 14-SEP-1998; 98WO-US019177.
PR 16-SEP-1998; 98WO-US019330.
PR 17-SEP-1998; 98WO-US019437.
PR 07-OCT-1998; 98WO-US021141.
PR 29-OCT-1998; 98WO-US022991.
PR 29-OCT-1998; 98WO-US022992.
PR 20-NOV-1998; 98WO-US024855.
PR 01-DEC-1998; 98WO-US025108.
PR 05-JAN-1999; 99WO-US000106.
PR 08-MAR-1999; 99WO-US005028.
PR 10-MAR-1999; 99WO-US005190.
PR 20-APR-1999; 99WO-US008615.
PR 14-MAY-1999; 99WO-US010733.
PR 02-JUN-1999; 99WO-US012252.
PR 01-SEP-1999; 99WO-US020111.
PR 08-SEP-1999; 99WO-US020594.
PR 13-SEP-1999; 99WO-US020944.
PR 15-SEP-1999; 99WO-US021090.
PR 15-SEP-1999; 99WO-US021547.

PR 05-OCT-1999; 99WO-US023089.
PR 29-NOV-1999; 99WO-US028214.
PR 30-NOV-1999; 99WO-US028313.
PR 30-NOV-1999; 99WO-US028409.
PR 01-DEC-1999; 99WO-US028301.
PR 01-DEC-1999; 99WO-US028634.
PR 02-DEC-1999; 99WO-US028551.
PR 02-DEC-1999; 99WO-US028564.
PR 02-DEC-1999; 99WO-US028565.
PR 16-DEC-1999; 99WO-US030095.
PR 20-DEC-1999; 99WO-US030911.
PR 20-DEC-1999; 99WO-US030999.
PR 22-DEC-1999; 99WO-US030720.
PR 30-DEC-1999; 99WO-US031243.
PR 30-DEC-1999; 99WO-US031274.
PR 05-JAN-2000; 2000WO-US000219.
PR 06-JAN-2000; 2000WO-US000277.
PR 06-JAN-2000; 2000WO-US000376.
PR 11-FEB-2000; 2000WO-US003565.
PR 18-FEB-2000; 2000WO-US004341.
PR 18-FEB-2000; 2000WO-US004342.
PR 22-FEB-2000; 2000WO-US004414.
PR 24-FEB-2000; 2000WO-US004914.
PR 24-FEB-2000; 2000WO-US005004.
PR 01-MAR-2000; 2000WO-US005601.
PR 02-MAR-2000; 2000WO-US005746.
PR 02-MAR-2000; 2000WO-US005841.
PR 10-MAR-2000; 2000WO-US006319.
PR 15-MAR-2000; 2000WO-US006884.
PR 20-MAR-2000; 2000WO-US007377.
PR 21-MAR-2000; 2000WO-US007532.
PR 30-MAR-2000; 2000WO-US008439.
PR 17-MAY-2000; 2000WO-US013705.
PR 22-MAY-2000; 2000WO-US014042.
PR 30-MAY-2000; 2000WO-US014941.
PR 02-JUN-2000; 2000WO-US015264.
PR 28-JUL-2000; 2000WO-US020710.
PR 11-AUG-2000; 2000WO-US022031.
PR 23-AUG-2000; 2000WO-US023522.
PR 24-AUG-2000; 2000WO-US023328.
PR 08-NOV-2000; 2000WO-US030952.
PR 10-NOV-2000; 2000WO-US030873.
PR 01-DEC-2000; 2000WO-US032678.
PR 20-DEC-2000; 2000US-00747259.
PR 28-DEC-2000; 2000WO-US034956.
PR 28-FEB-2001; 2001US-00796498.
PR 01-MAR-2001; 2001WO-US006520.
PR 09-MAR-2001; 2001US-00806666.
PR 14-MAR-2001; 2001US-00802706.
PR 22-MAR-2001; 2001US-00816744.
PR 05-APR-2001; 2001US-00828366.
PR 10-MAY-2001; 2001US-00854208.
PR 10-MAY-2001; 2001US-00854280.
PR 18-MAY-2001; 2001US-00860216.
PR 25-MAY-2001; 2001US-00866028.
PR 25-MAY-2001; 2001US-00866034.
PR 25-MAY-2001; 2001WO-US017092.
PR 01-JUN-2001; 2001US-00872035.
PR 01-JUN-2001; 2001WO-US017800.
PR 05-JUN-2001; 2001US-00874503.
PR 14-JUN-2001; 2001US-00882636.
PR 19-JUN-2001; 2001US-00886342.
PR 20-JUN-2001; 2001WO-US019692.
PR 21-JUN-2001; 2001US-00887879.
PR 22-JUN-2001; 2001WO-US020116.
PR 29-JUN-2001; 2001WO-US021066.
PR 09-JUL-2001; 2001WO-US021735.
PR 18-JUL-2001; 2001US-00908827.
PR 06-AUG-2001; 2001US-00924419.
PR 09-AUG-2001; 2001US-00927796.
PR 16-AUG-2001; 2001US-00931836.
PR 19-DEC-2001; 2001US-00028072.

XX (GETH) GENENTECH INC.
XX Baker KP, Beresini M, Deforge L, Desnoyers L, Filvaroff E, Gao W;
XX Gerritsen ME, Goddard A, Godowski PJ, Gurney AL, Sherwood S;
XX Smith V, Stewart TA, Tumas D, Watanabe CK, Wood WI, Zhang Z;
XX WPI; 2003-695927/66.
XX P-PSDB; ADB19200.
XX Novel secreted and transmembrane PRO polypeptides useful for stimulating
XX the release of tumor necrosis factor alpha and detecting the presence of
XX a tumor in a mammal.
XX Claim 2; Fig 191; 660pp; English.
XX The invention describes 305 nucleic acids encoding PRO (secreted and
XX transmembrane) polypeptides (I). (I) is useful for stimulating the
XX release of TNF-alpha from human blood, for modulating the uptake of
XX glucose or FFA by skeletal muscle cells or adipocyt
XX Sequence 1647 BP; 492 A; 341 C; 347 G; 467 T; 0 U; 0 Other;
SQ
Query Match 99.9%; Score 1625.4; DB 9; Length 1647;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 1626; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1 GCTTCAGCTGAAGAAAGAGAGAGAAATGAAGCGCTTCTGCTTCTGTTGTTCTTTATAA 60
Db 1 GCTTCAGCTGAAGAAAGAGAGAAATGAAGCGCTTCTGCTTCTGTTGTTCTTTATAA 60
QY 61 CATTTCTTCTGCATTTCCCTTAGTCGGATGACGGAAATGAGAAATATGCAACTCG 120
Db 61 CATTTCTTCTGCATTTCCCTTAGTCGGATGACGGAAATGAGAAATATGCAACTCG 120
QY 121 CTCAGGCATATCTCAACCAAGTTCTACTCTCTTGAATAGAGGGAATCATCTTGTTCAAA 180
Db 121 CTCAGGCATATCTCAACCAAGTTCTACTCTTGAATAGAGGGAATCATCTTGTTCAAA 180
QY 181 GCAAGAAATAGGAGTCTCATAGATGACAAAATTCGGGAAATCAAGCATTTTGGATTGA 240
Db 181 GCAAGAAATAGGAGTCTCATAGATGACAAAATTCGGGAAATCAAGCATTTTGGATTGA 240
QY 241 CAGTGACTGGAACCTGGAGCTCAACACCCCTTGAGATCATGAGACACCCAGGTGCGG 300
Db 241 CAGTGACTGGAACCTGGAGCTCAACACCCCTTGAGATCATGAGACACCCAGGTGCGG 300
QY 301 TGCCTGATGTGGGCCAGTATGGCTACACCCCTCCCTGGGTGGAGAAATACAACCTCACCT 360
Db 301 TGCCTGATGTGGGCCAGTATGGCTACACCCCTCCCTGGGTGGAGAAATACAACCTCACCT 360
QY 361 ACAGAAATAAATCTATATCTCCGGATATGGCAGAGCTCTGTGGATGAGGCTATCAAG 420
Db 361 ACAGAAATAAATCTATATCTCCGGATATGGCAGAGCTCTGTGGATGAGGCTATCAAG 420
QY 421 AAGGTTTGAAGTGTGGAGCAAGTCACTCCACTAAATTCACCAAGATTTCAAGGGGA 480
Db 421 AAGGTTTGAAGTGTGGAGCAAGTCACTCCACTAAATTCACCAAGATTTCAAGGGGA 480
QY 481 TTGCGACATCATGATTTGCTTTTAGGACTCGAGTCCATGCTCGGTCTCGCTATTTTG 540
Db 481 TTGCGACATCATGATTTGCTTTTAGGACTCGAGTCCATGCTCGGTCTCGCTATTTTG 540
QY 541 ATGGTCCCTTGGGAGTGTGTCGCCATGCTTTCTCTGCTCGGTCTGGGTGGTGACA 600
Db 541 ATGGTCCCTTGGGAGTGTGTCGCCATGCTTTCTCTGCTCGGTCTGGGTGGTGACA 600
QY 601 CTCATTTTCATGAGGATGAAACTGGACCAAGATGAGCAGGATTCACCTGTTCTTG 660
Db 601 CTCATTTTCATGAGGATGAAACTGGACCAAGATGAGCAGGATTCACCTGTTCTTG 660
QY 661 TGGCTGCTCATGAATTTGTCATGCACTGGGCTCTCTCACTCCAAATGATCAAAAGCCT 720
Db 661 TGGCTGCTCATGAATTTGTCATGCACTGGGCTCTCTCACTCCAAATGATCAAAAGCCT 720

Db 661 TGGCTGCTCATGAATTTGGTTCATGCACTGGGGCTCTCTCACTCCAAATGATCAAAACAGCCT 720
 Qy 721 TGATGTTCCCAAAATATGTCCTCCCTGGATCCAGAAAATACCCACTTCTCTCAGATGATA 780
 Db 721 TGATGTTCCCAAAATATGTCCTCCCTGGATCCAGAAAATACCCACTTCTCTCAGATGATA 780
 Qy 781 TCAATGGAATCCAGTCCATCTATGGAGTCTGCGCTTAAGTACCTGCTAAGCCAAAGGAAC 840
 Db 781 TCAATGGAATCCAGTCCATCTATGGAGTCTGCGCTTAAGTACCTGCTAAGCCAAAGGAAC 840
 Qy 841 CCACATATACCCCATGCGCTGACCCCTGACTTTTGAAGCTATCAAACTTTCGCGA 900
 Db 841 CCACATATACCCCATGCGCTGACCCCTGACTTTTGAAGCTATCAAACTTTCGCGA 900
 Qy 901 GAGAAGTAATGTTCTTTAAAGCGAGGACCTATGAGGAGTCTATATGATATCAAGGATG 960
 Db 901 GAGAAGTAATGTTCTTTAAAGCGAGGACCTATGAGGAGTCTATATGATATCAAGGATG 960
 Qy 961 TTGAGTTTGAATTAATGCTTTCATCTGCGCATCTCTGCCAGCTGATCGCAAGCTGCAT 1020
 Db 961 TTGAGTTTGAATTAATGCTTTCATCTGCGCATCTCTGCCAGCTGATCGCAAGCTGCAT 1020
 Qy 1021 ACAGAAACCCAGAGATAAGATTCTGTGTTTTTAAAGATGAAAACCTTCTGGATGATCAGAG 1080
 Db 1021 ACAGAAACCCAGAGATAAGATTCTGTGTTTTTAAAGATGAAAACCTTCTGGATGATCAGAG 1080
 Qy 1081 GATATGCTGCTTGGCAGATATCCCAATCCATCCATACATTAGTGTTCAGGACGCTG 1140
 Db 1081 GATATGCTGCTTGGCAGATATCCCAATCCATCCATACATTAGTGTTCAGGACGCTG 1140
 Qy 1141 TGAAGAAAATAGATGACCGCTGTGTGTAAGACACAAAGAAAACCTTCTTTTGTGG 1200
 Db 1141 TGAAGAAAATAGATGACCGCTGTGTGTAAGACACAAAGAAAACCTTCTTTTGTGG 1200
 Qy 1201 GCATTTGGTGTGGAGSTTTGATGAATGACCCAAACCATGACAAAGGATTCGCGCAGA 1260
 Db 1201 GCATTTGGTGTGGAGSTTTGATGAATGACCCAAACCATGACAAAGGATTCGCGCAGA 1260
 Qy 1261 GAGTGGTAAACACTTCTCTGGAATCAGTATCCGTTGTGATGCTGCTTCCAGTACAAG 1320
 Db 1261 GAGTGGTAAACACTTCTCTGGAATCAGTATCCGTTGTGATGCTGCTTCCAGTACAAG 1320
 Qy 1321 GATCTCTCTTTTTCAGCGCTGATCAAAAGCAATTTGAATCAACATTAAGACAAAGAATA 1380
 Db 1321 GATCTCTCTTTTTCAGCGCTGATCAAAAGCAATTTGAATCAACATTAAGACAAAGAATA 1380
 Qy 1381 TTACCCGAATCATGAGAACTAATCTTGTTTCAATGCAAAAGAACCAAGAACTCTCAT 1440
 Db 1381 TTACCCGAATCATGAGAACTAATCTTGTTTCAATGCAAAAGAACCAAGAACTCTCAT 1440
 Qy 1441 TTGGTTTGTATCAACAGGAAAGCACATTCAGGAGGATTAAGATATTTGTATCATATA 1500
 Db 1441 TTGGTTTGTATCAACAGGAAAGCACATTCAGGAGGATTAAGATATTTGTATCATATA 1500
 Qy 1501 AGAGTTTAAAGCTGTTTATTTTGTATGTTGTTTCAATTTGCTGAAAAACCTCTATTATC 1560
 Db 1501 AGAGTTTAAAGCTGTTTATTTTGTATGTTGTTTCAATTTGCTGAAAAACCTCTATTATC 1560
 Qy 1561 AATAAATTCATAGACCTAAAAATAAACCTCAACAGCTCTTTTAATAATAAATTCGCTTCAA 1620
 Db 1561 AATAAATTCATAGACCTAAAAATAAACCTCAACAGCTCTTTTAATAATAAATTCGCTTCAA 1620
 Qy 1621 AATAGAA 1627
 Db 1621 AATAGAA 1627

RESULT 13

ADB27740

ID ADB27740 standard; cDNA; 1647 BP.

XX

AC

ADB27740;

XX

DT 20-NOV-2003 (first entry)
 XX cDNA encoding human PRO polypeptide #96.
 DE Human; gene; ss; PRO; secreted polypeptide; transmembrane polypeptide;
 XX tumour necrosis factor-alpha; TNF-alpha; chondrocyte cell; tumour;
 KW cancer; adrenal; lung; colon; breast; prostate; rectum; kidney; cervix;
 KW liver; microvascular endothelial cell; glucose; PFA;
 KW skeletal muscle cell; adipocyte cell; pericyte cell;
 KW inner ear utricular supporting cell; T-lymphocyte cell;
 KW endothelial cell tube formation; bone disorder; cartilage disorder;
 KW sports injury; proteoglycan; articular cartilage defect; osteoarthritis;
 KW rheumatoid arthritis; haemoglobin-associated disorder thalassaemia;
 KW immune system cell infiltration.
 XX Homo sapiens.
 OS US2003082704-A1.
 XX 01-MAY-2003.
 PN 24-APR-2002; 2002US-00131819.
 PD 09-DEC-1999; 99US-0170262P.
 PF 01-DEC-2000; 2000WO-US032678.
 PR 19-DEC-2001; 2001US-00028072.
 XX (GETH) GENENTECH INC.
 PA Baker KP, Beresini M, Deforge L, Desnoyers L, Filvaroff E, Gao W;
 PI Gerritsen ME, Goddard A, Godowski PJ, Gurney AL, Sherwood S;
 PI Smith V, Stewart TA, Tumas D, Watanabe CK, Wood WI, Zhang Z;
 XX WPI; 2003-765415/72.
 DR P-PSDB; ADB27741.
 XX New PRO nucleic acid, useful for preparing a composition for treating
 PT e.g., tumor or for tissue typing.
 PT Claim 2; Fig 191; 637pp; English.
 PS The invention relates to isolated human PRO polypeptides (secreted and
 CC transmembrane polypeptides) and the polynucleotides encoding them. The
 CC invention also relates to an antibody which specifically binds to a PRO
 CC polypeptide, a method for stimulating the release of tumour necrosis
 CC factor-alpha (TNF-alpha) from human blood, a method for stimulating the
 CC proliferation or differentiation of chondrocyte cells and a method for
 CC detecting the presence of a tumour in a mammal (e.g. adrenal, lung,
 CC colon, breast, prostate, rectal, kidney, cervical and liver tumours). The
 CC polynucleotides are useful in molecular biology, including uses as
 CC hybridisation probes, in chromosome and gene mapping, in generating
 CC antisense RNA and DNA and in gene therapy. The polynucleotides may also
 CC be used in preparing PRO polypeptides by recombinant techniques and in
 CC generating either transgenic animals or knock-out animals which are
 CC useful in the development and screening of therapeutically useful
 CC reagents. The PRO polypeptides or antibodies are used in preparing a
 CC medicament for treating a condition responsive to the polypeptides or
 CC antibodies, such as tumours, for stimulating and inhibiting proliferation
 CC of human microvascular endothelial cells, for modulating the uptake of
 CC glucose or FFA by skeletal muscle cells or adipocyte cells, for
 CC stimulating differentiation of adipocyte cells, for stimulating
 CC proliferation of or gene expression in pericyte cells, for stimulating
 CC the proliferation of inner ear utricular supporting cells or T-lymphocyte
 CC cells, for inducing endothelial cell tube formation and for treating
 CC various bone and/or cartilage disorders such as sports injuries and
 CC arthritis. PRO polypeptides which stimulate the release of proteoglycans
 CC from cartilage are useful for treating sports-related joint problems,
 CC articular cartilage defects, osteoarthritis and rheumatoid arthritis. PRO
 CC polypeptides are also useful for treating various mammalian haemoglobin-
 CC associated disorders such as various thalassaemias and conditions which
 CC may benefit from enhanced local immune system cell infiltration. This
 CC sequence encodes a human PRO polypeptide of the invention. Note: The
 CC sequence data for this patent is also available in electronic format from


```

PF 16-MAY-2002; 2002US-00147508.
XX
PR 02-JUL-1998; 98US-0091519P.
PR 02-JUN-1999; 99WO-US012252.
PR 07-JUL-1999; 99US-0143048P.
PR 25-AUG-1999; 99US-00380137.
PR 30-MAR-2000; 2000WO-US008439.
PR 01-DEC-2000; 2000WO-US032678.
PR 19-DEC-2001; 2001US-00028072.
XX
PA (GETH ) GENENTECH INC.
XX
XX Baker KP, Beresini M, Deforge L, Desnoyers L, Fillvaroff E, Gao W,
PI Gerritsen ME, Goddard A, Godowski PJ, Gurney AL, Sherwood S;
PI Smith V, Stewart TA, Tumas D, Watanabe CK, Wood WI, Zhang Z;
XX WPI; 2003-786914/74.
DR P-PSDB; ADA86220.
XX
XX New PRO nucleic acid, useful for preparing a composition for treating
PT e.g., tumor or for tissue typing.
XX
PS Claim 2; Fig 191; 637pp; English.
XX
CC The invention describes 305 nucleic acids encoding PRO (secreted and
CC transmembrane) polypeptides (I). (I) is useful for stimulating the
CC release of TNF-alpha from human blood, for modulating the uptake of
CC glucose or FFA by skeletal muscle cells or adipocyte cells, for
CC stimulating the proliferation or differentiation of chondrocyte cells,
CC for stimulating the proliferation of or gene expression in pericyte
CC cells, for stimulating the release of proteoglycans from cartilage, for
CC stimulating the proliferation of inner ear utricular supporting cells,
CC for stimulating the proliferation of T-lymphocyte cells, for stimulating
CC the release of a cytokine from PBM cells, for inhibiting the binding of
CC A-peptide to factor VIIA, for inhibiting the differentiation of adipocyte
CC cells, for stimulating proliferation of endothelial cells, for detecting
CC the presence of tumour in a mammal. The tumour is lung, colon, breast,
CC prostate, rectal, cervical or liver tumour. The oligonucleotide probes
CC are useful for isolating genomic and cDNA nucleotide sequences or
CC antisense probes. (I) is also useful as therapeutic agent. PRO is useful
CC in assays to identify other proteins or molecules involved in binding
CC interaction. A polynucleotide (II) encoding (I) is useful in chromosome
CC and gene mapping, in generation of antisense RNA and DNA, in the
CC preparation of PRO polypeptide, for generating transgenic animals or
CC knockout animals which in turn are useful in the development and
CC screening of therapeutically useful reagents, in gene therapy, for
CC chromosome identification, as chromosome marker, and for generating
CC probes. An anti-(I)-antibody is useful in diagnostic assays for PRO, e.g.
CC detecting its expression in specific cells, tissues or serum, and for
CC affinity purification of PRO from recombinant cell culture or natural
CC sources. (I) and (II) are useful for tissue typing. This sequence encodes
CC a novel human secreted and transmembrane PRO polypeptide.
XX
SQ Sequence 1647 BP; 492 A; 341 C; 347 G; 467 T; 0 U; 0 Other;
Query Match
Best Local Similarity 99.9%; Score 1625.4; DB 9; Length 1647;
Matches 1626; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1 GCTTCAGCTGAAGAAGAGAGAGGAATGAAGCGCTTCCTGCTTCCTGTTTGGTTCTTTATAA 60
DB 1 GCTTCAGCTGAAGAAGAGAGAGGATGAAGCGCTTCCTGCTTCCTGTTTGGTTCTTTATAA 60
QY 61 CATTTTCTTCGATTTCCCTTAGTCGGATGACGGAAATGAAGAAATATGCAACTGG 120
DB 61 CATTTTCTTCGATTTCCCTTAGTCGGATGACGGAAATGAAGAAATATGCAACTGG 120
QY 121 CTCAGGCATATCTCAACAGTTCTACTCTCTGAAATAGAGGGATCATCTGTTCAA 180
DB 121 CTCAGGCATATCTCAACAGTTCTACTCTCTGAAATAGAGGGATCATCTGTTCAA 180
QY 181 GCAAGAATAGGAGTCTCATAGATGACAAAATTCGGGAAATGCAAGCAATTTTGGATTGA 240

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Db 421 AAGGTTTGAAGTGTGGAGCAAAAGTCACTCCACTAAATTCACCAAGATTTCCAAAGGGGA 480
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Db 481 TTGCAGACATCATGATTGCTTTAGACATCGAGTCGATCGGTGCTCGCTATTTTG 540
Qy 541 ATGGTCCCTTTGGAGTGTGTCCTTCCCTCGGTCCGGTCTGGGTGGTGACA 600
Db 541 ATGGTCCCTTTGGAGTGTGTCCTTCCCTCGGTCCGGTCTGGGTGGTGACA 600
Qy 601 CTCATTTTCATGAGGATGAAAACCTGCAACCAAGATGGACAGGATTCAACTTTGTTTG 660
Db 601 CTCATTTTCATGAGGATGAAAACCTGCAACCAAGATGGACAGGATTCAACTTTGTTTG 660
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Db 721 TGATGTTCCCAATATATGTCTCCTCGATCCCAAGAAATACCCACTTTCTCAGGATGATA 780
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Db 841 CCACATATACCCATGCTGACCTGACCTGACTTTTGACGCTATCAAACTTTCCGCA 900
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Db 1021 ACGAGAACCCAGAGATAGATTCTGGTTTTTAAAGATGAAAACCTCTGATGATCAGAG 1080
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Qy 1261 GAGTGTAAAAACACTTCTCGGAATCAGTATCCGTGTTGATGCTGTTTCCAGTACAAAG 1320
Db 1261 GAGTGTAAAAACACTTCTCGGAATCAGTATCCGTGTTGATGCTGTTTCCAGTACAAAG 1320
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Db 1321 GATTCCTTTTTCAGCCCTGGATCAAGCAATTTGAAATACAACTTAAGACAAAGAATA 1380
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Db 1381 TTACCCGAATCATGAACTATACCTTGGTTTCAATGCAAGAACCAAGAACTCCTCAT 1440
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Db 1441 TTGGTTTTGATATCAACAGGAAAAAGACATTCAGAGGCATTAAGATATTGTATCATA 1500
Qy 1501 AGAGTTTAAGCTGTTTTTTTGGTATTGTTCAATTTGCTGAAAAACACTTCTATTATC 1560
Db 1501 AGAGTTTAAGCTGTTTTTTTGGTATTGTTCAATTTGCTGAAAAACACTTCTATTATC 1560

Qy 1561 AATAAATTCATAGACCTAAATATACCTCAACAGGCTCTTTTAATATATATTTCTGCTTCAA 1620
Db 1561 AATAAATTCATAGACCTAAATATACCTCAACAGGCTCTTTTAATATATATTTCTGCTTCAA 1620
Qy 1621 AATAGAA 1627
Db 1621 AATAGAA 1627

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Job time : 841 secs

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OM nucleic - nucleic search, using sw model

Run on: November 15, 2004, 13:11:05 ; Search time 155 Seconds
(without alignments)
7460.990 Million cell updates/sec

Title: US-10-729-807-28

Perfect score: 1627

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Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 824507 seqs, 355394441 residues

Total number of hits satisfying chosen parameters: 1649014

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Issued Patents NA:*

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5: /cgn2.6/prodata/1/ina/PCUS COMB.seq:*

6: /cgn2.6/prodata/1/ina/backfiles1.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1627	100.0	1845	US-09-862-631-1	Sequence 1, Appli
2	1625.4	99.9	1847	US-10-140-002-191	Sequence 191, Appl
3	1417.8	87.1	1687	US-09-280-116-78	Sequence 78, Appl
4	447.6	27.5	1970	US-09-023-655-1264	Sequence 1264, Ap
5	447.6	27.5	1981	US-09-484-970B-62	Sequence 62, Appl
6	445.6	27.4	1801	US-09-023-655-1374	Sequence 1374, Ap
7	442.6	27.2	1434	US-09-023-655-1174	Sequence 1174, Ap
8	435.6	26.8	2223	US-09-178-002-3	Sequence 3, Appli
9	435.6	26.8	2223	US-09-023-655-1040	Sequence 1040, Ap
10	425.4	26.1	2314	US-09-178-002-1	Sequence 1, Appli
11	423	26.0	474	US-09-280-116-77	Sequence 77, Appl
12	389.4	23.9	1410	US-08-068-392-1	Sequence 1, Appli
13	389.4	23.9	1410	US-08-396-988-1	Sequence 1, Appli
14	379.2	23.3	1717	US-08-229-515A-12	Sequence 12, Appl
15	379.2	23.3	1717	US-08-645-865-12	Sequence 12, Appl
16	373.2	22.9	1521	US-08-994-689C-18	Sequence 18, Appl
17	373.2	22.9	2792	US-08-994-689C-8	Sequence 8, Appli
18	360.8	22.2	1160	US-07-780-973-15	Sequence 15, Appl
19	184	11.3	837	US-08-371-082-1	Sequence 1, Appli
20	184	11.3	1078	US-09-492-543-28	Sequence 28, Appl
21	184	11.3	1078	US-09-492-543-29	Sequence 29, Appl
22	184	11.3	1078	US-09-023-655-1368	Sequence 1368, Ap
23	141.8	8.7	989	US-09-862-631-2	Sequence 2, Appli
24	141.8	8.7	999	US-09-862-631-7	Sequence 7, Appli
25	141.8	8.7	1035	US-09-009-156-4	Sequence 4, Appli
26	141.8	8.7	1035	US-09-372-154-4	Sequence 4, Appli
27	140.8	8.7	1010	US-09-009-156-20	Sequence 20, Appl

28 140.8 8.7 1010 3 US-09-372-154-20 Sequence 20, Appli

29 140.2 8.6 825 3 US-08-896-062-1 Sequence 1, Appli

30 131 8.1 2123 4 US-09-194-468A-29 Sequence 29, Appli

31 122.2 7.5 536 1 US-08-303-270-3 Sequence 3, Appli

32 101.6 6.2 1923 3 US-09-294-841-1 Sequence 1, Appli

33 91 5.6 2116 3 US-09-000-041A-1 Sequence 1, Appli

34 91 5.6 2116 4 US-09-734-002-1 Sequence 1, Appli

35 86.8 5.3 2247 4 US-09-023-655-1410 Sequence 1410, Ap

36 86.8 5.3 2256 1 US-07-794-393-1 Sequence 1, Appli

37 86.8 5.1 2256 1 US-08-001-711-1 Sequence 1, Appli

38 83.6 5.1 2260 1 US-07-794-393-3 Sequence 3, Appli

39 83.6 5.1 2260 1 US-08-001-711-3 Sequence 3, Appli

40 80.8 5.0 2177 4 US-09-919-039-124 Sequence 124, App

41 80.4 4.9 3530 3 US-08-704-711A-10 Sequence 10, Appl

42 80.4 4.9 3530 3 US-09-521-220-10 Sequence 10, Appl

43 79.2 4.9 2109 4 US-09-799-451-345 Sequence 345, App

44 79.2 4.9 2333 1 US-08-392-678-33 Sequence 33, Appli

45 79.2 4.9 2334 1 US-08-457-304A-33 Sequence 33, Appli

ALIGNMENTS

RESULT 1

US-09-862-631-1

; Sequence 1, Application US/09862631

; Patent No: 6734005

; GENERAL INFORMATION:

; APPLICANT: Holmgren, Erik

; APPLICANT: Kihlen, Mats

; APPLICANT: Wood, Tim

; APPLICANT: Ekblom, Jonas

; TITLE OF INVENTION: No. 6734005el Matrix Metalloproteinases

; FILE REFERENCE: 00014regus

; CURRENT APPLICATION NUMBER: US/09/862,631

; CURRENT FILING DATE: 2000-05-22

; PRIOR APPLICATION NUMBER: 206119

; PRIOR FILING DATE: 2000-05-22

; NUMBER OF SEQ ID NOS: 8

; SOFTWARE: Patent in version 3.0

; SEQ ID NO 1

; LENGTH: 1845

; TYPE: DNA

; ORGANISM: Homo sapiens

US-09-862-631-1

Query Match 100.0%; Score 1627; DB 4; Length 1845;

Best Local Similarity 100.0%; Pred. No. 0;

Matches 1627; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GCTTCAGCTGAAGAAGAGAGAGGAATGAAGCGCTTCTGCTCTGTTGTTTCTTTATAA 60

DB 1 GCTTCAGCTGAAGAAGAGAGAGGAATGAAGCGCTTCTGCTCTGTTGTTTCTTTATAA 60

QY 61 CATTTTCTTCTGCAATTCCTTAGTCCGGATGACGGAATAAGAAAATATGCAACTGG 120

DB 61 CATTTTCTTCTGCAATTCCTTAGTCCGGATGACGGAATAAGAAAATATGCAACTGG 120

QY 121 CTCAGGCATATCTCAACCAAGTTCTACTCTCTTGAATAGAGGGGAATCATCTTGTTCAAA 180

DB 121 CTCAGGCATATCTCAACCAAGTTCTACTCTTGAATAGAGGGGAATCATCTTGTTCAAA 180

QY 181 GCAGAAATAGAGTCTCATAGATGACAAAATTCGGGAATGCAAGCAATTTTGGATTGA 240

DB 181 GCAGAAATAGAGTCTCATAGATGACAAAATTCGGGAATGCAAGCAATTTTGGATTGA 240

QY 241 CAGTGACTGGAAGAACTGCACTCAACACCTTGAGATCATGAAGACCCAGGTGTGGG 300

DB 241 CAGTGACTGGAAGAACTGCACTCAACACCTTGAGATCATGAAGACCCAGGTGTGGG 300

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QY	361	ACAGAAATAAATACTACTCCGAGATATGCAAGAGCTGCTGTGGATGAGGCTATCCAAG	420
Db	361	ACAGAAATAAATACTACTCCGAGATATGCAAGAGCTGCTGTGGATGAGGCTATCCAAG	420
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Db	421	AAGGTTTAGAAGTGTGGAGCAAAAGTCACTCCACTTAAATTCACCAAGATTTCAAGAGGGA	480
QY	481	TTGCAGACATCATGATTCCTTTTAGGACTCGAGTCCATGGTCCGTCCTCGCTATTTTG	540
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QY	601	CTCAATTTTATGAGGATGAATACTGGACCAAGGATGAGCAGGATTCAACTTGTTCCTG	660
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Db	661	TGGCTGCTCATGAATTTGGTCATGCACTGGGGCTCTCTCACTCCAATGATCAAAACAGCCT	720
QY	721	TGATGTTCCCAAAATATGTCCTCCCTGGATCCAGAAAATACCCACTTCTCAGGATGATA	780
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Db	781	TCATGGAATCCAGTCCATCATGAGGTCTGCTTAAGGTACCTGCTTAAGCAAGGAAC	840
QY	841	CCACTATACCCCATGCTGTGACCTGACCTTGTGACCTTATGACCTATCAAACTTTCGCGA	900
Db	841	CCACTATACCCCATGCTGTGACCTGACCTTGTGACCTTATGACCTATCAAACTTTCGCGA	900
QY	901	GAGAAGTAATGCTTTTAAAGGAGGACCTATGAGGATCTATATGATATCAAGGATG	960
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QY	961	TTGAGTTTGAATTAATGCTTCTGCGCATCTGCGAGCTGATCGAAGCTGAT	1020
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Db	1081	GATATGCTGCTTGGCAGATTTCCCAATCCATCCATACATAGGTTTCCAGGACCTG	1140
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Db	1321	GATTTCTTTTTCAGCGTGGATCAAGCAATTTGAATACAACTTAAGACAAAGAATA	1380
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RESULT 2

US-10-140-002-191

; Sequence 191, Application US/10140002

; Patent No. 6725730

; GENERAL INFORMATION:

; APPLICANT: Baker, Kevin P.

; APPLICANT: Beresini, Maureen

; APPLICANT: DeForge, Laura

; APPLICANT: Desnoyers, Luc

; APPLICANT: Filvaroff, Ellen

; APPLICANT: Gao, Wei-Qiang

; APPLICANT: Gerritsen, Mary B.

; APPLICANT: Goddard, Audrey

; APPLICANT: Godowski, Paul J.

; APPLICANT: Gurney, Austin L.

; APPLICANT: Sherwood, Steven

; APPLICANT: Smith, Victoria

; APPLICANT: Stewart, Timothy A.

; APPLICANT: Tamas, Daniel

; APPLICANT: Watanabe, Colin K

; APPLICANT: Wood, William

; APPLICANT: Zhang, Zemin

; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC

; FILE OF INVENTION: ACIDS ENCODING THE SAME

; FILE REFERENCE: P3330R1C59

; CURRENT APPLICATION NUMBER: US/10/140,002

; CURRENT FILING DATE: 2002-05-06

; Prior Application removed - See Palm or File Wrapper

; NUMBER OF SEQ ID NOS: 550

; SEQ ID NO 191

; LENGTH: 1647

; TYPE: DNA

; ORGANISM: Homo Sapien

US-10-140-002-191

Query Match 99.9%; Score 1625.4; DB 4; Length 1647;

Best Local Similarity 99.9%; Pred. No. 0;

Matches 1626; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY	1	GCTTCAGCTGAGAAAGAGAGGAATGAAGCGCTTCTGCTTCTGTTGTTGTTCTTTATAA	60
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Db	181	GCAAGAAATAGAGTCTCTCATAGATGACAAAAATTCGGGAAATGCAAGCAATTTTGGATTGA	240
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QY 541 |||||ATGCTCCCTTGGAGTGTGGCCATGCTTCTCTCTGCTCGGCTCTGGGTGTGACA 600
Db 541 |||||ATGCTCCCTTGGAGTGTGGCCATGCTTCTCTCTGCTCGGCTCTGGGTGTGACA 600
QY 601 |||||CTCATTTTGAAGGATGAATACTGCAACCAAGGATGAGCAGGATTCACCTTGTTCCTG 660
Db 601 |||||CTCATTTTGAAGGATGAATACTGCAACCAAGGATGAGCAGGATTCACCTTGTTCCTG 660
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QY 721 |||||TGATGTTCCCAATATATGCTCCCTGGATCCAGAAATACCCACTTTCTCAGGATGATA 780
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QY 781 |||||TCAATGGAAATCAGTCCATCTATGAGGCTGCTCCCTAAAGTACCTGCTAAGCCAAAGGAAC 840
Db 781 |||||TCAATGGAAATCAGTCCATCTATGAGGCTGCTCCCTAAAGTACCTGCTAAGCCAAAGGAAC 840
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Db 841 |||||CCACTATACCCCATGCTGTGACCTGACTTTGACGCTATCACTTTTCCGCA 900
QY 901 |||||GAGAGTAAATGTTCTTAAAGCAGCAGCTATGAGGATCTATTATGATATCAAGGATG 960
Db 901 |||||GAGAGTAAATGTTCTTAAAGCAGCAGCTATGAGGATCTATTATGATATCAAGGATG 960
QY 961 |||||TTGAGTTTGAATTAATTTGCTTCATTTGCGCATCTCTGCGCATCTCTGCGCATCTGCAAT 1020
Db 961 |||||TTGAGTTTGAATTAATTTGCTTCATTTGCGCATCTCTGCGCATCTCTGCGCATCTGCAAT 1020
QY 1021 |||||ACGAGAACCCAGAGATTAAGTCTGTTTAAAGATGAATAAATCTCTGGATGATCAGAG 1080
Db 1021 |||||ACGAGAACCCAGAGATTAAGTCTGTTTAAAGATGAATAAATCTCTGGATGATCAGAG 1080
QY 1081 |||||GATATGCTGTCTGCGCAGATTAATCCAAATCCATCATATTTAGTCTTTCAGGACGCTG 1140
Db 1081 |||||GATATGCTGTCTGCGCAGATTAATCCAAATCCATCATATTTAGTCTTTCAGGACGCTG 1140
QY 1141 |||||TGAAGAAATAGATGACGCGCTGTGTGATPAGACCAACCAAGAAATCTACTTTTGTGG 1200
Db 1141 |||||TGAAGAAATAGATGACGCGCTGTGTGATPAGACCAACCAAGAAATCTACTTTTGTGG 1200
QY 1201 |||||GCATTTGCTGCTGGAGTTTGAATGAATGACCCCAACCAATGACAAAGATTTCCCGCAGA 1260
Db 1201 |||||GCATTTGCTGCTGGAGTTTGAATGAATGACCCCAACCAATGACAAAGATTTCCCGCAGA 1260
QY 1261 |||||GAGTGTAAACACTTTTCTCGAATCAGTATCCGCTGCTGATCTGCTTCCAGTACAAG 1320
Db 1261 |||||GAGTGTAAACACTTTTCTCGAATCAGTATCCGCTGCTGATCTGCTTCCAGTACAAG 1320
QY 1321 |||||GATTTCTTTTTCAGCGCTGGATCAAGCAATTTGAATACAACATTAAGACAAAGAATA 1380
|||||
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Db 1321 |||||GATTTCTTTTTCAGCGCTGGATCAAGCAATTTGAATACAACATTAAGACAAAGAATA 1380
QY 1381 |||||TTACCCGAATCATGAGAACTAATACTTGTGTTTCAATGCAAGAAACCAAGAACTCTCAT 1440
Db 1381 |||||TTACCCGAATCATGAGAACTAATACTTGTGTTTCAATGCAAGAAACCAAGAACTCTCAT 1440
QY 1441 |||||TTGGTTTTGATATCAACAGGAAAGACACATTCAGAGGCAATAAGATATTTGATCATTA 1500
Db 1441 |||||TTGGTTTTGATATCAACAGGAAAGACACATTCAGAGGCAATAAGATATTTGATCATTA 1500
QY 1501 |||||AGAGTTTAAAGCTTGTTTTATTTTGTGTTTGTTCATTTGCTGAAAAACACTTTTATTC 1560
Db 1501 |||||AGAGTTTAAAGCTTGTTTTATTTTGTGTTTGTTCATTTGCTGAAAAACACTTTTATTC 1560
QY 1561 |||||ATAAATTCATGAGACCTTAAATTAACCTCAACAGGCTCTTTTATATAAATTTCTGCTTCAA 1620
Db 1561 |||||ATAAATTCATGAGACCTTAAATTAACCTCAACAGGCTCTTTTATATAAATTTCTGCTTCAA 1620
QY 1621 |||||AATAGAA 1627
Db 1621 |||||AATAGAA 1627

RESULT 3
US-09-280-116-78/c
; Sequence 78, Application US/09280116A
; Patent No. 6331427
; GENERAL INFORMATION:
; APPLICANT: Robison, Keith E.
; TITLE OF INVENTION: Nucleic Acid Molecules Encoding Human Protease Homologs
; FILE REFERENCE: 5800-24, 035800/176965
; CURRENT APPLICATION NUMBER: US/09/280,116A
; CURRENT FILING DATE: 1999-03-26
; NUMBER OF SEQ ID NOS: 268
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 78
; LENGTH: 1687
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: matrix metalloproteases
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (1) - (1687)
; OTHER INFORMATION: n = a, t, c or g
US-09-280-116-78

Query Match 87.1%; Score 1417.8; DB 3; Length 1687;
Best Local Similarity 99.8%; Pred. No. 0;
Matches 1430; Conservative 0; Mismatches 2; Indels 1; Gaps 1;

QY 136 TCATGATGACAAAATTCGGGAAATGCAAGCAATTTTGGATTGACAGTGTGAAAAAC 255
Db 1680 TCCGAGATGACAAAATTCGGGAAATGCAAGCAATTTTGGATTGACAGTGTGAAAAAC 1621
QY 256 TGGACTCAAAACACCTTCAGATCATGAGACACCCAGGTGTGGGTGCTGATGTGGGCC 315
Db 1620 TGGACTCAAAACACCTTCAGATCATGAGACACCCAGGTGTGGGTGCTGATGTGGGCC 1561
QY 316 AGTATGGCTACACCTTCCTGGGTGGAGAAAATCAACCTCACCTACAGAAATAATAACT 375
Db 1560 AGTATGGCTACACCTTCCTGGGTGGAGAAAATCAACCTCACCTACAGAAATAATAACT 1501
QY 376 ATACTCCGATATGACAGCTGCTGTGGATGAGGCTATCCAAGAGGTTTGAAGTGT 435
Db 1500 ATACTCCGATATGACAGCTGCTGTGGATGAGGCTATCCAAGAGGTTTGAAGTGT 1441
QY 436 GGAGCAAAAGTCACTCCACTTAAATTCACCAAGATTTCAAAGGGATTCAGACATCATGA 495
Db 1440 GGAGCAAAAGTCACTCCACTTAAATTCACCAAGATTTCAAAGGGATTCAGACATCATGA 1381
QY 496 TTGCTTTTGAAGTCACTGAGTCCATGCTGCTGCTGCTATTTTTCATGCTCCCTTGGGAG 555
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Db 1380 TTGCTTTAGGACTCGAGTCCATGGTGGTGTCTCGCTATTTTGTGGTCCCTTGGGAG 1321
QY 556 TGCTTGCCCATGCTTTCTCTCGTCCGGTCTGGGTGTGACACTCATTTTGTGATGAGG 615
Db 1320 TGCTTGCCCATGCTTTCTCTCGTCCGGTCTGGGTGTGACACTCATTTTGTGATGAGG 1261
QY 616 ATGAATACTGGACCAAGGATGGAGCAGGATCAACTTGTTCCTGTGGCTGCTCATGAAT 675
Db 1260 ATGAATACTGGACCAAGGATGGAGCAGGATCAACTTGTTCCTGTGGCTGCTCATGAAT 1201
QY 676 TTGCTCATGACCTGGGCTCTCTCACTCCCAATGATCAAAACAGCCTTCATGTTCCCAAT 735
Db 1200 TTGCTCATGACCTGGGCTCTCTCACTCCCAATGATCAAAACAGCCTTCATGTTCCCAAT 1141
QY 736 ATGCTCTCCCTGGATCCAGAAAATACCCACTTTCTCAGGATGATCAATGGAATCCAGT 795
Db 1140 ATGCTCTCCCTGGATCCAGAAAATACCCACTTTCTCAGGATGATCAATGGAATCCAGT 1081
QY 796 CCATCTATGGAGGTCTGCTTAAGTACCTGCTAAGCCAAAGGACCCACTATACCCCATG 855
Db 1080 CCATCTATGGAGGTCTGCTTAAGTACCTGCTAAGCCAAAGGACCCACTATACCCCATG 1021
QY 856 CTTGTGACCTGACTTCACTTTTCACTATCAAACTTTCCGAGAGAGTAAATGTTCT 915
Db 1020 CTTGTGACCTGACTTCACTTTTCACTATCAAACTTTCCGAGAGAGTAAATGTTCT 961
QY 916 TTAAGGACGACCTATGAGGAGTATATATGATATCAAGGATGTTGAGTTGAATTA 975
Db 960 TTAAGGACGACCTATGAGGAGTATATATGATATCAAGGATGTTGAGTTGAATTA 901
QY 976 TTGCTTCATTTGCGCATCTGCGCATCTGCGCATCTGCGCATCTGCGCATCTGCGCAT 1035
Db 900 TTGCTTCATTTGCGCATCTGCGCATCTGCGCATCTGCGCATCTGCGCATCTGCGCAT 841
QY 1036 ATAGATTTCTGTTTAAAGATGAAATCTCTGATGATCAGAGGATATGCTCTCTTC 1095
Db 840 ATAGATTTCTGTTTAAAGATGAAATCTCTGATGATCAGAGGATATGCTCTCTTC 781
QY 1096 CAGATTAATCCAAATCCATCATATAGTATTTTCCAGGA-CGTGTGAAGAAATAGAT 1154
Db 780 CAGATTAATCCAAATCCATCATATAGTATTTTCCAGGA-CGTGTGAAGAAATAGAT 721
QY 1155 GCAGCGCTGTGTATAGACACACAAAGAAACCTTCTTTTGGGCATTTGGTGTGG 1214
Db 720 GCAGCGCTGTGTATAGACACACAAAGAAACCTTCTTTTGGGCATTTGGTGTGG 661
QY 1215 AGGTTTGTATGAATGACCCAAACCATGGACAAAGATTTCCCGCAGAGAGTGTAAACAC 1274
Db 660 AGGTTTGTATGAATGACCCAAACCATGGACAAAGATTTCCCGCAGAGAGTGTAAACAC 601
QY 1275 TTTCTGTGAATCAGTATCCGTTGTGATGCTGCTTTCAGTACAAAGATTTCTTTTTC 1334
Db 600 TTTCTGTGAATCAGTATCCGTTGTGATGCTGCTTTCAGTACAAAGATTTCTTTTTC 541
QY 1335 AGCGTGTGATCAAGCAATTTGAATACAACTTAAGACAAAGATTTTACCAGGATCATG 1394
Db 540 AGCGTGTGATCAAGCAATTTGAATACAACTTAAGACAAAGATTTTACCAGGATCATG 481
QY 1395 AGAACTAATCTTGGTTTCAATGCAAGAAACCAAGAACTCCTCATTTGGTTTGTATC 1454
Db 480 AGAACTAATCTTGGTTTCAATGCAAGAAACCAAGAACTCCTCATTTGGTTTGTATC 421
QY 1455 AACAGGAAAAGACATTCAGGAGGATTAAGATTTTGTATCATAGAGTTTAAAGCTTG 1514
Db 420 AACAGGAAAAGACATTCAGGAGGATTAAGATTTTGTATCATAGAGTTTAAAGCTTG 361
QY 1515 TTTATTTTGTATTTGTTTCTTGTGTAAGAAACCTTCTATTTTATCAATAATTCATAGA 1574
Db 360 TTTATTTTGTATTTGTTTCTTGTGTAAGAAACCTTCTATTTTATCAATAATTCATAGA 301
QY 1575 CTTAAATTAACCTCAACAGGCTTTTAAATTAATTAATTCGTTTCAAAATAGAA 1627
Db 300 CTTAAATTAACCTCAACAGGCTTTTAAATTAATTAATTCGTTTCAAAATAGAA 248
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RESULT 4

```
US-09-023-655-1264
; Sequence 1264, Application US/09023655
; Patent No. 6607879
; GENERAL INFORMATION:
; APPLICANT: Cocks, Benjamin G.
; APPLICANT: Susan G. Stuart
; APPLICANT: Jeffrey J. Seilhamer
; TITLE OF INVENTION: COMPOSITION FOR THE DETECTION OF BLOOD CELL GENE
; TITLE OF INVENTION: EXPRESSION
; NUMBER OF SEQUENCES: 1508
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: INCYTE PHARMACEUTICALS, INC.
; STREET: 3174 PORTER DRIVE
; CITY: PALO ALTO
; STATE: CALIFORNIA
; COUNTRY: USA
; ZIP: 94304
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Word Perfect 6.1 for Windows/MS-DOS 6.2
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/023,655
; FILING DATE: HEREWITH
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Zeller, Karen J.
; REGISTRATION NUMBER: 37,071
; REFERENCE/DOCKET NUMBER: PA-0001 US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (650) 855-0555
; TELEFAX: (650) 845-4166
; INFORMATION FOR SEQ ID NO: 1264:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1970 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; IMMEDIATE SOURCE:
; LIBRARY: GENBANK
; CLONE: g30125
US-09-023-655-1264
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Query Match 27.5%; Score 447.6; DB 4; Length 1970;
Best Local Similarity 61.1%; Pred. No. 5.1e-121;
Matches 837; Conservative 0; Mismatches 509; Indels 24; Gaps 6;

QY 98 AAATGAAGAAAATATGCAACTGGCTCAGGCATATCTCAACCCAGTTCTACTCTCTTGAAT 157
Db 146 ACAAGACAGATGTGGACTTAGTCCAGAAATACCTGGAATAATACACCTTGAAGAA 205
QY 158 AGAAGGGAATCATCTTGTCAAAGCAAGATAGGAGTCTCATAGATGACAAAATTCGGGA 217
Db 206 TGATGGGAGGCAAGTTGAAAAGCGGAGAAATAGTGGCCAGTGGTTGAAAATTTGAAGCA 265
QY 218 AATGCAAGCATTTTGGATTGACAGTCACTGGGAAATCTGACCTCAACACCTTTGAGAT 277
Db 266 AATGAGGAATTCCTTGGCTGAAAGTACTGGGAAACCAAGATGCTGAAACCTTGAAGGT 325
QY 278 CATGAAGACACCCAGGTGTGGGTGCTGTAGTGTGGGCCAGTATGGCTACAC-----CCT 331
Db 326 GATGAGCAGCCAGATGTGGAGTGCCTGATGTGCTCAGTTTGTCTCTCACTGAGGGGAA 385
QY 332 CCCTGGGTGGAGAAAATACACCTCACTACAGATAATAACTATATCTCCGATATGGC 391
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386 CCCTCGTGGGAGCAACACATCTGACCTACAGGAATGAAATTTACACGCCAGATTGTC 445
392 ACAGAGCTGCTGTGATGAGCTATCCAGAGGTTTGAAGTGTGAGCAAGTCACTCC 451
446 AAGAGCAGATGTGACCATGCCATTGAGAAAGCCTTCCAACTCTGGAGTAATGTGCACAC 505
452 ACTAAATATCCACCAAGATTTCAAAGGGATTCAGACATCATGATTCCTTTAGGACTCG 511
506 TCTGACATTCACCAAGTCTCTGAGGTCAAGCAGACATCATGATATCTTTGTGACGGG 565
512 AGTCCATGTGCGGTCTCTCGCTATTTTGAAGTTCCTTGGAGTGTCTGGCCATGCCCTT 571
566 AGATCATCGGAGCAACTCTCC---TTTGTAGTACCTGGAGGAAATCTTCTCATGCTTT 622
572 TCCTCTGTGTCGGGTCTGGGTGACATCTATTTGTAGAGTCAAAACTTGGACCAA 631
623 TCAACAGGCCCGAGGATTTGGAGGGATGCTCATTTTGTGAAGATGAAGGTGGACCAA 682
632 GGATGAGCAGGATTCAACTTTGTTTGTGGTGTCTCATGAATTTGGTCAATGCTGGG 691
683 CAATTTTCAAGAGTACAACTTACATCTGTGTGGGTCTAGAACTGGCCATTTCTTTGG 742
692 GCTCTCTCACTCAATGATCAAAACAGCTTGTATGTTCCCAAAATATGTCTCCCTGGATCC 751
743 ACTCTCCCATTTCTACTGATATCGGGGCTTTGATGTACCTTAGCTACACCTTCACTG--- 798
752 CAGAAATACCCATTTCTCAGGATGATATCAATGGAATCCAGTCCATCTATGAGGTCT 811
799 --GTGATGTTACGTAGCTAGCTAGGATGACATTTGATGGCATCCAAAGCATATATGAGCGTTC 856
812 GCTAAGTACCTGTGTAAGCAAGGAACCCACTATACCCCATGCTGTGACCCCTGACATT 871
857 CCAAAA---TCTGTCCGCCATCGGCCACAAACCCCAAGCATGTGACAGTAAGCT 913
872 GACTTTGAGCTATCACAACTTTCGAGAGAGTAATGTTCTTTAAAGGCGAGGACCT 931
914 AACTTTGATGATATAACTACGATTCGGGAGAGTGATGTTCTTTAAAGACAGATTTCTA 973
932 ATGGAGATCTATTATGATATACGAGTGTGAGTTGAAATTTGCTTTCATTTCTGGCC 991
974 CATGGCAAAATCCCTTACCCGAGTGTAGCTCAATTTCTTTCTGTTTCTGGCC 1033
992 ATCTCTGCCAGCTGATCTCAAGCTGCATACGA---GAACCCCGAGAGATAAGTCTGTG 1048
1034 ACACTGCCAATGGCTTGAAGCTGCTTACGAAATTTGCCGACAGAGATGAAGTCGGTT 1093
1049 TTTTAAAGATGAACCTTCTGATGATACAGAGATGCTGTTTCCAGATTTATCCCAA 1108
1094 TTTCAAAGGGAATAAGTACTGGGCTGTTCCAGGACAGAAATGTCTACACGGATACCCCAA 1153
1109 ATCCATCCATA--CATAGGTTTTCAGGACGTGTGAAGAAATAGATGCGCGCTCTG 1165
1154 GGACATCTACAGCTCTTTGGCTTCCCTAGAACTGTGAAGCATATCGATGCTGCTTTTC 1213
1166 TGATAAGCAACAAGAAAAACCTTCTTTTGGGCATTTGGTGTGAGGATTTGATGA 1225
1214 TCAGGAAAAACA CTGGA AAAACCTTCTTTTGTGTAACAATACTGGAGTATGATGA 1273
1226 AATGACCCAAACATGGCAAAAGGATTCGCCAGAGAGTGGTAAACAATTTCCTGGAAT 1285
1274 ATATAACCGATCTATGGATTCAGGTTATCCCAAAATGATAGACATGACTTTCTCTGGAAT 1333
1286 CAGTATCCGTGTGATGCTGCTTCCAGTACAAAGGATTTCTTTTTCAGCGGTGGATC 1345
1334 TGGCCACAAGTTGATGCAAGTTTTCATGAAGATGGAATTTTCTATTTCTTTTCATGGAAAC 1393
1346 AAAGCAATTTGAATACAACTTAAGCAAAAGAAATATTACCCGAATCATGAGAACTAAATAC 1405
1394 AAGACAAATACAAATTTGATCTCTAAACGAAGAAATTTTGAATCTCCGAAAGCTAAATAG 1453
1406 TTGGTTTCAATGGAAGAAACCAAGAACTCTCTCATTTGGTTTTGATATCA 1455
1454 CTGGTTCACTCGAGGAAAAATTTGAACATTAATAATTTGAATGGAAAAACA 1503

RESULT 5

US-09-484-970B-62
; Sequence 62, Application US/09484970B
; Patent No. 6426186
; GENERAL INFORMATION:
; APPLICANT: Jones, Karen A.
; APPLICANT: Volkmueth, Wayne
; APPLICANT: Walker, Michael G.
; TITLE OF INVENTION: BONE REMODELING GENES
; FILE REFERENCE: PB-0014 US
; CURRENT APPLICATION NUMBER: US/09/484,970B
; CURRENT FILING DATE: 2000-01-18
; NUMBER OF SEQ ID NOS: 172
; SOFTWARE: PERL Program
; SEQ ID NO 62
; LENGTH: 1981
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc feature
; OTHER INFORMATION: Incyte ID No. 6426186 245334.1
US-09-484-970B-62

Query Match 27.5%; Score 447.6; DB 4; Length 1981;
Best Local Similarity 61.1%; Pred. No. 5.1e-121;
Matches 837; Conservative 0; Mismatches 509; Indels 24; Gaps 6;

QY 98 AATGAAGAAAAATATGCAACTGGCTCAGCATATCTCAACCCAGTCTTACTCTCTTGAAT 157
DB 157 ACNAGAGCAGATGTGGACTTAGTCCGAAATACCTTGGAAATACTCAACCTGAAGAA 216
QY 158 AGAGGGAATCATCTTTGTTTCAAAGCAAGAAATAGGAGTCTCATAGATGACAAATTCGGGA 217
DB 217 TGATGGGCGCAAGTTGAAAAGCGGAGAAATAGTGGCCAGTGGTTGAAAATTTGAAGCA 276
QY 218 AATGCAAGCATTTTGTGGATTGACAGTGAAGTGGAAATCGGACTCAACACCCCTTGAAT 277
DB 277 AATGCAAGCAATTTTGTGGCTGAAAGTGTGACTGGGAAACAGATGCTGAAACCCCTGAAGT 336
QY 278 CATGAAGACACCCAGTGTGGGTGCTGATGTGGCCAGTATGGCTACAC-----CCT 331
DB 337 GATGAAGACGCCAGATGTGGAGTGCCTGATGTGGCTCAGTTTGTCTCCTCAGTAGGGGAA 396
QY 332 CCCTGGTGGAGAAATAACAACCTCACCTACAGAAATAATAAATACTATCTCCGATATGGC 391
DB 397 CCCTGCTGGGAGCAACACATCTGACCTACAGGATGAAATTAACGCCAGATTTGCC 456
QY 392 AGAGCTGCTGTGATGAGGCTATCCAGAGGTTTAGAAGTGTGGAGCAAAAGTCACTCC 451
DB 457 AAGAGCAGATGTGGACCATGCAATTTGAGAAAGCCCTTCCAACCTCGAGTAATGTCAACC 516
QY 452 ACTAAATTCACCAAGATTTCAAAGGGATTCAGACATCATGATTTGCCCTTTAGGACTCG 511
DB 517 TCTGACATTCACCAAGTCTCTGAGGGTCAACAGACATCATGATATCTTTTGTCAAGGG 576
QY 512 AGTCCATGTGCGTGTCTCGCTATTTTGAAGTTCCTTTGGAGTGTCTGGCCATGCTCTT 571
DB 577 AGATCATCGGACAACTCTCC---TTTGTAGTACCTGGAGGAAATCTTTGCTCATGCTTT 633
QY 572 TCCTCTGTTCGGGTCTGGGTGAGCACTCATTTTGAAGAGTGAAGAACTGACCAAA 631
DB 634 TCAACAGGCCCGAGGATTTGGAGGGGATGCTCAATTTGATGAAGATGAAGGTGGACCAA 693
QY 632 GGATGAGCAGGATTCAACTTTGTTTGTGGTCTCATGAATTTGTCTATGCACTGG 691
DB 694 CAATTTCAAGAGTACAACTTACATCTGTTTGGGCTCATGAATCTGGCCATTTCTCTGG 753
QY 692 GCTCTCTCACTCAATGATCAAAACAGCCTTGAATGTTCCCAAAATATGTTCTCCCTGGATCC 751
DB 754 ACTCTCCCATTTCTACTGATATCGGGGCTTTGATGTACCTTAGCTACACCTTCAGTG---- 809

APPLICATION NUMBER: US/09/023,655
FILING DATE: HEREWITH
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Zeller, Karen J.
REGISTRATION NUMBER: 37,071
REFERENCE/DOCKET NUMBER: PA-0001 US
TELECOMMUNICATION INFORMATION:
TELEPHONE: (650) 855-0555
TELEFAX: (650) 845-4166
INFORMATION FOR SEQ ID NO: 1374:
SEQUENCE CHARACTERISTICS:
LENGTH: 1801 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
IMMEDIATE SOURCE:
LIBRARY: GENBANK
CLONE: g36632
US-09-023-655-1374

Query Match 27.4%; Score 445.6; DB 4; Length 1801;
Best Local Similarity 60.2%; Pred. No. 1.9e-120;
Matches 865; Conservative 0; Mismatches 529; Indels 42; Gaps 6;

752 CAGAAATACCACTTTCTCAGGATGATATCAATGAATCCAGTCCACTATCATGGGTCT 811
Db | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
810 --GTGATGTTTCAGTAGCTCAGGATGATTAATGATGCATCCAAGCCATATATGACGTT 867
Qy | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
812 GCCTAAGGTACTGCTAAGCAAAGAACCCATATACCCTATGCCCTGCGACCTGACTT 871
Db | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
868 CCAAAA--TCTGTCCAGCCATCGGCCCAACAACCCCAAGCGTGACAGTAAGCT 924
Qy | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
872 GACTTTTCAGCTATCACAACTTTCCGACAGAGATGATGTTCTTTAAAGCGAGGACCT 931
Db | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
925 AACCTTTGATGCTATACTAGTTCGGGGAGAAGTGAATGTTCTTTAAAGACAGATCTTA 984
Qy | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
932 ATGGAGGATCTATTATGATATACAGGATGTTGAGTTTGAATTAATTCCTTCATTCGGCC 991
Db | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
985 CATGGCGCAAAATCCCTTCTACCCGGAAGTTGAGTCAATTTCAATTCGTTTTCTGGCC 1044
Qy | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
992 ATCTCTGCCAGCTGATCTGCAAGCTGCATAGA--GAACCCACAGATAGATTCGTT 1048
Db | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
1045 ACAACTGCCAAATGGGCTTGAAGCTGCTTACGAATTTGCCACAGAGATGAAGTCCGGTT 1104
Qy | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
1049 TTTTAAAGATGAAAATCTCTGATGATCAGAGGATATGCTGTCGTGCGAGATTAATCCAA 1108
Db | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
1105 TTTCAGAGGGAATAAGTACTGGGCTGTTTCAGGACAGATGCTACACGATACCCAA 1164
Qy | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
1109 ATCCATCCATA---CATTAGTTTTCCAGGACGTGTGAAGAAAATAGATGACGCGCTG 1165
Db | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
1165 GGACATCTACAGCTCTTTGGCTTCCCTAGAACGTGAAGCATATCGATGCTCTTTC 1224
Qy | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
1166 TGATAGACCAACAAGAAACCTACTCTTTTGGGGCATTTGGTCTGGAGGTTTGAATGA 1225
Db | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
1225 TGAGGAAAAACACTGGAAGAAACCTACTCTTTTGTCTAACAAATACTGGAGGTATGATGA 1284
Qy | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
1226 AATGACCCAAACATGCAAGAGGATCCCGACAGAGTGTGAAGACACTTTTCCTGGAAT 1285
Db | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
1285 ATATAAAGATCTATGATCCAGGTATCCCAAAATGATAGACATGACTTTCTGGAAT 1344
Qy | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
1286 CAGTATCCGTGTGATGCTGCTTTCCAGTACAAAGGATTTCTTTTCAGCCGCTGGATC 1345
Db | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
1345 TGGCCAAAGTTGATGCAAGTTTTCATGAGATGATTTTCTATTTCTTTCATGGAAC 1404
Qy | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
1346 AAAGCAATTTGATACCAACATTAAGACAAAGAAATTAACCGAATCATAGAACTATATAC 1405
Db | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
1405 AAGACAATACAAAATTTGATCTTAAACGAAGAGATTTTGACTCTCCAGAAAGTAATAG 1464
Qy | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
1406 TTGGTTTCATCAAGAACCAAGAACTCCTCATTTGTTTGTATCA 1455
Db | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
1465 CTGGTTCAACTCGAGAAAAATTGAACATTACTAATTTGAATGGAAMACA 1514

RESULT 6
US-09-023-655-1374
Sequence 1374, Application US/09023655
Patent No. 6607879
GENERAL INFORMATION:
APPLICANT: Benjamin G.
APPLICANT: Susan G. Stuart
APPLICANT: Jeffrey J. Seilhamer
TITLE OF INVENTION: COMPOSITION FOR THE DETECTION OF BLOOD CELL GENE
TITLE OF INVENTION: EXPRESSION
NUMBER OF SEQUENCES: 1508
CORRESPONDENCE ADDRESS:
ADDRESSEE: INCYTE PHARMACEUTICALS, INC.
STREET: 3174 PORTER DRIVE
CITY: PALO ALTO
STATE: CALIFORNIA
COUNTRY: USA
ZIP: 94304
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Word Perfect 6.1 for Windows/MS-DOS 6.2
CURRENT APPLICATION DATA:


```

RESULT 8
US-09-178-002-3
; Sequence 3, Application US/09178002
; Patent No. H001973
; GENERAL INFORMATION:
; APPLICANT: Hu, Shou-Ih
; TITLE OF INVENTION: Human Neutrophil Collagenase Splice Variant
; FILE REFERENCE: CGC 2048
; CURRENT APPLICATION NUMBER: US/09/178,002
; CURRENT FILING DATE: 1998-10-22
; NUMBER OF SEQ ID NOS: 9
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 3
; LENGTH: 2223
; TYPE: DNA
; ORGANISM: Homo sapiens

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QY		813	CTTAAGGTACTGCTAAAGCCCAAGACATTCCTCGTGGTTTG	920
Db		861	TCAAGCAACCCTATTCCAACCTACTGGACCAAGCACCCCAAACCTGTGACCCCAGTTTG	932
QY		873	ACTTTTGACGCTATCACACTTCCGCAGAGAAGCTAATGTTCTTTAAAGGCAGGCACCTA	932
Db		921	ACATTTTGATGCTATCACCACTCCGCTGGAGAAATCTTTCTTTTAAAGACAGGTACTTC	980
QY		933	TGAGGATCTATTATGATATACCGGATGTTGCAGTTTGAATTAATTCGTTCTCATTTCTGGCCA	992
Db		981	TGGAGAGGGCATCCTCAGCTACAAAGAGTCGAATGAAATTTTCTCTATTCTTGGCCA	1040
QY		993	TCCTGCGCAGCTGATCTGCAAGCTGCATACGAGAA---CCCCAGAGATAAGATCTCGGTT	1049
Db		1041	TCCCTTCCAACCTGGTATACAGGCTGCTTATGAAGATTTTGACAGAGACCTCATTTTCCCTA	1100

1050 TTTAAAGATGAAACCTCTTGGATGATCAGAGGATATGCTGTCTTGGCCAGATTATCCCAA 1109
1101 TTTAAAGGCAACCAATACCTCTGGCTCTGAGTGGCTATGATATCTGCAAGGTTATCCCAAG 1160
1110 TCCATCCATACATAGTGTCTTCCAGGACGCTGTGAAGAAATAGATGAGCGCTGTGTGAT 1169
1161 GATATATCAAACTATGCTTCTCCAGCAGCGCTCCAGCAATGACGAGCTGTTTCTA- 1219
1170 AAGACCAAGAAACCTACTTCTTGTGGCATTTGGTGGCTGTGGAGTTTGATGAATG 1229
1220 -----CAGAAGTAAACATCTTCTTGTAAATGACCAATCTGGAGATATGAACCAA 1274
1230 ACCCAACCATGACAAAGATTTCCGACAGAGTGTGAACACATTTCTCTGCAATCAGT 1289
1275 AGACAATTCATGAGCGAGTTATCCCAAGCATATCAGTGCCTTTCAGGAATAGAG 1334
1290 ATCCGTTGTATGCTCTTCCAGTACAAAGGATTTCTTTTTCAGCGCTGTGATCAAAG 1349
1335 AGTAAAGTTGATCAGTTTTTCCAGCAAGAACATTTCTTCCATGCTTTCAGTGGACCAAGA 1394
1350 CAATTTGAATACAACTTAAGACAAAGATATTACCGAATCATGAGAACTAATCTTGG 1409
1395 TATTACGCAATTCATTTATGCTCAGAGATTACAGAGTTCCAGAGTTCCAAAGAGCAATAATGG 1454
1410 TTTCAATGCAAGA 1423
1455 CTTAACTGTAGATA 1468

RESULT 9

US-09-023-655-1040
; Sequence 1040, Application US/09023655
; Patent No. 6607879
; GENERAL INFORMATION:
; APPLICANT: Cocks, Benjamin G.
; APPLICANT: Susan G. Stuart
; APPLICANT: Jeffrey J. Seilhamer
; TITLE OF INVENTION: COMPOSITION FOR THE DETECTION OF BLOOD CELL GENE
; TITLE OF INVENTION: EXPRESSION
; NUMBER OF SEQUENCES: 1508
; CORRESPONDENCE ADDRESS:
; ADDRESSES: INCYTE PHARMACEUTICALS, INC.
; STREET: 3174 PORTER DRIVE
; CITY: PALO ALTO
; STATE: CALIFORNIA
; COUNTRY: USA
; ZIP: 94304
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Word Perfect 6.1 for Windows/MS-DOS 6.2
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/023,655
; FILING DATE: HEREWITH
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Zeller, Karen J.
; REGISTRATION NUMBER: 37,071
; REFERENCE/DOCKET NUMBER: PA-0001 US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (650) 855-0555
; TELEFAX: (650) 845-4166
; INFORMATION FOR SEQ ID NO: 1040:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 2223 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear

; IMMEDIATE SOURCE:
; LIBRARY: GENBANK
; CLONE: g180617
; US-09-023-655-1040

Query Match 26.8%; Score 435.6; DB 4; Length 2223;
Best Local Similarity 60.8%; Pred. No. 1.8e-117;
Matches 809; Conservative 0; Mismatches 504; Indels 21; Gaps 5;

QY	99	AATGAAGAAATATGCAACTGGCTCAGGCATATCTCAACCAGTTTCTACTCTCTTGAATA	158
Db	147	AAAGAGAAATAACAAAACCTGTTTCAGGACTACTCTGAAAGATTTACCAATTACCAAGC	206
QY	159	GAAGGAAATCATCTTGTTCAAAGCAAGATAGGAGTCTCATAGATGACAAAAATTCGGAA	218
Db	207	AACCATGATCAGTCTCAAGGAAGAAATGACCTAAATGTGATCGTTGAAAGCTTAAAGAA	266
QY	219	ATCAAGCAATTTTTTGGATTGACAGTGACTGGGAAACTGGACTCAAAACACCTTGAGATC	278
Db	267	ATGACCGGATTTTTTGGTTTGAATGACGGGAAGCCAAATGAGGAAACTCTGGACATG	326
QY	279	ATGAAGACACCCAGGTGTGGGTGCTGATGTGGGCCAGTATGGCTACACCC-----TC	332
Db	327	ATGAAAGAGCTCGCTGTGGAGTGCCTGACAGTGGTGGTTTATGTTAAACCCAGGAAAC	386
QY	333	CTGGGTGGAGAAATACAACTCAGTACAGAAATATAAATACTCCGGATATGGCA	392
Db	387	CCCAAGTGGGAACGCCTAACTTGACTACAGGATTCGAAACTATATACCCACAGCTGTCA	446
QY	393	CGAGCTGCTGTGATGAGGCTATCCAAAGAGGTTTAGAGTGTGGAGCAAGTCACTCCA	452
Db	447	GAGGCTGAGGTAGAAAGAGCTATCAAGGATGCTTTGAACTCTGGAGTGTGCATCACCT	506
QY	453	CTAAAATTCACCAAGATTTCAAAGGGGATTCAGAGCATCATGATTTGCCCTTTAGGACTCA	512
Db	507	CTCATCTTCACCAAGATCTCACAGGAGAGGAGATATCAACATTTGCTTTTACCAAGA	566
QY	513	GTCCATGTTGGTGTCTCTGCTATTTTATGTTGCCCTTGGAGTGTTCGGCATGCTTT	572
Db	567	GATCAGGTGACAAATTTCTCA---TTTGATGACCAATGGAATCTTCTCTCATGCTTT	623
QY	573	CCTCTGTTCCGGTCTGGTGTGCTGACACTATTTGATGAGGATCAAACTGGACCAAG	632
Db	624	CAGCAGGCAAGGATTTGGAGAGATGCTCATTTGATGCCGAAGAAACATGGACCAAC	683
QY	633	GATGAGCAGGATTCACACTTTTCTTGGCTGCTCATGAAATTTGGTCATGCACTGGGG	692
Db	684	ACCTCCGCAAAATTACAACTTTTCTTGTGCTGCTCATGATTTGGCATTTCTTTGGG	743
QY	693	CTCTCTCACTCAATGATCAAAACAGCTTGTATGTTCCCAAATATGTTCTCCCTGATGCC	752
Db	744	CTCGCTCACTCTCTGACCTTGTGCTGATGATATCCCACTATGCTTTTACAGGAAACC	803
QY	753	AGAAAATACCACTTTTCTCAGGATGATATCAATGAAATCCAGTCCATCTATGGAGTCTG	812
Db	804	AGCACTACTCTCTCTCAAGATGATGATGAGGATTCAGGCCATCTATGGA---CTT	860
QY	813	CCTAAGGTACCTGCTTAAGCCAAAGGAACCACTATACCCCATGCTGTGACCCCTGACTTG	872
Db	861	TCAAGCAACCTTATCCAACCTACTGGACCAAGCACACCCAAACCTGTGACCCCACTTG	920
QY	873	ACTTTTGAGGTATCAAACTTTTCGGCAGAGAGTAATGTTCTTTTAAAGGAGGACCACTA	932
Db	921	ACATTTGATGCTATCACCACACTCCGTGGAGAAATCTTTTCTTTTAAAGACAGGTACTTC	980
QY	933	TGGAGGATCTATTATGATATCAGGATGTTGAGTTGAAATTAATGCTTCACTTCGGCA	992
Db	981	TGGAGAGGATCTCTCAGCTACAAAGAGTCCAAATGAAATTTATTTCTTCTTCTTCTG	1040
QY	993	TCTCTGCCAGCTGATCTGCAAGCTGCATACGAGAA---CCCCAGAGATAAGATCTGTT	1049
Db	1041	TCCCTTCCAACTGGTATACAGGCTGCTTATGAGATTTTGACAGAGACCTCATTTTCTTA	1100

QY 1050 TTTAAGATGAAACTTCTGGATGATCAGAGGATATGCTCTCTGCGAGATATCCAAA 1109
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Db 1101 TTTAAGGCAACCAATACTGGGCTCTGAGTGGCTATGATATTTGCAAGGTATCCCAAG 1160
| | | | |
QY 1110 TCCATCCATACATTAAGTCTTCCAGGACGCTGTAAGAAATAGATGAGCGCTCTGTGAT 1169
| | | | |
Db 1161 GATATATCAAACTATGCTTCCAGCAGCGTCCAGCAATGACGAGCTGTTTCTA- 1219
| | | | |
QY 1170 AAGACCAACAGAAAACTACTTCTTGTGGGCAATTTGGTCTGGAGGTTTGATGAATG 1229
| | | | |
Db 1220 -----CAGAAGTAAACATACTTCTTGTAAATGACCAATCTGGAGATATGATAACAA 1274
| | | | |
QY 1230 ACCCAACCATGAGCAAGATTTCCCGCAGAGAGTGTAAACACTTTCTGGGAATCAGT 1289
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Db 1275 AGACAATTCATGAGCGCAGGTATCCCAAGAGCATATCAGGTGCTTTCCAGGAATAGAG 1334
| | | | |
QY 1290 ATCCGCTGTCATGCTGCTTTCCAGTACAAAGGATTTCTTTTTCAGCGCTGGATCAAG 1349
| | | | |
Db 1335 AGTAAAGTGTAGTCAAGTCTTCCAGCAAGACATTTCTTCCATGCTTCAGTGGACCAAGA 1394
| | | | |
QY 1350 CAATTTGATACAACTAAGACAAAGAAATATTAACCGAATCATGAGAACTAATACTTGG 1409
| | | | |
Db 1395 TATTACGCAATTTGATCTATTGCTCAGAGAGTTACAGAGTTGCAAGAGGCAATAAATGG 1454
| | | | |
QY 1410 TTTCAATGCAAGA 1423
| | | | |
Db 1455 CTAACTGTAGATA 1468
| | | | |

RESULT 10

US-09-178-002-1
; Sequence 1, Application US/09178002
; Patent No. H001973
; GENERAL INFORMATION:
; APPLICANT: Hu, Shou-Ih
; TITLE OF INVENTION: Human Neutrophil Collagenase Splice Variant
; FILE REFERENCE: CGC 2048
; CURRENT APPLICATION NUMBER: US/09/178,002
; CURRENT FILING DATE: 1998-10-22
; NUMBER OF SEQ ID NOS: 9
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1
; LENGTH: 2314
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (232)..(1566)
US-09-178-002-1

Query Match 26.1%; Score 425.4; DB 1; Length 2314;
Best Local Similarity 60.6%; Pred. No. 1.8e-114;
Matches 794; Conservative 0; Mismatches 496; Indels 21; Gaps 5;

QY 122 TCAGGCATATCTCAACAGTCTTCTCTCTTCAAAATAGAGGAATCATCTTGTTCAAAAG 181
| | | | |
Db 261 TAATGACTACCTGGAAAGTTCTCAATATCAACAGCACCATGATCATGCTACAGGNA 320
| | | | |
QY 182 CAAGAATAGGAGTCTCATAGATGACAAAATTCGGGAATTCGAAGCATTTTTTGGATTTGAC 241
| | | | |
Db 321 GAATGGCACTAATGTGATGCTTTGAAAGCTTAAAGAAATGACGCGATTTTTTGGGTGAA 380
| | | | |
QY 242 AGTGACTGMAAATCGGACTCAACACCTTTCAGATCATGAGACACCCAGCTGTGGGT 301
| | | | |
Db 381 TGTGACGGGGAAGCCAAATGAGGAACTCTGACATGATGAAAGAGCCCTCGCTGTGGAGT 440
| | | | |
QY 302 GCTGATGTGGCCAGTATGGCTTACACCC-----TCCCTGGGTGGAGAAAATACAACCT 355
| | | | |
Db 441 GCTGACAGTGTGGTGTATTTATTTAATCCCGAGGAACCCCAAGTGGGAACGCATACCTT 500
| | | | |
QY 356 CACCTACAGAAATAAATACTACTCCGGATATGGCAGAGCTGTCTGTGATGAGGCTAT 415
| | | | |
Db 501 GACCTACAGGATTCGAAACTATACCCCAACAGCTGTGAGAGGTGAGGTAGAAAGAGCTAT 560
| | | | |

RESULT 11
US-09-280-116-77
; Sequence 77, Application US/09280116A

QY 416 CCAAGAAGGTTTAAAGTGTGGAGCAAAAGTCACTCCACTAAATAATTCACCAAGATTTCCAAA 475
| | | | |
Db 561 CAAGATGCTTTGAATCTGGAGTGTTCATCACCTCTCATCTTACCAGGATCTCACA 620
| | | | |
QY 476 GGGGATTTGCAGACATCATGATTCCTTTAGGATCTCGAGTCCATGGTCCGGTGTCTCCGCTA 535
| | | | |
Db 621 GGGAGAGGCAGATATCAACATTTGCTTTTACCAGAGAGATCAAGGTGACAAATTCCTC- - -C 677
| | | | |
QY 536 TTTTGTATGTTCCTTGGAGTGTCTGGCATGCTTTCCTCTCTGGTCCGGTCTGGGTGG 595
| | | | |
Db 678 ATTTGTATGGACCAATGGAATCTCTGCTCATGCTTTTCAGCAGGCCCAAGATATGGAGG 737
| | | | |
QY 596 TGACACTCATTTTGTATGAGGATGAAACTGGAACCAAGGATGGAGCAGGATTCACATTTGTT 655
| | | | |
Db 738 AGATGCTCATTTTGTATGCTCCGAGAAACATGGAACCAACACCTCCGCAAAATACAACTTTGT 797
| | | | |
QY 656 TCTTGTGGCTGCTCATGAATTTGTCATGCACTGGGGCTCTCTCACTCCAAATGATCAAAAC 715
| | | | |
Db 798 TCTTGTGCTGCTCATGAATTTGGCCATTTCTTTGGGCTCGCTCACTCTCTGACCTTGG 857
| | | | |
QY 716 AGCCTTGATGTTCCCAATTTATGTCCTCTGGATCCCGAGAAATATACCCACTTTCTCAGGA 775
| | | | |
Db 858 TGCCTTGATGTTATCCCAACTATGCTTTTCAGGGAACCAAGCAATCTACTCTCCCTCAGA 917
| | | | |
QY 776 TGATATCAATGGAATCCAGTCCATCTATGAGGCTCTGCTTAAGGTACTGCTAAGCCAAA 835
| | | | |
Db 918 TGACATCGATGGCATTCAGGCCATCTATGA- - -CTTTCAAGCAACCTATCCAACTAC 974
| | | | |
QY 836 GGAAACCCATATACCCCATGCTGTGACCTGACTGCTGACTTTTGACGCTATCAACATTT 895
| | | | |
Db 975 TGGACCAAGCACACCCAAACCTCTGACCCAGTTTGACATTTGATGCTATCACCACT 1034
| | | | |
QY 896 CCGCAGAGAGTAAATGTTCTTTAAGCAGCACCTATGGAGGATCTATTATGATATCAC 955
| | | | |
Db 1035 CCGTGGAGAAATACTTTTCTTTAAGACAGAGTACTTTCTGGAGAGGCACTCTCAGCTACA 1094
| | | | |
QY 956 GGATGTTGAGTTTGAATTAATTTGCTTCTGCTGCTCTCTGCGAGTGTCTGCTGCAAGC 1015
| | | | |
Db 1095 AAGAGTGAATGAATTTATTTCTTCTTCTGCTGCTCTCTGCTGCTGCTGCTGCTGCTGCT 1154
| | | | |
QY 1016 TGCATACGAGAA- - -CCCCAGAGATAGATCTGGTCTGCTGCTTAAAGATGAAATCTGCTGAT 1072
| | | | |
Db 1155 TGCTTATGAAGATTTTGACAGAGACCTCAITTTTCTATTTTAAAGGCAACCAATACCTGGC 1214
| | | | |
QY 1073 GATCAGAGGATATGCTGCTTGGCAGATTTATCCCAATCCCATCATATAGTATGCTTTTCC 1132
| | | | |
Db 1215 TCTGAGTGGCTATGATATCTGCAAGGTTATCCCAAGGATATATCAAACTATGCTTCCCTC 1274
| | | | |
QY 1133 AGGAGCTGTGAAGAAATAGATGAGCGCTCTGTGATTAAGACCAAGAAACCACTACTTT 1192
| | | | |
Db 1275 CAGCAGCGTCCAAAGCAATTTGACGAGCTGTTTCTTA- - - - -CAGAGTAAACATACTT 1328
| | | | |
QY 1193 CTTTGTGGGCAATTTGCTGCTGAGGTTTGTGAATGACCCCAACCATGGACCAAGGATTT 1252
| | | | |
Db 1329 CTTTGTAAATGACCAATTTCTGGAGATATGATAACCAAGACAAATTCATGGAGCCAGGTTA 1388
| | | | |
QY 1253 CCGCAGAGAGTGGTAAACACTTTCTCGGAATCAGTATCCGTTGTGATGCTGCTTTTCCA 1312
| | | | |
Db 1389 TCCCAAGACATATCAGGTGCTTTCCAGGAATAGAGATGAAGTTGATGACGATTTTCCA 1448
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QY 1313 GTACAAAGGATTTCTTTTTCAGCGGTGGATCAAGCAATTTGAAATCAACATTAAGAC 1372
| | | | |
Db 1449 GCAAGAACATTTCTTCCATGCTTTCAGTGGACCAAGATATTACGATTTGATCTTATTGC 1508
| | | | |
QY 1373 AAAGATATATACCCCAATCATGAGAACTAATACTTGGTTTCAATCAAGA 1423
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Db 1509 TCAGAGAGTTACCGAGTTGCAAGAGGCAATAAATGGCTTAACCTAGATA 1559
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; Patent No. 6331427
; GENERAL INFORMATION:
; APPLICANT: Robison, Keith E.
; TITLE OF INVENTION: Nucleic Acid Molecules Encoding Human Protease Homologs
; FILE REFERENCE: 5800-24, 035800/176965
; CURRENT APPLICATION NUMBER: US/09/280,116A
; CURRENT FILING DATE: 1999-03-26
; NUMBER OF SEQ ID NOS: 268
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 77
; LENGTH: 474
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: matrix metalloproteases
; NAME/KEY: misc feature
; LOCATION: (1)..(474)
; OTHER INFORMATION: n = a, t, c or g
US-09-280-116-77

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Query Match      26.0%; Score 423; DB 3; Length 474;
Best Local Similarity 100.0%; Pred. No. 3.7e-114;
Matches 423; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 641 AGGATTCAACTTCTTCTTGTGGCTGCTCATGAATTTGGTCATGCACTGGGGCTCTCTCA 700
DB |||||
QY 701 CTCGAATGATCAACAGCCTTGATGTTCCAAATTAATGTTCTCCCTGGATCCCAAGAAATA 760
DB |||||
QY 761 CCCACTTCTCAGGATGATATCAATGGAATCCAGTCCATCATATGAGGTCTGCTTAAGGT 820
DB |||||
QY 821 ACCTGCTAAGCCAAAGAACCCACTATACCCATGCTGTGACCTGACTTGACTTTTGA 880
DB |||||
QY 881 CGTATFACAACCTTCCGAGAGAGTAATGTTCTTTAAAGGAGGACCACTATGAGGAT 940
DB |||||
QY 941 CTATTATGATACAGGATGTTGAGTTGAAATTAATGTTCTTCTGCGCATCTCTGCC 1000
DB |||||
QY 1001 AGCTGATCTGCAAGCTGCTACAGAACCCAGAGATAAGATTCTGTTTTTAAAGATGA 1060
DB |||||
QY 1061 AAA 1063
DB |||
QY 471 AAA 473

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RESULT 12

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US-08-068-392-1
; Sequence 1, Application US/08068392
; Patent No. 6150152
; GENERAL INFORMATION:
; APPLICANT: Shapito, Steven M.
; TITLE OF INVENTION: Human Macrophage Metalloprotease
; NUMBER OF SEQUENCES: 3
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Scott J. Meyer, Monsanto Co., A3SM
; STREET: 800 N. Lindbergh Blvd.
; CITY: St. Louis
; STATE: Missouri
; COUNTRY: USA
; ZIP: 63167

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; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/068,392
; FILING DATE: 19930528
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Meyer, Scott J.
; REGISTRATION NUMBER: 25275
; REFERENCE/DOCKET NUMBER: 07-24 (12406)A
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (314)694-3117
; TELEFAX: (314)694-5435
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1410 base pairs
; TYPE: NUCLEIC ACID
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 1..1410
US-08-068-392-1

Query Match      23.9%; Score 389.4; DB 3; Length 1410;
Best Local Similarity 59.0%; Pred. No. 5.1e-104;
Matches 786; Conservative 0; Mismatches 526; Indels 21; Gaps 6;

QY 103 AAGAAATATGCAACTGGCTCAGGCATATCTCAACAGTTCTTACTCTCTTGAATAGAAG 162
DB |||||
QY 163 GGAATCATCTTGTTCAAAGCAAGATA---GAGTCTCATAGATGACAAAATTCGGGAAA 219
DB |||||
QY 220 TGAAGAGCATTTTGTGATTGACAGTGACCTGGAACAACTGGACTCAACACCCCTTGATCA 279
DB |||||
QY 280 TGAAGACACCCAGGTGTGGGGTGCCTGATGTGGGCCAGTATGGCTACACCC-----TCC 333
DB |||||
QY 334 CTGGGTGGAGAAAATACAACTCACCTACAGAAATAATAAATACTACTCCGGATATGCGAC 393
DB |||||
QY 394 GAGCTGCTGTGATGAGGCTATCCAAGAGGTTTGAAGTGTGGAGCAAAAGTCACTCCAC 453
DB |||||
QY 454 TAAATTCACCAAGATTTCAAAGGGATGACAGATCATGATTCCTTTAGACTCGAG 513
DB |||||
QY 514 TCCATGGTTCGGTGTCTCTGCTATTTTGTGTTCCCTTGGAGTGTCTGGCCATGCTTTTC 573
DB |||||
QY 574 CTCCTGGTCCGGTCTGGGTGGTGAACCTCATTTTGTGAGGATGAAATCGACCAAG 633
DB |||||
QY 634 ATGGAGCAGGATTAACATTTGTTTCTTGTGGTGTGCTCATGAATTTGGTATGACATGGGGC 693
DB |||||
QY 694 TCTCTCACTCCATGATCAACAGCCTTGATGTTCCCAAATTTATGTCCTCCCTGGATCCA 753

```

Db 677 TTGGCCATCTTAGTATCCAAAGCTGTAAATGTTCCCACTCAAAATATGTCACATCA 736
Qy 754 GAAATACCCACTTTCTCAGGATGATATCAATGGAATCCAGTCCATCTATGAGGTCTGC 813
Db 737 ACATATTCGCTCTCTGCTGATGACATACGTGGCAATTCAGTCCCTGTATGAGACCAA 796
Qy 814 CTAAGGTACCTGTGAAGCAAA---GGAAACCACTATACCCCATGCTGTGACCTGACT 870
Db 797 AAGAGAACCAACGCTTGCCAAATCTGACAAATTCAGAACCAAGCTCTCTGTGACCCCAAT 856
Qy 871 TGACTTTTGAAGCTATCACAATCTTCGACAGAGAAATGTTCTTTAAAGGCGAGGAC 930
Db 857 TGAGTTTGTGCTGTCTACCTGCGGAAATAGATCTTTTCTTCAAGACAGGTCT 916
Qy 931 TATGAGAGATCTATTATGATATACGAGTGTGAGTTTGAATTAATATGCTTCTATCTGGC 990
Db 917 TCTGGCTGAAGTTTCTGAGAGACCAAGACCAAGTGTAAATTAATTTCTTCTTATGGC 976
Qy 991 CATCTTGCAGCTGATCTGAAGCTGCATACGAGA---ACCCAGAGATAGATCTGG 1047
Db 977 CAACCTTGCCTGCTGGCATTGAAGCTGCTTATGAATTTGAAGCAGAAATCAAGTTTTC 1036
Qy 1048 TTTTAAAGATGAAACTTCTGGATGATCAGAGGATATGCTGTCTTGCAGATTATCCCA 1107
Db 1037 TTTTAAAGATGACAAATCTAGTTTAAATAGCAATTTAAGACAGGCAAAATATCCCA 1096
Qy 1108 AATCCATCCATACATTAGTTTCCAGGACGTGTGAAGAAATAGATGACGCGCTGTGT 1167
Db 1097 AGAGCATACATCTTTTGGTTTCTTAACTTTTGTGAAAAAATTTGATGCACTGTGTTA 1156
Qy 1168 ATAAGACCAAGAAACCTACTCTTTTGGGCAATTTGCTGGAGGTTTGAATGAA 1227
Db 1157 ACCACGTTTTATAGGACCTACTCTTTTGTAGATAACCAATTTGGAGGTATGATGAA 1216
Qy 1228 TGACCCAAACCATGCAAGAGATTCGCGAGAGAGTGTGTAACCACTTTCTGGAATCA 1287
Db 1217 GGAGACAGATGATGGACCTGTTATCCAACTGATACCAAGAACTTCCAAAGATCG 1276
Qy 1288 GTATCCGTTGTAGTGTCTTCCAGT---ACAAAGGATCTTCTTTTTCAGCGGTGAT 1344
Db 1277 GGCCTAAATTTGATGCACTCTTATTTCTAAACCAATACTACTATTTCTTCCAAAGAT 1336
Qy 1345 CAAGCAATTTGAATACAAATTAAGACAAAGATTTACCGGATCATGAGACTAATA 1404
Db 1337 CTAACCAATTTGAATATGACTTCTTCTCAACGATCACCAAAACACTGAAGAAATA 1396
Qy 1405 CTTCGTTTCAATG 1417
Db 1397 GCTGGTTGGTTG 1409

RESULT 13
US-08-396-988-1
; Sequence 1, Application US/08396988
; Patent No. 6204043
; GENERAL INFORMATION:
; APPLICANT: Shaprio, Steven M.
; TITLE OF INVENTION: Human Macrophage Metalloproteinase
; NUMBER OF SEQUENCES: 3
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Scott J. Meyer, Monsanto Co., A3SM
; STREET: 800 N. Lindbergh Blvd.
; CITY: St. Louis
; STATE: Missouri
; COUNTRY: USA
; ZIP: 63167
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/396,988
; FILING DATE: 01-MAR-1995
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/068,392
; FILING DATE: 28-MAY-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Meyer, Scott J. 25275
; REGISTRATION NUMBER:
; REFERENCE/DOCKET NUMBER: 07-24(12406)A
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (314)694-3117
; TELEFAX: (314)694-5435
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1410 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: cdna
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 1..1410
; US-08-396-988-1

Query Match 23.9%; Score 389.4; DB 3; Length 1410;
Best Local Similarity 59.0%; Pred. No. 5.1e-104; Indels 21; Gaps 6;
Matches 786; Conservative 0; Mismatches 526;
Qy 103 AAGAAATATGCAACTGGCTCAGGCATATCTCAACCAAGTCTTACTCTCTGAAATAGAG 162
Db 80 AAATATATGCTATTTGGTGAGAGATCTTAGAAAAATTTATATGGCCTTGAGATAACA 139
Qy 163 GGAATCATCTTGTTCAGAGCAAGATA---GGAGTCTCATAGATGACAAAATTCGGGAA 219
Db 140 AACTTCCAGTGACAAAAATGAATATATAGTGGAAATCTTAATGAAGAAAAATCCAAAGAA 199
Qy 220 TGCAAGCATTTTGGATTTGACAGTCACTGCAAAACTGGACTCAAAACACCTTGAGATCA 279
Db 200 TGCAGCACTTCTGGTCTGAAGTGACCGGCACTGGACACATCTACCTTGGAGATGA 259
Qy 280 TGAAGACACCCAGGTGTGGGTGCTGATGTGGGCCAGTATGGCTTACACCC-----TCC 333
Db 260 TGCAGCACCTCGATGTGGAGTCCCGATGTCATCACTTCAGGGAAATGCGAGGGGCG 319
Qy 334 CTGGGTGGAGAAATACAACTCCTACATACAGAAATAAATACTATCTCGGATATGGCAC 393
Db 320 CCGTATGGAGGAAACATTTATATCACTACAGAAATCAATTAATACACCTGACATGAACC 379
Qy 394 GAGCTGTGTGATGAGGCTATCCAAGAAAGGTTTGAAGTGTGGAGCAAGTCACTCCAC 453
Db 380 GTGAGATGTTGACTACGCAATCGGAAAGCTTTCCAGTATGAGTAAATGTACCCCT 439
Qy 454 TAAATTCACCAAGATTTCAAGGGGATTCAGACATCATGATTCCTTTAGGATCGAG 513
Db 440 TGAATTCAGCAAGATTAACACAGCATGGCTGACATTTTGGTGGTTTTTGGCCGTGGAG 499
Qy 514 TCCATGGTGGGTCTCTGCTATTTTGGTGGTCCCTTGGAGTGTCTGGCATGCTTTC 573
Db 500 CTCATGGAGACTTCCATGC---TTTGAAGGCAAGGTGGAAATCTTACCCATGCTTTG 556
Qy 574 CTCCTGGTCCGGGTCTGGGTGGTGCACACTCAATTTTGTAGAGATGAAACTGGACCAAG 633
Db 557 GACCTGGATCTGGCATTGGAGGGATGCACATTCGATGAGGACGAATTTCTGGACTAC 616
Qy 634 ATGAGACAGGATCAACTTTTCTTGTGGTGTCTCATGAATTTGGTCAATGATGATGGG 693
Db 617 ATTGAGGAGGCAAACTTTGTTCTCTCACTGTCTTTCAGAGATTTGGCCATTTCTTAGGTC 676
Qy 694 TCTCTCACTCCAAATGATCAACAGCTTGTATGTTTCCCAAAATTTATGCTCTCCCTGGATCCCA 753
Db 677 TTGGCCATTTAGTATCCAAAGGCTGTAAATGTTTCCCACTCAAAATATGTCACATCA 736

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GenCore version 5.1.6
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OM protein - nucleic search, using frame_plus_p2n model

Run on: November 15, 2004, 21:08:48 ; Search time 136 Seconds
(without alignments)
2681.137 Million cell updates/sec

Title: US-10-729-807-10

Perfect score: 2763

Sequence: 1 MKRLLLLCLFFITFSAPFL.....SLSLFFIGVHLKNTSIYQ 513

Scoring table: BLOSUM62

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Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 824507 seqs, 355394441 residues

Total number of hits satisfying chosen parameters: 1649014

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Command line parameters:

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-LOOPEXT=0 -UNITS=bits -START=1 -END=1 -MATRIX=blomsum62 -TRANS=human40.cdi
-LIST=45 -DOCALIGN=200 -THR SCORE=pct -THR MAX=100 -THR MIN=0 -ALIGN=15
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-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database :

Issued Patents NA:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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1	2763	100.0	1845	US-09-862-631-1	Sequence 1, Appli
2	2752	99.6	1647	US-10-140-002-191	Sequence 191, Appl
3	2455	88.9	1687	US-09-280-116-78	Sequence 78, Appl
4	1254	45.4	1434	US-09-023-655-1174	Sequence 1174, Ap
5	1250	45.2	1801	US-09-023-655-1374	Sequence 1374, Ap
6	1198.5	43.4	1717	US-08-229-515A-12	Sequence 12, Appl
7	1198.5	43.4	1717	US-08-645-865-12	Sequence 12, Appl
8	1161.5	42.0	1970	US-09-023-655-1264	Sequence 1264, Ap
9	1161	42.0	2223	US-09-178-002-3	Sequence 3, Appli
10	1161	42.0	2223	US-09-023-655-1040	Sequence 1040, Ap
11	1153.5	41.7	1981	US-09-484-970B-62	Sequence 62, Appl
12	1133	41.0	1410	US-08-068-392-1	Sequence 1, Appli

13	1133	41.0	1410	3	US-08-396-988-1	Sequence 1, Appli
14	1132	41.0	1521	4	US-08-994-689C-18	Sequence 18, Appl
15	1132	41.0	2792	4	US-08-994-689C-8	Sequence 8, Appli
16	1127	40.8	2314	1	US-09-178-002-1	Sequence 1, Appli
17	1033.5	37.4	1160	3	US-07-780-973-15	Sequence 15, Appl
18	786.5	28.5	474	3	US-09-280-116-77	Sequence 77, Appl
19	769.5	27.9	2123	4	US-09-194-468A-29	Sequence 29, Appl
20	718	26.0	1923	3	US-09-294-841-1	Sequence 1, Appli
21	715.5	25.9	3530	3	US-08-704-711A-10	Sequence 10, Appl
22	715.5	25.9	3530	3	US-09-521-220-10	Sequence 10, Appl
23	713.5	25.8	2116	3	US-09-000-041A-1	Sequence 1, Appli
24	713.5	25.8	2116	4	US-09-734-002-1	Sequence 2, Appli
25	713	25.8	3403	3	US-08-448-489-2	Sequence 2, Appli
26	713	25.8	3437	3	US-08-704-711A-9	Sequence 9, Appli
27	713	25.8	3437	3	US-09-521-220-9	Sequence 9, Appli
28	713	25.8	3437	4	US-09-919-497-34	Sequence 34, Appl
29	672	24.3	3456	3	US-08-704-711A-8	Sequence 8, Appli
30	672	24.3	3456	3	US-09-521-220-8	Sequence 8, Appli
31	600	21.7	825	4	US-08-896-062-1	Sequence 1, Appli
32	597	21.6	2335	4	US-09-799-451-346	Sequence 346, App
33	594.5	21.5	837	1	US-08-371-082-1	Sequence 1, Appli
34	594.5	21.5	1078	3	US-09-492-543-28	Sequence 28, Appl
35	594.5	21.5	1078	3	US-09-492-543-29	Sequence 29, Appl
36	594.5	21.5	1078	4	US-09-023-655-1368	Sequence 1368, Ap
37	594	21.5	2334	1	US-08-457-304A-33	Sequence 33, Appl
38	594	21.5	2334	1	US-08-456-701A-33	Sequence 33, Appl
39	594	21.5	2334	4	US-08-684-932A-33	Sequence 33, Appl
40	594	21.5	2334	4	US-09-023-655-996	Sequence 996, App
41	590	21.4	2260	1	US-07-794-393-3	Sequence 3, Appli
42	590	21.4	2260	1	US-08-001-711-3	Sequence 3, Appli
43	580	21.0	2247	4	US-09-023-655-1410	Sequence 1410, Ap
44	580	21.0	2256	1	US-07-794-393-1	Sequence 1, Appli
45	580	21.0	2256	1	US-08-001-711-1	Sequence 1, Appli

ALIGNMENTS

RESULT 1
US-09-862-631-1
; Sequence 1, Application US/09862631
; Patent No. 6734005
; GENERAL INFORMATION:
; APPLICANT: Holmgren, Erik
; APPLICANT: Kihlen, Mats
; APPLICANT: Wood, Tim
; APPLICANT: Ekblom, Jonas
; TITLE OF INVENTION: No. 6734005el Matrix Metalloproteinases
; FILE REFERENCE: 00014regUS
; CURRENT APPLICATION NUMBER: US/09/862,631
; CURRENT FILING DATE: 2000-05-22
; PRIOR APPLICATION NUMBER: 206119
; PRIOR FILING DATE: 2000-05-22
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 1
; LENGTH: 1845
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-862-631-1

Alignment Scores:
Pred. No.: 0
Score: 2763.00
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Query Match: 100.00%
DB: 4
Length: 1845
Matches: 513
Conservative: 0
Mismatches: 0
Indels: 0
Gaps: 0

US-10-729-807-10 (1-513) x US-09-862-631-1 (1-1845)

Qy 1 MetLysArgLeuLeuLeuLeuCysLeuPheLeuThrPheSerSerAlaPheProLeu 20

Db 24 ATGAAGCGCTTCGCTTCCTGTTGTTCTTTATACATTTCTTCGATTCCTCCCTTA 83

QY	21	ValArgMetThrGluAsnGluGluAAsnMetGlnLeuAlaGlnAlaTyrLeuAsnGlnPhe	40
Db	84	GTCCGGATGACGGAATAAGAAAAATATGCAACTGGCTCAGGCATATCTCAACAGCTTC	143
QY	41	TyrSerLeuGluIleGluGlyAsnHisLeuValGlnSerLysAsnArgSerLeuIleAsp	60
Db	144	TACTCTCTTGAATAGAGGAATCATCTTGTTCAAAGCAAGAAATAGAGTCTCATAGAT	203
QY	61	AspLysIleArgGluMetGlnAlaPhePheGlyLeuThrValThrGlyLysLeuAspSer	80
Db	204	GACAAAATTCGGGAATGCAAGCATTTTGTGATTTGACAGTGACTGGAAACCTGACTCA	263
QY	81	AsnThrLeuGluIleMetLysThrProArgCysGlyValProAspValGlyGlnTyrGly	100
Db	264	AACACCTTGAGATCATGAACACACCCAGGTGTGGGTGCTGATGTGGGCGACATATGGC	323
QY	101	TyrThrLeuProGlyTyrArgLysTyrAsnLeuThrTyrArgIleIleAsnTyrThrPro	120
Db	324	TACACCTCTCCCTGGGTGAGAAATACAACTCCTACAGTAATAAATACTATCTCCG	383
QY	121	AspMetAlaArgAlaAlaValAspGluAlaIleGlnGluGlyLeuGluValThrSerLys	140
Db	384	GATATGCACGAGCTGCTGTGGATGAGGCTATCCAAAGAGTTTAGAAGTGTGGAGCAAA	443
QY	141	ValThrProLeuLysPheThrLysIleSerLysGlyIleAlaAspIleMetIleAlaPhe	160
Db	444	GTCACTCCACTAAATTCACCAAGATTTCAAAGGGGATTCAGACATCATGATTTGCCTTT	503
QY	161	ArgThrArgValHisGlyArgCysProArgTyrPheAspGlyProLeuGlyValLeuGly	180
Db	504	AGGACTCGAGTCCATGGTGGTGCTCCTCGCTATTTTGTGATGTCCTTGGGAGTGTGGC	563
QY	181	HisAlaPheProProGlyProGlyLeuGlyGlyAspThrHisPheAspGluAspGluAsn	200
Db	564	CATGCCCTTCTCTCTGGTCCGGGTCTGGTGGTGCACCTCATTTTGTATGAGGATGAAAC	623
QY	201	TrpThrLysAspGlyAlaGlyPheAsnLeuPheLeuValAlaAlaHisGluPheGlyHis	220
Db	624	TGGACCAAGATGGAGCAGGATTCAACTTGTCTGTGGTGTCTCATGAATTTGGTCAT	683
QY	221	AlaLeuGlyLeuSerHisSerAsnAspGlnThrAlaLeuMetPheProAsnTyrValSer	240
Db	684	GCACCTGGGCGCTCTCTCATCTCAATGATCAACAGCCTTGATGTTCCCAAAATATGCTCC	743
QY	241	LeuAspProArgLysTyrProLeuSerGlnAspIleAsnGlyIleGlnSerIleTyr	260
Db	744	CTGGATCCAGAAATACCCACTTCTCAGGATGATATCAATGGAATCCAGTCCATCTAT	803
QY	261	GlyGlyLeuProLysValProAlaLysProLysGluProThrIleProHisAlaCysAsp	280
Db	804	GGAGGTCTGCCTAAGGTACTCTAAGCCAAAGGAACCCACTATACCCCATGCCCTGTGAC	863
QY	281	ProAspLeuThrPheAspAlaIleThrThrPheArgArgGluValMetPhePheLysGly	300
Db	864	CCTGACTTGACCTTTTGACGCTATCAACTTTCGACAGAGTAATGTCTTTAAAGGC	923
QY	301	ArgHisLeuTrpArgIleTyrTyrAspIleThrAspValGluPheGluLeuIleAlaSer	320
Db	924	AGGCACCTATGAGGATCTATTATGATATCAGGATGTGAGTTTGAATTAATTCCTTCA	983
QY	321	PheTrpProSerLeuProHisAspLeuGlnAlaIleTyrGluAsnProArgAspLysIle	340
Db	984	TTCTGGCCATCTCTGCCACTGATCTGCAAGCTGCATAGCAGAACCCAGATAGATTT	1043
QY	341	LeuValPheLysAspGluAsnPheTrpMetIleArgGlyTyrAlaValLeuProAspTyr	360
Db	1044	CTGGTTTTTAAGATGAAAACTTCTGGATGATCAGAGGATATGCTCTCTGACAGATTAT	1103
QY	361	ProLysSerIleHisThrLeuGlyPheProGlyArgValLysLysIleAspAlaVal	380
Db	1104	CCCAAAATCCATCATATAGTGTTCAGGAGCGTGTGAAGAAAAATAGATGACGCGTC	1163

QY	381	CysAspLysThrThrArgLysThrTyrPhePheValGlyIleTrpCysTrpArgPheAsp	400
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QY	401	GluMetThrGlnThrMetAspLysGlyPheProGlnArgValLysHisPheProGly	420
Db	1224	GAATGACCCCAACCATGGACAAAGGATTCGCCGACAGAGTGGTAAACACACTTTCTCTGGA	1283
QY	421	IleSerIleArgValAspAlaAlaPheGlnTyrLysGlyPhePhePheSerArgGly	440
Db	1284	ATCAGTATCCGTGTGATGCTGCTTTCCAGTACAAAGATTTCTCTTTTTCAGCCGTGGA	1343
QY	441	SerLysGlnPheGluTyrAsnIleLysThrLysAsnIleThrArgIleMetArgThrAsn	460
Db	1344	TCAAAGCAATTTGAATACACATTAACACAAAGAAATATTACCCGAATCATGAGAACTAAT	1403
QY	461	ThrTrpPheGlnCysLysGluProLysAsnSerSerPheGlyPheAspIleAsnLysGlu	480
Db	1404	ACTTGGTTTCAATGCAAAAGAACCAAGAACTCCTCATTTGTTTGTATATCAACAGGAA	1463
QY	481	LysAlaHisSerGlyGlyIleLysIleLeuTyrHisLysSerLeuSerLeuPheIlePhe	500
Db	1464	AAACACATTCAGAGGCGCATTAAGATATTGTATCATAGAGTTTAAGCTTCTTTATTTT	1523
QY	501	GlyIleValHisLeuLeuLysAsnThrSerIleTyrGln	513
Db	1524	GGTATTGTTTCATTTGCTGAAAAACACATTTCTATTATCAA	1562

RESULT 2

US-10-140-002-191

Sequence 191, Application US/10140002

Patent No. 6725730

GENERAL INFORMATION:

APPLICANT: Baker, Kevin P.

APPLICANT: Beresini, Maureen

APPLICANT: DeForge, Laura

APPLICANT: Desnoyers, Luc

APPLICANT: Filvaroff, Ellen

APPLICANT: Gao, Wei-Qiang

APPLICANT: Gerritsen, Mary E.

APPLICANT: Goddard, Audrey

APPLICANT: Godowski, Paul J.

APPLICANT: Gurney, Austin L.

APPLICANT: Sherwood, Steven

APPLICANT: Smith, Victoria

APPLICANT: Stewart, Timothy A.

APPLICANT: Tumas, Daniel

APPLICANT: Watanabe, Colin K

APPLICANT: Wood, William

APPLICANT: Zhang, Zemin

TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC

TITLE OF INVENTION: ACIDS ENCODING THE SAME

FILE REFERENCE: P3330R1C59

CURRENT APPLICATION NUMBER: US/10/140,002

CURRENT FILING DATE: 2002-05-06

Prior Application removed - See Palm or File Wrapper

NUMBER OF SEQ ID NOS: 550

SEQ ID NO 191

LENGTH: 1647

TYPE: DNA

ORGANISM: Homo Sapien

US-10-140-002-191

Alignment Scores:

Pred. No.: 0

Score: 2752.00

Percent Similarity: 99.81%

Best Local Similarity: 99.81%

Query Match: 99.60%

DB: 4

Length: 1647

Matches: 512

Conservative: 0

Mismatches: 1

Indels: 0

Gaps: 0

US-10-729-807-10 (1-513) x US-10-140-002-191 (1-1647)

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 QY 21 ValArgMetThrGluAsnGluGluAsnMetGlnLeuAlaGlnAlaTyrLeuAsnGlnPhe 40
 DB 84 GTCCCGGATGACCGAATAATGAAGAAATATGCAACTGGCTCAGGCATATCTCAACAGATTC 143
 QY 41 TyrSerLeuGluIleGluGlnHisLeuValGlnSerLysAsnArgSerLeuIleAsp 60
 DB 144 TACTCTCTTGAATAGAGGGAATCATCTTGTTCAAAGCAAGATAGGAGTCTCATAGAT 203
 QY 61 AspLysIleArgGluMetGlnAlaPhePheGlyLeuThrValThrGlyLysLeuAspSer 80
 DB 204 GACAAATTCGGAAATGCAAGCAATTTTGGATTGACAGTGACCTGGAAACCTGGACTCA 263
 QY 81 AsnThrLeuGluIleMetLysThrProArgCysGlyValProAspValGlyGlnTyrGly 100
 DB 264 AACACCTTGAGATCATGAAGACACCCAGGTGTGGGTGCTGATGTGGCCAGTATGCG 323
 QY 101 TyrThrLeuProGlyTyrArgLysTyrAsnLeuThrTyrArgLleIleAsnTyrThrPro 120
 DB 324 TACACCTCCCTGGGTGGAGAAATACACCTCACCTACAGAATAATAAACTATATCTCG 383
 QY 121 AspMetAlaArgAlaValAspGluAlaIleGlnGluGlyLeuGluValTyrSerLys 140
 DB 384 GATATGGACAGAGCTGCTGTGATGAGGTATCCAAAGAGGTTTAGAAGTGTGGAGCAAA 443
 QY 141 ValThrProLeuLysPheThrLysIleSerLysGlyIleAlaAspIleMetIleAlaPhe 160
 DB 444 GTCACTCCACTAAATTCACCAAGATTTCAAAGGGGATTCAGAGCATCATGATTCCTTT 503
 QY 161 ArgThrArgValHisGlyArgCysProArgTyrPheAspGlyProLeuGlyValLeuGly 180
 DB 504 AGGACTCGAGTCCATGGTGGGTGCTCTCGCTATTTTGATGGTCCCTGGGAGTGTCTGGC 563
 QY 181 HisAlaPheProGlyProGlyLeuGlyAspThrHisPheAspGluAspGluAsn 200
 DB 564 CATGCTTTCTCTCTGCTGGGTCTGGGTGGTGACATCATTTTGATGAGATGAAGAAC 623
 QY 201 TrpThrLysAspGlyAlaGlyPheAsnLeuPheLeuValAlaHisGluPheGlyHis 220
 DB 624 TGGACCAAGATGGAGCAGGATTCAACTTGTCTGTGGTCTCATGAATTTGGTCTAT 683
 QY 221 AlaLeuGlyLeuSerHisSerAsnAspGlnThrAlaLeuMetPheProAsnTyrValSer 240
 DB 684 GCATGGGGCTCTCTCATCTCAATGATCAACAGCCTTGATGTTCACCAATATATGCTCC 743
 QY 241 LeuAspProArgLysTyrProLeuSerGlnAspIleAsnGlyIleGlnSerIleTyr 260
 DB 744 CTGGATCCAGAAATATCCCACTTCTCAGGATGATATCAATGGAATCCAGTCCATCTAT 803
 QY 261 GlyGlyLeuProLysValProAlaLysProLysGluProThrIleProHisAlaCysAsp 280
 DB 804 GGAGGTCTGCTTAAGGTACCTGCTAAGCAAGCAAGAAACCACTATACCCCATGCTGTGAC 863
 QY 281 ProAspLeuThrPheAspAlaIleThrThrPheArgArgGluValMetPhePheLysGly 300
 DB 864 CTTGACTTGACTTTTGACGCTATCACTTCCGACAGAGTAATGTTCTTTAAAGGC 923
 QY 301 ArgHisLeuTyrArgIleTyrTyrAspIleThrAspValGluPheGluLeuIleAlaSer 320
 DB 924 AGGCACCTATGAGGATCTATATGATATCACGGATGTTGAGTTGAATTAATTCCTTCA 983
 QY 321 PheTyrProSerLeuProAlaAspLeuGlnAlaIleTyrGluAsnProArgAspLysIle 340
 DB 984 TTCTGGCCATCTCTCCAGCTGATCTGCAAGCTGCATACAGAAACCCAGAGATAAGATT 1043
 QY 341 LeuValPheLysAspGluAsnPheTyrMetIleArgGlyTyrAlaValLeuProAspTyr 360
 DB 1044 CTGGTTTTAAAGATGAAGAACTTCTGGATGATCAGAGGATATGCTGTCTGCCAGATTAT 1103
 QY 361 ProLysSerIleHisThrLeuGlyPheProGlyArgValLysLysIleAspAlaVal 380

DB 1104 CCCAATCCATCATACATTAGTTTTCAGACGCTGTGAAGAAATAGATGACCCGTC 1163
 QY 381 CysAspLysThrThrArgLysThrTyrPhePheValGlyIleTyrCysTyrPheArgPheAsp 400
 DB 1164 TGTGATAAGACCAACAGAAACCTTACTTCTTGTGGGCATTTGGTGTCTGGAGGTTTGAT 1223
 QY 401 GluMetThrGlnThrMetAspLysGlyPheProGlnArgValValIshisPheProGly 420
 DB 1224 GAAATGACCCCAACCATGGACAAGGATTCGCGCAGAGAGTGGTAAACACATTTCTCTGA 1283
 QY 421 IleSerIleArgValAspAlaAlaPheGlnTyrLysGlyPhePhePhePheSerArgGly 440
 DB 1284 ATCAGTATCCGTTGTGATGCTGCTTTCAGTACAAAGGATTCCTTTTTCAGCCGTGA 1343
 QY 441 SerLysGlnPheGluTyrAsnIleLysThrLysAsnIleThrArgIleMetArgThrAsn 460
 DB 1344 TCAAGCAATTTGAATACAAATTAAGACAAAGATATATCCCGAATCATGAGAACTAAT 1403
 QY 461 ThrTyrPheGlnCysLysGluProLysAsnSerSerPheGlyPheAspIleAsnLysGlu 480
 DB 1404 ACTTGGTTTCAATGCAAGAACCAAGAACTCCTCATTTGGTTTGTATATCAACAGGAA 1463
 QY 481 LysAlaHisSerGlyGlyIleLysIleLeuTyrHisLysSerLysSerLeuPheIlePhe 500
 DB 1464 AAAGCACATTCAGGAGGCATAAAGATATGTATCATAGAGTTTAAGCTTGTATTATTT 1523
 QY 501 GlyIleValHisLeuLeuLysAsnThrSerIleTyrGln 513
 DB 1524 GGTATTGTTTCTTCTGTAAGAAACACTTCTATTTATCA 1562

RESULT 3

US-09-280-116-78/c
 ; Sequence 78, Application US/09280116A
 ; Patent No. 6331427
 ; GENERAL INFORMATION:
 ; APPLICANT: Robison, Keith E.
 ; TITLE OF INVENTION: Nucleic Acid Molecules Encoding Human Protease Homologs
 ; FILE REFERENCE: 5800-24, 035800/176965
 ; CURRENT APPLICATION NUMBER: US/09/280,116A
 ; CURRENT FILING DATE: 1999-03-26
 ; NUMBER OF SEQ ID NOS: 268
 ; SOFTWARE: PatentIn Ver. 2.0
 ; SEQ ID NO 78
 ; LENGTH: 1687
 ; TYPE: DNA
 ; ORGANISM: Homo sapiens
 ; FEATURE:
 ; OTHER INFORMATION: matrix metalloproteases
 ; FEATURE:
 ; NAME/KEY: misc_feature
 ; LOCATION: (1)..(1687)
 ; OTHER INFORMATION: n = a, t, c or g
 US-09-280-116-78

Alignment Scores:
 Pred. No.: 3.83e-288 Length: 1687
 Score: 2455.00 Matches: 454
 Percent Similarity: 99.78% Conservative: 0
 Best Local Similarity: 99.78% Mismatches: 0
 Query Match: 88.85% Indels: 1
 DB: 3 Gaps: 0

US-10-729-807-10 (1-513) x US-09-280-116-78 (1-1687)

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 DB 1675 GATGACAAATTCGGGAATTCGAAGCAATTTTGGATTGACAGTGACTGGAAACTGAC 1616
 QY 80 SerAsnThrLeuGluIleMetLysThrProArgCysGlyValProAspValGlyGlnTyr 99
 DB 1615 TCAACACCTTTGAGATCATGAGACACCCAGGTTGGGGTGCCTGATGTGGCCAGTAT 1556

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QY 100 GlyTyrThrLeuProGlyTrpArgLysTyrAsnLeuThrTyrArgIleIleAsnTyrThr 119
Db 1555 GGCTACACCTCCCTCGGTGGAGAAATACAACTCACCTACAGATATATAACTATPACT 1496
QY 120 ProAspMetAlaArgAlaAlaValAspGluAlaIleGlnGluGlyLeuGluValTrpSer 139
Db 1495 CCGGATATGCCAGAGCTGCTGTGGATGAGGCTATCCAAGAAGGTTTAGAAGTGTGGAGC 1436
QY 140 LysValThrProLeuLysPheThrLysIleSerLysGlyIleAlaAspIleMetIleAla 159
Db 1435 AAAGTCACTCCACTAAATTCACCAAGATTCAAAGGGGATTCAGACATCATGATGCC 1376
QY 160 PheArgThrArgValHisGlyArgCysProArgTyrPheAspGlyProLeuGlyValLeu 179
Db 1375 TTTAGGACTCGAGTCGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1316
QY 180 GlyHisAlaPheProGlyProGlyProGlyLeuGlyGlyAspThrHisPheAspGluAspGlu 199
Db 1315 GGCATGCTCTTCTCTGCTCGGGTCTGGGTGGTGCACACTCATTTTGAAGAGGATGAA 1256
QY 200 AsnTrpThrLysAspGlyAlaGlyPheAsnLeuPheValAlaAlaHisGluPheGly 219
Db 1255 AACTGGACCAAGATGAGCAGGATTCAACTTGTCTTGTGGCTGCTCATGAATTTGGT 1196
QY 220 HisAlaLeuGlyLeuSerHisSerAsnAspGlnThrAlaLeuMetPheProAsnTyrVal 239
Db 1195 CATGCATGGGGCTCTCTCACTCAATGATCAACAGCCCTGATGTTCCCAATATATGTC 1136
QY 240 SerLeuAspProArgLysTrpProLeuSerGlnAspAspIleAsnGlyIleGlnSerIle 259
Db 1135 TCCCTGGATCCAGAAATACCCACTTCTCAGGATGATATCAATGAAATCCAGTCCATC 1076
QY 260 TyrGlyLeuProLysValProAlaLysProLysGluProThrIleProHisAlaCys 279
Db 1075 TATGGAGTCTGCTAGGTACCTGCTAAGCCTAAGCAAGGAACCCACTATACCCCATGCTGT 1016
QY 280 AspProAspLeuThrPheAspAlaIleThrPheArgArgGluValMetPhePheLys 299
Db 1015 GACCTGACTTGCTTTTGACGCTATCACAACTTTCGCGAGAGTAATGTTCTTTAAA 956
QY 300 GlyArgHisLeuTrpArgIleTyrTyrAspIleThrAspValGluPheGluLeuIleAla 319
Db 955 GGCAGGCACTATGAGGATCTATATGATATACGAGATGTGAGTTGATTAATGCT 896
QY 320 SerPheTrpProSerLeuProAlaAspLeuGlnAlaIleTyrGluAsnProArgAspLys 339
Db 895 TCATTCTGGCCATCTCTGCCAGCTGATCTGCAAGCTCATACGAGACCCAGAGATAAG 836
QY 340 IleLeuValPheLysAspGluAsnPheTrpMetIleArgGlyTyrAlaValLeuProAsp 359
Db 835 ATCTGTTGTTTAAAGATGAAACTTCTGGATGATCAGGATATGCTGCTGCCAGAT 776
QY 360 TyrProLysSerIleHisThrLeuGlyPheProGly-ArgValLysLysIleAspAlaAl 379
Db 775 TATCCCAATCCATCCATACATTAGGTTTCCAGGACCGTGTGAAGAAATAGATGCAGC 716
QY 379 aValCysAspLysThrThrArgLysThrTyrPhePheValGlyIleTrpCysTrpArgPh 399
Db 715 CGTCTGTGTAAGACCAAGAAACCTACTCTTTGTGGCATTTTGGTCTGCGAGGTT 656
QY 399 eAspGluMetThrGlnThrMetAspLysGlyPheProGlnArgValValLysHisPhePr 419
Db 655 TGATGAATGACCCAAACCATGGCAAGAGATTCGCGAGAGAGTGTGTAACACTTTCC 596
QY 419 oGlyIleSerIleArgValAspAlaAlaPheGlnTyrLysGlyPhePhePheSerAr 439
Db 595 TGGAAATCAGTATCGCTGTGATGCTGCTTCCAGTACAAAGGATTCCTCTTTTTCAGCCG 536
QY 439 gGlySerLysGlnPheGlnTyrAsnIleLysThrIysAsnIleThrArgIleMetArgTh 459
Db 535 TGGATCAAGCAATTTGAATCAACATTAAGACAAAGAAATATTACCGAATCATGAGAAC 476
QY 459 rAsnThrTrpPheGlnCysLysGluProLysAsnSerSerPheGlyPheAspIleAsnLy 479
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Db 475 TAATACTTGGTTTCAATGCAAAAGAACCAAAAGAACTCTCATTTGGTTTTCATATCAACA 416
QY 479 sGluLysAlaHisSerGlyGlyIleLysIleLeuTyrHisLysSerLeuSerLeuPheIl 499
Db 415 GGAAGAAAGCACATTCAGGAGGCATAAAGATATTGTATCATATAAGAGTTTAAGCTTGTAT 356
QY 499 ePheGlyIleValHisLeuLeuLysAsnThrSerIleTyrGln 513
Db 355 TTTTGTATTGTTTCAATTTGCTGTAACAACTCTCTATTATCAAA 313
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RESULT 4

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US-09-023-655-1174
; Sequence 1174, Application US/09023655
; Patent No. 6607879
; GENERAL INFORMATION:
; APPLICANT: Cocks, Benjamin G.
; APPLICANT: Susan G. Stuart
; APPLICANT: Jeffrey J. Seilhamer
; TITLE OF INVENTION: COMPOSITION FOR THE DETECTION OF BLOOD CELL GENE
; TITLE OF INVENTION: EXPRESSION
; NUMBER OF SEQUENCES: 1508
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: INCYTE PHARMACEUTICALS, INC.
; STREET: 3174 PORTER DRIVE
; CITY: PALO ALTO
; STATE: CALIFORNIA
; COUNTRY: USA
; ZIP: 94304
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Word Perfect 6.1 for Windows/MS-DOS 6.2
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/023,655
; FILING DATE: HEREWITH
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Zeller, Karen J.
; REGISTRATION NUMBER: 37,071
; REFERENCE/DOCKET NUMBER: PA-0001 US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (650) 855-0555
; TELEFAX: (650) 845-4166
; INFORMATION FOR SEQ ID NO: 1174:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1434 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; IMMEDIATE SOURCE:
; LIBRARY: GENEANK
; CLONE: g186618
; US-09-023-655-1174
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Alignment Scores:
Pred. No.: 3,4e-142 Length: 1434
Score: 1254.00 Matches: 247
Percent Similarity: 66.04% Conservative: 70
Best Local Similarity: 51.46% Mismatches: 145
Query Match: 45.39% Indels: 18
DB: 4 Gaps: 9
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US-10-729-807-10 (1-513) x US-09-023-655-1174 (1-1434)

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QY 1 MetLysArgLeuLeuLeuLeuCysLeuPhePheIleThrPheSerSerAlaPheProLeu 20
Db 1 ATGAAGAGTCTTCCAACTCTACTGTGTGCGTGCGAGCTTGTCTAGCCTATCCATTG 60
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QY 21 ValArgMetThrGluAsnGlu-----AsnMetGlnLeuAlaGlnIleTyrLeuAsnGln 39
Dd |||::: ::||| ||| ||| ||| ||| ||| |||
61 GATCGAGCTGCAAGGGTGAGCACACCGCATGAACCTTTGTTCAGAATAATCTGAAACAAC 120
QY 40 PheTyrSerLeuGluIleGluGlyAsnHisLeuValGlnSerLysAsnArgSerLeuile 59
 ::||| :||| ::||| ::||| ::||| ::|||
Dd 121 TACTATCAGACCTCGAAAAAAGATGTGAACAAGTTTGTTAGGAGAAAAGGACAGTGGTCCCTGTT 180
QY 60 AspAspLysIleArgGluMetGlnAlaPhePheGlyLeuThrValThrGlyLysLeuAsp 79
Dd 181 GTTAAAAAATCCGAGAAATGCAGAAAGTTCTCTGGATTGGAGGTGACGGGGAAGCTGGAC 240
QY 80 SerAsnThrLeuGluIleMetLysThrProArgCysGlyValProAspValcylGlnTyr 99
Dd 241 TCCGACACTCTGGAGGTGATSGCGAAGCCCAGGTGTGGAGTTCCTGAGCTTGGTCACTTC 300
QY 100 GlyTyrThrLeuProGly-----TiprArgLysTyrAsnLeuThrTyrArgIlelle 116
 |||| ||| | ||| ||| ||| |||
Dd 301 ---AGAACCTTTCTGTGCATCCCCGAAGTGGAGGAAAAACCCACCCTTACATACAGATTGTG 357
QY 117 AsnTyrThrProaspMetAlaArgAlaAlaValAspGluAlaIleGlnGluGlyLeuGlu 136
 :||| :||| ::||| ::||| ::||| ::|||
Dd 358 AATTATACACGATTTGCCAAAAGATGCTGTTGATTCTGCTGTGTGAGAAAGCTCTGAAA 417
QY 137 ValTrpSerLysValThrProLeuLysPheThrLysIleSerLysGlyIleAlaAspile 156
 :||| :||| ::||| ::||| ::||| ::|||
Dd 418 GTCTGGGAAGAGGTGACTCCACTCACATTCTCCAGGCTGTATGAAGAGAGAGCTGATATA 477
QY 157 MetIleAlaPheArgThrArgValHisGlyArg---CysProArgTyrPheAspGlyPro 175
 ||||| :||| ||| ||| ||| ||| |||
Dd 478 ATGATCTCTTTTCGATTAGAGAACATGGAGACTTTTACCCT-----TTTGATGGACCT 531
QY 176 LeuGlyValLeuGlyHisAlaPheProGlyProGlyLeuGlyGlyAspThrHisPhe 195
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Dd 532 GGAAATGTTTTGGCCCATGCTATGCTCCCTCGGCGCAGGATTAATGAGATGCCACTTT 591
QY 196 AspGluAspGlnAsnTrpThrLysAspGlyAlaGlyPheAsnLeuPheLeuValAlaala 215
 :||| :||| ::||| ::||| ::||| ::|||
Dd 592 GATGATGATGAACAATGACAAAAGGATACAAACAGGAGCCAATTTATTTCTCGTTGCTGCT 651
QY 216 HisGluPheGlyHisAlaLeuGlyLeuSerHisSerAsnAspGlnThrAlaLeuMetPhe 235
 ||||| :||| ||| ||| ||| ||| |||
Dd 652 CATGAATTGGCCACTCCCTGGGTCTTTTCACTCAGCCAACTGAAGCTTGATGTAC 711
QY 236 ProAsnTyrValSerLeu----ApproArgLysTyrProLeuSerGlnAspApilleAsn 254
 :||| :||| ::||| ::||| ::||| ::|||
Dd 712 CCACCTCATCACTCACTCACAGACCTGACTCGGTTCCGCTGTCTCAAGATGATATAAAT 771
QY 255 GlyIleGlnSerIleTyrGly-----GlyLeuProLysValProAla 268
 ||||| :||| ||| ||| ||| ||| |||
Dd 772 GGCATTTCAGTCCCTCATGAGACCTCCCTCGACTCCCTGAGAGCCCTCGGTACCCACG 831
QY 269 Lys-----ProLysGluProThriLeProHisAlaCysAspProAspLeuthrPheAsp 286
 :||| :||| ::||| ::||| ::||| ::|||
Dd 832 GAACCTGTCCCTCCAGAACCTGGGAGCCAGCCAACTGTGATCTGCTTTTGTCTTTGAT 891
QY 287 AlaIleThrThrPheArgArgGluValMetPhePhelysGlyArgHisLeuftrpArgIle 306
 :||| :||| ::||| ::||| ::||| ::|||
Dd 892 GCCTGCAGCACTCTGAGGGAGAGAAATCCCTGATCTTTAAAGACAGGCACCTTTTGGCGCAA 951
QY 307 TyrTyraSpilethrAspValGluPheGluLeulleAlaSerPhetrpProSerLeupro 326
 :||| :||| ::||| ::||| ::||| ::|||
Dd 952 TCCTCAGGAAGCTTGNACCTGAATTCATTTGATCTCTTCATTTTGGCCATCTCTTCCT 1011
QY 327 AlaaspleuGlnAlalatyrglu----AsnProArgAspLysIleLeuValPheLysAsp 345
 :||| :||| ::||| ::||| ::||| ::|||
Dd 1012 TCAGGGCTGTGATCCCGCATATGAAGTTACTAGCAAGGACCTCGTGTTCATTTTAAAGGA 1071
QY 346 GluAsnPheTrpMetIleArgGlyTyrAlaValLeuProAspTyrProLysSerIleHis 365
 :||| :||| ::||| ::||| ::||| ::|||
Dd 1072 AATCAATTCTGGGCCATCAGAGAAATGAGGTACGAGCTGGATACCCAGAGCATCCAC 1131

QY	366	ThrieUglyPheProGlyArgValLysLysLysIleAsPaLaIaValCysAspLysThr	395
Db	1132	ACCTTAGTTTCCTCCAACCGTGAGAAATCGATGCAGCAATTTCGGATAAGGAAAAG	1191
QY	386	ArgLysThrTyrPhePheValGlyIleTpCysTipArgPheAspGluMetThrGlnThr	405
Db	1192	AACAAACAATATTCITTTGTAGAGGACAAATACCTGGAGATTTCATGAGAAGAAATTC	1251
QY	406	MetAspLysGlyPheProGlnArgValValLysHisPheProGlyIleSerIleArgVal	425
Db	1252	ATGGAGCCAGGCVTTCCCAAGCAAATAGCTGAAGACTTTCACGGGATTGACTCAAAAGATT	1311
QY	426	AspAlaAalpheGlnTyrLysGlyPhePhePhePheSerArgGlySerLysGlnPheGlu	445
Db	1312	GATGCTGTTTTGAAGAATTTGGTCTCTTTTATTTCTTTACTGGATCTTCACAGTTGGAG	1371
QY	446	TyrAsnIleLysThrLysAsnIleThrArgIleMetArgThrAsnThrTrpPheGlnCys	465
Db	1372	TTTGACCCAAATGCCAAAGAAAGTGACACACACTTTGAAGAGTAACAGCTGGCTTAATCT	1431
RESULT 5			
US-09-023-655-1374			
; Sequence 1374, Application US/09023655			
; Patent No. 6607879			
; GENERAL INFORMATION:			
; APPLICANT: Cocks, Benjamin G.			
; APPLICANT: Susan G. Stuart			
; APPLICANT: Jeffrey J. Seilhamer			
; TITLE OF INVENTION: COMPOSITION FOR THE DETECTION OF BLOOD CELL GENE			
; TITLE OF INVENTION: EXPRESSION			
; NUMBER OF SEQUENCES: 1508			
; CORRESPONDENCE ADDRESS:			
; ADDRESSEE: INCYTE PHARMACEUTICALS, INC.			
; STREET: 3174 PORTER DRIVE			
; CITY: PALO ALTO			
; STATE: CALIFORNIA			
; COUNTRY: USA			
; ZIP: 94304			
; COMPUTER READABLE FORM:			
; MEDIUM TYPE: Floppy disk			
; COMPUTER: IBM PC compatible			
; OPERATING SYSTEM: PC-DOS/MS-DOS			
; SOFTWARE: Word Perfect 6.1 for Windows/MS-DOS 6.2			
; CURRENT APPLICATION DATA:			
; APPLICATION NUMBER: US/09/023,655			
; FILING DATE: HERewith			
; CLASSIFICATION:			
; PRIOR APPLICATION DATA:			
; APPLICATION NUMBER:			
; FILING DATE:			
; CLASSIFICATION:			
; ATTORNEY/AGENT INFORMATION:			
; NAME: Zeller, Karen J.			
; REGISTRATION NUMBER: 37,071			
; REFERENCE/DOCKET NUMBER: PA-0001 US			
; TELECOMMUNICATION INFORMATION:			
; TELEPHONE: (650) 855-0555			
; TELEFAX: (650) 845-4166			
; INFORMATION FOR SEQ ID NO: 1374:			
; SEQUENCE CHARACTERISTICS:			
; LENGTH: 1801 base pairs			
; TYPE: nucleic acid			
; STRANDEDNESS: single			
; TOPOLOGY: linear			
; IMMEDIATE SOURCE:			
; LIBRARY: GENBANK			
; CLONE: g36632			
US-09-023-655-1374			
Alignment Scores:			
Pred. No.: 1.51e-141 Length: 1801			
Score: 1250.00 Matches: 246			
Percent Similarity: 66.04% Conservative: 71			

Best Local Similarity: 51.25% Mismatches: 145
 Query Match: 45.24% Indels: 18
 DB: 4 Gaps: 9

US-10-729-807-10 (1-513) x US-09-023-655-1374 (1-1801)

QY 1 MetLysArgLeuLeuLeuLeuCysLeuPhePheLeuThrPheSerSerAlaPheProLeu 20
 DB 44 ATGAGAGTCTTCCATCTACTGTTGCTGTGCGGAGTTTGTCTCAGCCCTATCCATTG 103
 QY 21 ValArgMetThrGluAsnGluGlu---AsnMetGlnLeuAlaGlnAlaTyrLeuAsnGln 39
 DB 104 GATGGAGCTGCAAGGGGTAGGACACAGCATGAACCTTGTTCAGAAATATCTAGAAAC 163
 QY 40 PheTyrSerLeuGluLeuGluGlnAsnHisLeuValGlnSerLysAsnArgSerLeuLeu 59
 DB 164 TACTACGACTCAAAAGAGATGTGAAACAGTGTGTTAGGAGAAAGGACAGTGTCTCTGT 223
 QY 60 AspAspLysIleArgGluMetGlnAlaPhePheGlyLeuThrValThrGlyLysLeuAsp 79
 DB 224 GTTAAATAATCCGAGAAATGCAAGATTCCTTTGGATTGGAGGTGACGGGAAAGCTGGAC 283
 QY 80 SerAsnThrLeuGluLeuMetLysThrProArgCysGlyValProAspValGlyGlnTyr 99
 DB 284 TCCGACACTCTGAGGTGATGCGCAAGCCAGGTGTGGAGTCTCTGATGTGTCTCACTTC 343
 QY 100 GlyTyrThrLeuProGly-----TyrArgLysTyrAsnLeuThrTyrArgIleIle 116
 DB 344 ---AGAACCTTCTCTGTCATCCCGAGTGGAGGAGAAACCCACCTTACATACAGAGTTGTG 400
 QY 117 AsnTyrThrProAspMetAlaArgAlaAlaValAspGluAlaIleGlnGluGlyLeuGlu 136
 DB 401 AATTATACACCATTTGCCAAGATGCTGTTGATTCCTGCTGTGTGAGAAAGCTCGAAA 460
 QY 137 ValTyrSerLysValThrProLeuLysPheThrLysIleSerLysGlyIleAlaAspIle 156
 DB 461 GTCTGGAGAGGTGACTCCACTCACATCTCCAGGCTGTATGAGGAGAGGCTGATATA 520
 QY 157 MetIleAlaPheArgThrArgValHisGlyArg---CysProArgTyrPheAspGlyPro 175
 DB 521 ATGATCTCTTTGTCAGTTAGAGACATGAGACTTTTACCCT-----TTTGATGGACCT 574
 QY 176 LeuGlyValLeuGlyHisAlaPheProGlyProGlyLeuGlyGlyAspThrHisPhe 195
 DB 575 GGAATATTTTGGCCCATGCTACTGCTCCCTGGGCGAGGATTAATGGAGATGCCACTTT 634
 QY 196 AspGluAspGluAsnThrThrLysAspGlyValaGlyPheAsnLeuPheLeuValAlaAla 215
 DB 635 GATGATGATGAACATGACAAAGATACACAGGACCAATTTATTTCTCGTTGCTGCT 694
 QY 216 HisGluPheGlyHisAlaLeuGlyLeuSerHisSerAsnAspGlnThrAlaLeuMetPhe 235
 DB 695 CATGAATTTGGCCACTCCCTGGGTCTCTTTCACTCAGCCCAACACTGAAGCTTTTGATGAC 754
 QY 236 ProAsnTyrValSerLeu---AspProArgLysTyrProLeuSerGlnAspAspIleAsn 254
 DB 755 CCATCTATCACTCACTCAACAGACTGACTCGGTTCGCTCTCAAGATGATATAAT 814
 QY 255 GlyIleGlnSerIleTyrGly-----GlyLeuProLysValProAla 269
 DB 815 GGCATTGATCTCTATGACCTCCCTGACTCCCTGAGACCCCTGCTGATCCACAG 874
 QY 269 Lys-----ProLysGluProThrIleProHisAlaCysAspProAspLeuThrPheAsp 286
 DB 875 GAACCTGTCTCCAGAACCTGGGACGCCCAACTGTGATCTGCTGTCTCTGCTTGTAT 934
 QY 287 AlaIleThrThrPheArgArgValMetPhePheLysGlyArgHisLeuTyrArgIle 306
 DB 935 GCTGTGAGACTCTGAGGGGAGAAATCTGTATCTTTAAGACAGGCACTTTTGGCGCAA 994
 QY 307 TyrTyrAspIleThrAspValGluPheGluLeuIleAlaSerPheThrProSerLeuPro 326
 DB 995 TCCCTCAGGAAGCTTGAACCTGAATTGCAATTTGATCTCTCTCATTTTGGCCATCTCTCT 1054

QY 327 AlaAspLeuGlnAlaAlaTyrGlu---AsnProArgAspLysIleLeuValPheLysAsp 345
 DB 1055 TCAGCGGTGATGCCGATCATGAAGTTACTAGCAGGAGCTCGTTTTCATTTTAAAGGA 1114
 QY 346 GluAsnPheTyrMetIleArgGlyTyrAlaValLeuProAspTyrProLysSerIleHis 365
 DB 1115 ATCATTTCTGGCCCATCAGAGGAATGAGGTACGAGCTGGATACCCCAAGAGCATCCAC 1174
 QY 366 ThrLeuGlyPheProGlyArgValLysLysIleAspAlaValCysAspLysThrThr 385
 DB 1175 ACCTAGGTTTCCCTCCACCGGTGAGGAAATCGATGCGAGCCATTTCTGATAAGGAAAAG 1234
 QY 386 ArgLysThrTyrPhePheValGlyIleTyrCysTyrArgPheAspGluMetThrGlnThr 405
 DB 1235 AACAAACATATTTCTTTGAGGACAAATACTGGAGATTGTGATGAGAGAAATTC 1294
 QY 406 MetAspLysGlyPheProGlnArgValValLysHisPheProGlyIleSerIleArgVal 425
 DB 1295 ATGGAGCCAGGCTTTCACCAAGCAATAGCTGAAGACTTTCAGGGATTCAGTCAAGATT 1354
 QY 426 AspAlaAlaPheGlnTyrLysGlyPhePhePhePheSerArgLysSerLysGlnPheGlu 445
 DB 1355 GATGCTGTTTGAAGAATTTGGGTTCTTTATTTCTTACTGGATCTTCACAGTTGGAG 1414
 QY 446 TyrAsnIleLysThrLysAsnIleThrArgIleMetArgThrAsnThrTyrPheGlnCys 465
 DB 1415 TTGGACCAATGCCAAGAAAGTGACACACTTTGAGAGATTAACAGCTGGCTTAATGT 1474

RESULT 6

US-08-229-515A-12
 ; Sequence 12, Application US/08229515A
 ; Patent No. 5518885
 ; GENERAL INFORMATION:
 ; APPLICANT: RAZIUDIN
 ; APPLICANT: SARKAR, FAZLUL H
 ; TITLE OF INVENTION: ERBB2 PROMOTER BINDING PROTEIN IN
 ; TITLE OF INVENTION: NEOPLASTIC DISEASE
 ; NUMBER OF SEQUENCES: 19
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: NEEDLE & ROSENBERG PC
 ; STREET: 127 Peachtree Street, Suite 1200
 ; CITY: Atlanta
 ; STATE: Georgia
 ; COUNTRY: usa
 ; ZIP: 30303
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: PatentIn Release #1.0, Version #1.30
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/229,515A
 ; FILING DATE: 19 APR 1994
 ; CLASSIFICATION: 435
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: PERRYMAN, DAVID G
 ; REGISTRATION NUMBER: 33,438
 ; REFERENCE/DOCKET NUMBER: 1414.608
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: 404-688-0770
 ; TELEFAX: 404-688-9880
 ; INFORMATION FOR SEQ ID NO: 12:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 1717 base pairs
 ; TYPE: nucleic acid
 ; STRANDEDNESS: single
 ; TOPOLOGY: linear
 ; US-08-229-515A-12

Alignment Scores: 2.56e-135 Length: 1717
 Pred. No.: 1198.50 Matches: 243
 Score:

Percent Similarity: 64.24% Conservative: 66
Best Local Similarity: 50.52% Mismatches: 151
Query Match: 43.38% Indels: 21
DB: 1 Gaps: 9

US-10-729-807-10 (1-513) x US-08-229-515A-12 (1-1717)

QY 1 MetLysArgLeuLeuLeuLeuLeuLeuLeuPhePheIleThrPheSerSerAlaPheProLeu 20
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QY 21 -----ValArgMetThrGluAsnGluGluAsnMetGlnLeuAlaGlnAlaTyrLeu 37
DB CATGGGCGAGTGAGA-----CAAGACCACTCAACCATGGATCTTGGCTCAGCAATACCTA 151
QY 38 AsnGlnPheTyrSerLeuGluLeuGluLeuGluLeuValGlnSerLysAsnArgSer 57
DB GAAATAATCTACCACTTTAGAAAAAATGAGAAACAAATTTTCAAAAGAAAGACAGTAGT 211
QY 58 LeuIleAspAspLysLeuLeuLeuMetGlnAlaPhePheGlyLeuThrValThrGlyLys 77
DB 212 CTGTGTCTCAAAAATTTGAGAAATGAGAAATGAGAAATGAGAAATGAGAAATGAGAAAT 271
QY 78 LeuAspSerAsnThrLeuLeuLeuMetLysThrProArgCysGlyValProAspValGly 97
DB 272 CTGGACTCGAACACTGTGGAGATGATGACAGAGCCCGGTGTGGTGTCCCGACCTTGGT 331
QY 98 GlnTyrGlyTyrThrLeuProGly-----TrpArgLysTyrAsnLeuThrTyrArg 114
DB 332 GCGTTCAGT---ACCTTTCAGGTTTCCACCCAAATGGAGGAAAAACCACTCTCTACAGG 388
QY 115 IleIleAsnTyrThrProAspMetAlaArgAlaAlaValAspGluAlaIleGlnGluGly 134
DB 389 ATTGTGAATTATACCTGGATTACCAAGAGAGAGTGGATCTGCCATTGAGAGAGCT 448
QY 135 LeuGluValTyrSerLysValThrProLeuLysPheThrLysIleSerLysGlyIleAla 154
DB 449 TTGAAGGTCTGGAGAGGTGACCCCACTCACTTCTCCAGGATCTCTGAAGGAGAGCT 508
QY 155 AspileMetIleAlaPheArgThrArgValHisGlyArg---CysProArgTyrPheAsp 173
DB 509 GACATAATGATCTCTCTTTCAGTGTGGAGAACATGGAGACTTTTACCT-----TTTGAT 562
QY 174 GlyProLeuGlyValLeuGlyHisAlaPheProGlyProGlyLeuGlyGlyAspThr 193
DB 563 GGAGTGGGACAGACTTGGCTCATGCTCCCTCCACCTGGCTGGATTTTATGGAGATGCT 622
QY 194 HisPheAspGluAspGluAsnThrThrLysAspGlyAlaGlyPheAsnLeuPheLeuVal 213
DB 623 CACTTCGATGATGATGAGAAATGGTCACTGGGACCTTCAGGACCAATTTATCTCTGTT 682
QY 214 AlaAlaHisGluPheGlyHisAlaLeuGlyLeuSerHisSerAsnAspGlnThrAlaLeu 233
DB 683 GCTCGGATGAACCTGGTCACTCCCTGGGTCTCTTTCACTCAAAACAAACAAAGAAATCTCTG 742
QY 234 MetPheProAsnTyr---ValSerLeuAspProArgLysTyrProLeuSerGlnAspAsp 252
DB 743 ATGTACCCAGTCTACAGTTCTCCAGGACCAAGCCAAATTCGCTTCTCAGGATGAT 802
QY 253 IleAsnGlyIleGlnSerIleTyrGlyGlyLeuProLys----- 265
DB 803 ATAGAGGGCATTCATCCCTGTATGGAGCCGCCCTCTCTGATGCCACAGTGTCTCT 862
QY 266 ValProAlaLysProLysGluProThrIleProHisAlaCysAspProAspLeuThrPhe 285
DB 863 GTGCCCTCTGTCTCTCCAAAACCTGAGACCCCACTGCAAAATGTGATCTCTCTCTCTCT 922
QY 286 AspAlaIleThrThrPheArgGluValMetPhePheLysGlyArgHisLeuThrArg 305
DB 923 GATCGACTCACCATGCTCAGAGGGAATCTCTATTTTAAAGACAGACACTTCTGGCGT 982
QY 306 IleTyrTyrAspIleThrAspValGluPheGluLeuIleAlaSerPheThrProSerLeu 325

DB 983 AGAACCCAGTGAATCCCGAGCCTGAATTCATTTGATTTTCAGCATTTTGGCCCTCTCTT 1042
QY 326 ProAlaAspLeuGlnAlaAlaTyrGlu---AsnProArgAspLysIleLeuValPheLys 344
DB 1043 CCTTCAGGCTTAGATGCTGCTATGAGGCAATAAACAAGACAGAGATTCTGATTTTAA 1102
QY 345 AspGluAsnPheTyrMetIleArgGlyTyrAlaValLeuProAspTyrProLysSerIle 364
DB 1103 GGAAGTCAGTCTGGCGCTCCGAGAAATGAAGTCCAAAGCAGGTTTACCAAGAGGATC 1162
QY 365 HisThrLeuGlyPheProGlyArgValLysLysIleAspAlaAlaValCysAspLysThr 384
DB 1163 CACACTCTTGGCTTCTCTCCACCGTGAAGAGATGATGACCTGTTTGTGAAAGGAG 1222
QY 385 ThrArgLysThrTyrPhePheValGlyIleTyrCysTyrPhePheAspGluMetThrGln 404
DB 1223 AAGAAGAAGAGCTATTTCTTGTAGTGACAAATCTCGAGATTGATGAGACAAGACAG 1282
QY 405 ThrMetAspLysGlyPheProGlnArgValLysHisPhePheProGlyIleSerIleArg 424
DB 1283 CTTATGGATAAAGGCTTCCCGAGACTGATTAACAGATGACTTCCCAAGAAATTGAGCCACA 1342
QY 425 ValAspAlaAlaPheGlnTyrLysGlyPhePhePhePheSerArgGlySerLysGlnPhe 444
DB 1343 GTTGATGCTGTGTACATGCTTGGGTTTTTATTTCTTCTGTGGATCATCAGATTTC 1402
QY 445 GluTyrAsnIleLysThrLysAsnIleThrArgIleMetArgThrAsnThrTyrPheGln 464
DB 1403 GAGTTTGACCCCAATGTCAGGACGCTGACACACACTGAAGACGACACAGCTGGCTGTG 1462
QY 465 Cys 465
DB 1463 TGC 1465

RESULT 7
US-08-645-865-12
; Sequence 12, Application US/08645865
; Patent No. 5654406
; GENERAL INFORMATION:
; APPLICANT: RAZIUDIN
; APPLICANT: SARKAR, FAZLUL H
; TITLE OF INVENTION: ERBB2 PROMOTER BINDING PROTEIN IN
; TITLE OF INVENTION: NEOPLASTIC DISEASE
; NUMBER OF SEQUENCES: 19
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: NEEDLE & ROSENBERG PC
; CITY: Atlanta
; STATE: Georgia
; COUNTRY: usa
; ZIP: 30303
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/645,865
; FILING DATE: 14 MAY 1996
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: PERRYMAN, DAVID G
; REGISTRATION NUMBER: 33,438
; REFERENCE/DOCKET NUMBER: 1414.608
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 404-688-0770
; TELEFAX: 404-688-9880
; INFORMATION FOR SEQ ID NO: 12:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1717 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear

336 ---ProArgAspLysIleLeuValPheLysAspGluAsnPheTrpMetIleArgGlyTyr 350
1077 TTTGACAGAGACTCATTTCTCTATTATAAGGCAACCACTACTGGGCTCTGAGTGGCTAT 1136
355 AlaValLeuProAspTyrProLysSerIleHisThrLeuGlyPheProGlyArgValLys 374
1137 GATATTCTGCAAGGTATCCCAAGGATATATCAAACTATGGCTTCCACAGCGTCCAA 1196
375 LysIleAspAlaValCysAspLysThrThrArgLysThrTyrPhePheValGlyIle 394
1197 GCAATTGACGAGCTGTTTCTTACAGAAGT-----AAAACATACTTCTTTGTAATGAC 1250
395 TrpCysTrpArgPheAspGluMetThrGlnThrMetAspLysGlyPheProGlnArgVal 414
1251 CAATTCTGAGATATGATTAACCAAGACAAATTTCATGGAGCCAGGTATATCCAAAGACATA 1310
415 ValLysHisPheProGlyIleSerIleArgValAspAlaAlaPheGlnTyrLysGlyPhe 434
1311 TCAGGTGCCTTTCAGGATAGAGATAGAGATAAGTTGATGTCAGTTTCCAGCAAGAACATTC 1370
435 PhePhePheSerArgGlySerLysGlnPheGluTyrAsnIleLysThrLysAsnIleThr 454
1371 TTCATGCTTCAGTCGACCAAGATATAGCATTTGATCTTATTGCTCAGAGATTACC 1430
455 ArgIleMetArgThrAsnThrTrpPheGlnCysLys 466
1431 AGAGTTGCAAGGCAATAAATGGCTTAAGTCTGAGTAACTGATGAG 1466

RESULT 10
US-09-023-655-1040
; Sequence 1040 Application US/09023655
; Patent No. 6607879
; GENERAL INFORMATION:
; APPLICANT: Cocks, Benjamin G.
; APPLICANT: Susan G. Stuart
; APPLICANT: Jeffrey J. Seilhamer
; TITLE OF INVENTION: COMPOSITION FOR THE DETECTION OF BLOOD CELL GENE
; TITLE OF INVENTION: EXPRESSION
; NUMBER OF SEQUENCES: 1508
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: INCYTE PHARMACEUTICALS, INC.
; STREET: 3174 PORTER DRIVE
; CITY: PALO ALTO
; STATE: CALIFORNIA
; COUNTRY: USA
; ZIP: 94304
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Word Perfect 6.1 for Windows/MS-DOS 6.2
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/023,655
; FILING DATE: HEREWITH
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Zeller, Karen J.
; REGISTRATION NUMBER: 37,071
; REFERENCE/DOCKET NUMBER: EA-0001 US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (650) 855-0555
; TELEFAX: (650) 845-4166
; INFORMATION FOR SEQ ID NO: 1040:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 2223 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear

997 CCCAAACCCCTGTGACCCCGAGTTTGACATTTTGATGCTATCATCCACACATCCCGTGAGAAATA 955

296 MetPhePheLysGlyArgHisLeuTyrArgIleTyrTyrAspIleThrAspValGluPhe 315

957 CTTTCTTTTAAAGACAGACTACTCTGGAGAGGCGATCCTCAGCTACAAAGAGTGCMAATG 1016

316 GluLeuIleAlaSerPheTyrProSerLeuProAlaAspLeuGlnAlaAlaTyrGluAsn 335

1017 AATTTTATTCTCTATTCTGCGCCATCCCTCCAACTGCTATACAGGCTGCTTATGAAGAT 1076

336 ---ProArgAspLysIleLeuValPheLysAspGluAsnPheTyrMetIleArgGlyTyr 354

1077 TTTGACAGACAGCTCAATTTTCTATTTTAAAGGCCAACCAATACTGGGCTCTGAGTGGCTAT 1136

355 AlaValLeuProAspTyrProLysSerIleHisThrLeuGlyPheProGlyArgValLys 374

1137 GATATCTGCAAGGTATCCCAAGGATATATCAAACTATGGCTTCCCGACAGCGGCCAA 1196

375 LysIleAspAlaAlaValCysAspLysThrArgLysThrTyrPhePheValGlyLe 394

1197 GCAATTCAGCGAGCTGTTTCTACAGAAGT-----AAACATACTTCTTTGTAATGAC 1250

395 TrpCysTrpArgPheAspGluMetThrGlnThrMetAspLysGlyPheProGlnArgVal 414

1251 CAATTCGGAGATATGATAACCAAGACAATTCATGGAGCCAGGTTTATCCCAAAGACATA 1310

415 ValLysHisPheProGlyIleSerIleArgValAspAlaAlaPheGlnTyrLysGlyPhe 434

1311 TCAGGTGCTTTCCAGGAAATAGAGATTAAGTGTATGATCAGTTTCCAGCAAGAACATTC 1370

435 PhePhePheSerArgGlySerLysGlnPheGluTyrAsnIleLysThrLysAsnIleThr 454

1371 TTCATGCTTCAGTGGACCAAGATATTACGCATTTGATCCTTATGCTCAGAGAGTTACC 1430

455 ArgIleMetArgThrAsnThrTyrPheGlnCysLys 466

1431 AGAGTTGCAAGGCGCAATAAATGCTTAACGTGAGA 1466

RESULT 11

US-09-484-970B-62

Sequence 62, Application US/09484970B

Patent No. 6426186

GENERAL INFORMATION:

APPLICANT: Jones, Karen A.

APPLICANT: Volkmut, Wayne

APPLICANT: Walker, Michael G.

TITLE OF INVENTION: BONE REMODELING GENES

FILE REFERENCE: PB-0014 US

CURRENT APPLICATION NUMBER: US/09/484,970B

CURRENT FILING DATE: 2000-01-18

NUMBER OF SEQ ID NOS: 172

SOFTWARE: PERL Program

SEQ ID NO 62

LENGTH: 1981

TYPE: DNA

ORGANISM: Homo sapiens

FEATURE:

NAME/KEY: misc feature

OTHER INFORMATION: Incyte ID No. 6426186 245334.1

US-09-484-970B-62

Alignment Scores:

Pred. No.: 9 61e-130 Length: 1981

Score: 1153.50 Matches: 232

Percent Similarity: 66.31% Conservative: 77

Best Local Similarity: 49.79% Mismatches: 146

Query Match: 41.75% Indels: 11

DB: 4 Gaps: 8

US-10-729-807-10 (1-513) x US-09-484-970B-62 (1-1981)

Qy 7 LeuCysLeuPheIleThrPheSerSerAlaPheProLeuValArgMetThrGluAsn 26

Db 104 CTGCTGCTGTTCTGGGGTGTGTGTCTCACAGCTTCCAGCGACTCTAGAAACACAA --- 160
QY 27 GluGluAsnMetGlnLeuAlaGlnAlaTyrLeuAsnGlnPheTyrSerLeuGluLeuGlu 46
Db 161 GAGCAAGATGTGGACTTAGCTCAGAAATACCTGGAAATATACCAACCTGGAAGATGAT 220
QY 47 GlyAsnHisLeuValGlnSerLysAsnArgSerLeuLeuAspLysIleArgGluMet 66
Db 221 GGGAGGCAAGTTTGAAGCGGAGAAATAGTGGCCCGAGTGTGTTGAATAATTAAGCAATG 280
QY 67 GlnAlaPhePheGlyLeuThrValThrGlyLysLeuAspSerAsnThrLeuGluLeuMet 86
Db 281 CAGGAATTTCTTGGGCTGAAAGTGAATGCGGAAACCAAGATGCTCAACCCCTGGAAGTGTG 340
QY 87 LysThrProArgCysGlyValProAspValGlyGlnTyrGlyTyrThr ---LeuPro 104
Db 341 AAGCAGCCAGATGTGGAGTGTGATGTGGTGTGCTGCTCCTCAGCGGGAGAACCT 400
QY 105 GlyTyrArgLysTyrAsnLeuThrTyrArgIleIleAsnTyrThrProAspMetAlaArg 124
Db 401 CCTGGGAGCAACACATCTGACATGACATGACATGACATGACATGACATGACATGACAT 460
QY 125 AlaAlaValAspGluAlaIleGlnGlyLeuGluValTyrSerLysValThrProLeu 144
Db 461 GCAGATGTGACCATGCCATTCAGAAAGCCTTCCAACTCTGGAGTAATGTCAACCTCTG 520
QY 145 LysPheThrLysIleSerLysGlyIleAlaAspIleMetIleAlaPheArgThrArgVal 164
Db 521 ACATTCACCAAGTCTCTGAGGCTCAAGGAGCATCATCATCATCATCATCATCATCATCAT 577
QY 165 HisGlyArgCysProArgTyrPheAspGlyProLeuGlyValLeuGlyHisAlaPhePro 184
Db 578 GATCATCGGAGCAACTCTCTTTTGTATGAGACCTGGAGGAACTTCTCTATGCTTTTCAA 637
QY 185 ProGlyProGlyLeuGlyGlyAspThrHisPheAspGluAspGluAsnTrpThrLysAsp 204
Db 638 CCAGGCCCAAGTATTGGAGGGATGCTCATTTTGTATGAGACCTGGAGGAACTTCTCTATGCTTTTCAA 697
QY 205 GlyAlaGlyPheAsnLeuPheLeuValAlaAlaHisGlyPheGlyHisAlaLeuGlyLeu 224
Db 698 TTCAGAGATACAACTATCATCGTGTGGGCTCATGAACTCGGCCATTTCTCTTGGACTC 757
QY 225 SerHisSerAsnAspGlnThrAlaLeuMetPheProAsnTyrVal ---SerLeuAspPro 243
Db 758 TCCCATTTACTGATATCGGGCTTTGTATGATGATGATGATGATGATGATGATGATGAT 817
QY 244 ArgLysTyrProLeuSerGlnAspIleAsnGlyIleGlnSerIleTyrGlyGlyLeu 263
Db 818 CAG-----CTAGCTCAGGATGACATTTGATGATGATGATGATGATGATGATGATGAT 865
QY 264 ProLysValProAlaLysProLysGluProThrIleProHisAlaCysAspProAspLeu 283
Db 866 TCCCAAAATCCTGTCAGCCCATCGGCCCAACAAACCCCAAGCGGTGACAGTAAGCTA 925
QY 284 ThrPheAspAlaIleThrPheArgArgGluValMetPhePheLysGlyArgHisLeu 303
Db 926 ACCTTTGATGCTATACTAGATTCGGGAGAGTGTGTTCTTTAAAGACAGATTTCTAC 985
QY 304 TrpArgIleTyrTyrAspIleThrAspValGluPheGluLeuIleAlaSerPheTrpPro 323
Db 986 ATCGGCACAAATCCCTTCTACCGGGAAGTTGAGCTCAATTTTCAATTTCTGTTTCTGGCCA 1045
QY 324 SerLeuProAlaAspLeuGlnAlaTyrGlu ---AsnProArgAspLysIleLeuVal 342
Db 1046 CAACTGCCAAATCGGCTTGAAGCTGTCTTACGAATTTGCCGACAGATGAATGCCGTTT 1105
QY 343 PheLysAspGluAsnPheTrpMetIleArgGlyTyrAlaValLeuProAspTyrProLys 362
Db 1106 TTCAAAGGAATTAAGTACTGCTGTTTCGGGACAGAAATGTGTACACGATACCCCAAG 1165
QY 363 SerIleHis ---ThrLeuGlyPheProGlyArgValLysIleAspAlaValCys 381
Db 1166 GACATCTACAGCTCCTTTGGCTTTCCCTTAGAACTGTGAAGCATATCATGCTGCTCTTCT 1225

QY 382 AspLysThrThrArgLysThrTyrPhePheValGlyIleTyrCysTyrArgPheAspGlu 401
Db 1226 GAGGAAACACCTGGAAACACCTCTCTTTGTTGTACAAATATCTGGAGGTATGATGAA 1285
QY 402 MetThrGlnThrMetAspLysGlyPheProGlnArgValValLysHisPheProGlyIle 421
Db 1286 TATAAACGATCTATGATCCAGGTTATCCCAAAATGATAGCACATGACTTCTCTGGAAT 1345
QY 422 SerIleArgValAspAlaAlaPheGlnTyrLysGlyPhePhePhePheSerArgGlySer 441
Db 1346 GCCCAACAAGTTGATGCACTTTTCATGAAAGATGATTTCTTATTTCTTCATGGAACA 1405
QY 442 LysGlnPheGluTyrAsnIleLysThrLysAsnIleThrArgIleMetArgThrAsnThr 461
Db 1406 AGACATACAAATTTGATCTTAAACAGAGAGAAATTTGACTCTCCAGAAAGTAATAGC 1465
QY 462 TrpPheGlnCysLysGlu 467
Db 1466 TGGTTCACTGCAGGAAA 1483

RESULT 12
US-08-068-392-1
; Sequence 1, Application US/08068392
; Patent No. 6150152
; GENERAL INFORMATION:
; APPLICANT: Shaparo, Steven M.
; TITLE OF INVENTION: Human Macrophage Metalloproteinase
; NUMBER OF SEQUENCES: 3
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Scott J. Meyer, Monsanto Co., A3SM
; STREET: 800 N. Lindbergh Blvd.
; CITY: St. Louis
; STATE: Missouri
; COUNTRY: USA
; ZIP: 63167
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; FILING DATE: 19930528
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Meyer, Scott J.
; REGISTRATION NUMBER: 25275
; REFERENCE/DOCKET NUMBER: 07-24 (12406) A
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (314)694-3117
; TELEFAX: (314)694-5435
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1410 base pairs
; TYPE: NUCLEIC ACID
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 1..1410
US-08-068-392-1

Alignment Scores:
Pred. No.: 1,72e-127 Length: 1410
Score: 1133.00 Matches: 229
Percent Similarity: 64.56% Conservative: 77
Best Local Similarity: 48.31% Mismatches: 152
Query Match: 41.01% Indels: 16
DB: 3 Gaps: 10

US-10-729-807-10 (1-513) x US-08-068-392-1 (1-1410)

Percent Similarity:	64.56%	Conservative:	77
Best Local Similarity:	48.31%	Mismatches:	15
Query Match:	41.01%	Indels:	16
DB:	3	Gaps:	10

US-10-729-807-10 (1-513) x US-08-396-988-1 (1-1410)

Qy	3	ArgLeuLeuLeuLeuCysLeuPhePheIleThrPheSerSerAlaPheProLeuValArg	22
Db	4	AAGTTCTTCTAATATCGCTCGCAGGCCACTGCTCTTGAGAGCTCTCCCTCGAACACG	63
Qy	23	MetThrGluAsnGluAsnMetGlnLeu--AlaGlnAlaTyrlauAsnGlnPheTyr	41
Db	64	TCTACAGCGCTGGAAAAATAATGTGCTATTGTTGGTGAGAGATACCTTAGAAAAATTTAT	123
Qy	42	SerLeuGluIleGluGlyAsnHisLeuValGlnSerLysAsnArg-----SerLeu	58
Db	124	GGCCTTGAGAVA-----AACAAATTCACAGTGACAAAATGAATATAGTGCAAACTTA	177
Qy	59	IleAspAspLyIleArgGluMetGlnAlaPhePheGlyLeuThrValThrGlyLysLeu	78
Db	178	ATGAAGGAAGAANAATCCAAGAAATGACAGCACTTCTTGGGTCTGAAAGTGACCGGGCAACTG	237
Qy	79	AspSerAsnThrLeuGluIleMetLysThrProArgCysGlyValProAspValGlyGln	98
Db	238	GACACATCTACCCTGGAGATGATGCAGCACCTCGATGTGGAGTCCCCGATGTCATCAT	297
Qy	99	TyrGlyTyrThrLeuProGly-----TrpArgLysTyrAsnLeuThrTyrArgIle	115
Db	298	TTC---AGGGAATATCCACAGGGGGCCGCTATGCGAGGAACAATATATCATCACTACAGAAATC	354
Qy	116	IleAsnTyrThrProAspMetAlaArgAlaAlaValAspGluAlaIleGlnGluGlyLeu	135
Db	355	AATAATTACACACCTGCATGAACCGTGAGGATGTGACTACGCAATCGGAAAGCTTTC	414
Qy	136	GluValTrpSerLysValThrProLeuLysPheThrLysIleSerLysGlyIleAlaAsp	155
Db	415	CAAGTATGAGTAATGTTACCCCCTGAAATTCAGCAAGATTAACACAGCATGGCTGAC	474
Qy	156	IleMetIleAlaPheArgThrArgValHisGlyArgCysProArgTyrPheAspGlyPro	175
Db	475	ATTTGGTGTTTTTGCCGTGGAGCTCATGGAGACTTC---CATGCTTTTGATGGCAA	531
Qy	176	LeuGlyValLeuGlyHisAlaPheProGlyProGlyLeuGlyGlyAspThrHisPhe	195
Db	532	GGTGAATCCTAGCCATGCTTTTGGACCTGATCTGGCATTTGGAGGGGATGCATATTC	591
Qy	196	AspGluAspGluAsnTrpThrLysAspGlyAlaGlyPheAsnLeuPheLeuValAla	215
Db	592	GATGAGGACGAATCTCGACATACACATTCAGGAGGACCAAACTGTGCTCTCACTGCTGT	651
Qy	216	HisGluPheGlyHisAlaLeuGlyLeuSerHisSerAsnAspGlnThrAlaLeuMetPhe	235
Db	652	CACGAGATTGGCCATTCTTAGTCTTGCCATTCTAGTGATCCAAAGGCTGTAATGTC	711
Qy	236	ProLeuTyrValSerLeuAspProArgLysTyrProLeuSerGlnAspAspIleAsnGly	255
Db	712	CCCACCTCAAAATATGTCGACATCAACACATTTCCGCTCTCTGCTGATGACATACGTGGC	771
Qy	256	IleGlnSerIleTyrGlyLeuProLysValProAlaLeuProLysGluPro-----	273
Db	772	ATTGATCCCTGTATGGAGAC---CCAAAGAGAACCCACGCTTGCCTCAATCTGACAAAT	828
Qy	274	ThrIleProHisAlaCysAspProAspLeuThrPheAspAlaIleThrThrPheArgArg	293
Db	829	TCAGAACACAGCTCTCTGTGACCCCAATTTGAGTTTTGATGCTGTCTCACTACCGTGGAAAT	888
Qy	294	GluValMetPhePheLysGlyArgHisLeuTrpArgIleTyrTyrAspIleThrAspVal	313
Db	889	AAGATCTTTTCTTCAAGACAGGGTCTCTGGCTGAAGGTTTCTTGAGAGACCAAGACC	948
Qy	314	GluPheGluLeuIleAlaSerPheTrpProSerLeuProAlaAspLeuGlnAlaIleTyr	333

RESULT 14

RESCHI 14
US-08-994-689C-18

03 08 2024 002C 18
; Sequence 18, Application US/08994689C

; Patent No. 6613958

; GENERAL INFORMATION:

APPLICANT: Neuhold, Lisa

APPLICANT: Killar, Loran

; TITLE OF INVENTION: TRANSGENIC ANIMAL MODEL FOR

; TITLE OF INVENTION: DEGENERATIVE DISEASES OF CARTILAGE

; NUMBER OF SEQUENCES: 21

; CORRESPONDENCE ADDRESS:

; ADDRESS: Darby & Darby PC

STREET: 805 Third Avenue

CITY: New York

STATE: NY
COUNTY: ROCK

COUNTRY: U.
ZIP: 10033

; ZIP: 10022
; COMPUTER READABLE FORM.

```

; COMPUTER READABLE FORM:
;
; MEDTIM TYPE: Diskette

```

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; MEDIUM TYPE: DISKETTE
: : IBM COMPATIBLE

```

```

; IBM COMPATIBLE
; OPERATING SYSTEM: DOS

```

OPERATING SYSTEM: DOS
SOFTWARE: FastSEO for Windows Version 2.0

```

; SOFTWARE:  FASTSEQ 101
;
; CURRENT APPLICATION DATA:

```

; CONSENT ALL INFORMATION DATA.
; APPLICATION NUMBER: US/08/994,689C

FILING DATE: 1997-12-10

CLASSIFICATION: 800

;
;
PRIOR APPLICATION DATA:

APPLICATION N

FILING DATE:

ATTORNEY/AGENT INFORMATION:

```
; NAME: Green, Reza
```

; REGISTRATION NUMBER: 38,475

REFERENCE/DOCKET NUMBER: 0630/0D532

TELECOMMUNICATION INFORMATION:
 TEL. EDICONT 012 527 7700

TELEPHONE: 212-527-7700
TELEFAX: 212-762-6337

TELEFAX: 212-753-6237
TELEFAX: 236687

TELEX: 236687
INFORMATION FOR SEQ ID NO: 18.

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; INFORMATION FOR SEQ ID NO:
: SEQUENCE CHARACTERISTICS:

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; SEQUENCE CHARACTERISTICS:
; LENGTH: 1521 base pairs

NAME: nucleic acid

STRANDEDNESS: since

TOPOLOGY: linear

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; MOLECULE TYPE: cDNA
US-08-994-689C-18

Alignment Scores:
Pred. No.: 2,58e-127 Length: 1521
Score: 1132.00 Matches: 221
Percent Similarity: 63.45% Conservative: 62
Best Local Similarity: 49.55% Mismatches: 151
Query Match: 40.97% Indels: 12
DB: 4 Gaps: 8

US-10-729-807-10 (1-513) x US-08-994-689C-18 (1-1521)

Qy 26 AsnGluGluAsnMetGlnLeuAlaAlaTyrLeuAsnGlnPheTyr---SerLeuGlu 44
Db 98 TCTGAGAAAGACCTCCAGCTTTGCGAGCGCTTACCTGAGATCATATACCAATCTTACAAAT 157
Qy 45 IleGluGlyAsnHisLeuValGlnSerLysAsnArgSerLeuIleAspAspLysIleArg 64
Db 158 CTCGGGGA-----ATCCTGAAGGAGNATGCAGCAAGCTCCATGACTGAGAGGCTCGGA 211
Qy 65 GluMetGlnAlaPhePheGlyLeuThrValThrGlyLysLeuAspSerAsnThrLeuGlu 84
Db 212 GAAATGCACTTTCTTTCGGCTTAGAGGTGACTGCGCAAACTTGACGATAACACCTTAGAT 271
Qy 85 IleMetLysThrProArgCysGlyValProAspValGlyGlnTyrGlyTyr----- 101
Db 272 GTCATGAAAGCAAGCAAGATCGGGGTGTGCTGATGGTGAAATACAAATGTTTCCCTCGA 331
Qy 102 ThrLeuProGlyTrpArgLysTyrAsnLeuThrTyrArgIleIleAsnTyrThrProAsp 121
Db 332 ACTCTTAA---TGGTCCAAATGAATTAACCTACAGATTGGAATTACACCCCTGAT 388
Qy 122 MetAlaArgAlaAlaValAspGluAlaIleGlnGluGlyLeuGluValTrpSerLysVal 141
Db 389 ATGACTCATTTCTGAAGTCGAAAGGCAATTCAAAAAGCCCTTCAAGATTGTCGCGATGA 448
Qy 142 ThrProLysPheThrLysIleSerLysGlyLeuAlaPheIleMetIleAlaPheArg 161
Db 449 ACTCTCTGAATTTTACAGATTTTACAGATGGCAATGCTGACATCATGATCTCTTTTGA 508
Qy 162 ThrArgValHisGlyArg--CysProArgTyrPheAspGlyProLeuGlyValLeuGly 180
Db 509 ATTAAGGAGCATGCGGACTTCTACCCA-----TTTGATGGCCCTCTGGCTGCTGCT 562
Qy 181 HisAlaPheProGlyProGlyLeuGlyAspThrHisPheAspGluAspGluAsn 200
Db 563 CATGCTTTTCTCTCGGCCCAATATTATGGAGGAGATGCCCAATTTTGATGATGATGAAACC 622
Qy 201 TrpThrLysAspGlyAlaGlyPheAsnLeuPheLeuValAlaAlaHisGluPheGlyHis 220
Db 623 TGGCAAGTAGTTCAAAGGCTCAACACTTTTCTGTGCTGCGATGAGTTCGGCCAC 682
Qy 221 AlaLeuGlyLeuSerHisSerAsnAspGlnThrAlaLeuMetPheProAsnTyrValSer 240
Db 683 TCCTTAGTCTTGACCACTCCAGGACCTCGAGCACTCATGTTTCTTATCTACACCTAC 742
Qy 241 LeuAspProArgLysTyrProLeuSerGlnAspIleAsnGlyIleGlnSerIleTyr 260
Db 743 ACCGGCAAAAGCCACTTTATCTCTGATGACGATGTACAAAGGATCCAGTCTCTCTAT 802
Qy 261 GlyGlyLeuProLysValProAlaLysProLysGluProThrIleProHisAlaCysAsp 280
Db 803 GGTCCAGGAGATGAAGACCCC---AACCTTAACATCCAAAACGCCAGCAAAATGTGAC 859
Qy 281 ProAspLeuThrPheAspAlaIleThrThrPheArgArgGluValMetPhePheLysGly 300
Db 860 CTTTCTTATCCCTTGATGCCATTACCACTCCGAGGAGAAACATGATCTTTAAAGAC 919
Qy 301 ArgHisLeuThrArgIleTyrTyrAspIleThrAspValGluPheGluLeuIleAlaSer 320
Db 920 AGATTCTCTGGCGCTGCATCCTCAGCAGGTGATGCGGAGCTGTTTAAACGAAATCA 979

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Qy 321 PheTrpSerLeuProAlaAspLeuGluAlaAlaTyrGluAsnPro---ArgAspLys 339
Db 980 TTTTGGCCAGAACTTCCCAACCGTATTGATGCTGCATATGAGCACCTTCTCATGACCTC 1039
Qy 340 IleLeuValPheLysAspGluAsnPheTrpMetIleArgGlyTyrAlaValLeuProAsp 359
Db 1040 ATCTTCATCTTCAGAGGTAGAAAATTTTGGCTCTTAATGGTTATGACATCTCGAAGGT 1099
Qy 360 TyrProLysSerIleHisThrLeuGlyPheProGlyArgValLysLysIleAspAlaAla 379
Db 1100 TATCCCAAAAAATATCTGAACCTGGGTCTTCCAAAAGAAAGTTAAGAAGATAAGTGCAGCT 1159
Qy 380 ValCysAspLysThrThrArgLysThrTyrPhePheValGlyIleTyrCysTyrArgPhe 399
Db 1160 GTTCATCTTGGAGNATACAGCAAGACTCTCTGTCTCAGAAACACGAGTCTGGAGATAT 1219
Qy 400 AspGluMetThrGlnThrMetAspLysGlyPheProGlnArgValValLysHisPhePro 419
Db 1220 GATGATACTAACCATAATTATGATAAAGACTATCCGAGACTAATAGAAGAAGACTTCCCA 1279
Qy 420 GlyIleSerIleArgValAspAlaAlaPheGlnTyrLysGlyPhePhePheSerArg 439
Db 1280 GGAATTCGTGATAAAGTAGATGCTCTCTATGAGAAAATGTTATATCTATTTTCAAC 1339
Qy 440 GlySerLysGlnPheGluTyrAsnIleLysThrLysAsnIleThrArgIleMetArgThr 459
Db 1340 GGACCCATACAGTTTGAATACAGCATCTGGAGTAACCGTATTTGTCGGTCTATCCAGCA 1399
Qy 460 AsnThrTrpPheGlnCys 465
Db 1400 AATTCATTTTGTGGTGT 1417

RESULT 15
US-08-994-689C-8
; Sequence 8, Application US/08994689C
; Patent No. 6613958
; GENERAL INFORMATION:
; APPLICANT: Neuhold, Lisa
; APPLICANT: Killar, Loran
; TITLE OF INVENTION: TRANSGENIC ANIMAL MODEL FOR
; TITLE OF INVENTION: DEGENERATIVE DISEASES OF CARTILAGE
; NUMBER OF SEQUENCES: 21
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Darby & Darby PC
; STREET: 805 Third Avenue
; CITY: New York
; STATE: NY
; COUNTRY: USA
; ZIP: 10022
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FASTSEQ for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/994,689C
; FILING DATE: 1997-12-19
; CLASSIFICATION: 800
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Green, Reza
; REGISTRATION NUMBER: 38,475
; REFERENCE/DOCKET NUMBER: 0630/0D532
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 212-527-7700
; TELEFAX: 212-753-6237
; TELEX: 236687
; INFORMATION FOR SEQ ID NO: 8:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 2792 base pairs
; TYPE: nucleic acid

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; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
US-08-994-689C-8

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Alignment Scores:

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Pred. No.: 6,91e-127 Length: 2792
Score: 1132.00 Matches: 221
Percent Similarity: 63.45% Conservative: 62
Best Local Similarity: 49.55% Mismatches: 151
Query Match: 40.97% Indels: 12
DB: 4 Gaps: 8

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US-10-729-807-10 (1-513) x US-08-994-689C-8 (1-2792)

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DB 595 TCTGAGGAAGACCTCCAGTTTGCAGAGCGCTACTGAGATCATACTACCAAT 654
QY 45 IleGluGlyAsnHisLeuValGlnSerLysAsnArgSerLeuIleAspAspLysIleArg 64
DB 655 CTCGGGGGA-----ATCTGAAGGAGAGATGCAGCAAGCTCCATGACTGAGAGGCTCCGA 708
QY 65 GluMetGlnAlaPhePheGlyLeuThrValThrGlyLysLeuAspSerAsnThrLeuGlu 84
DB 709 GAAATGCAGCTCTTCTTCGCTTAGAGGTGACTGGCAAACTTGACGATTAACACCTTAGAT 768
QY 85 IleMetLysThrProArgCysGlyValProAspValGlyGlnTyrGlyTyr----- 101
DB 769 GTCATGAAAAAGCAAGATGCGGGGTTGTCGATGTGGGTGAATACAAATGTTTTCCCTCGA 828
QY 102 ThrLeuProGlyTyrArgLysTyrAsnLeuThrTyrArgIleIleAsnTyrThrProAsp 121
DB 829 ACTCTTAA--TGGTCCAAATGAATTTAACTCAGAAATGTGGAATTAACACCCCTGAT 885
QY 122 MetAlaArgAlaAlaValAspGluAlaIleGlnGluGlyLeuGluValTyrSerLysVal 141
DB 886 ATGACTCATCTGAGTGCAGAAAGGCAATTCAMAAAGCCCTCAAAAGTTTGGTCCGATGA 945
QY 142 ThrProLeuLysPheThrLysIleSerLysGlyIleAlaAspIleMetIleAlaPheArg 161
DB 946 ACTCCTCTGAATTTTACCAGACTTCACGATGGCAATTTGCTGACATCATGATCTCTTTTGA 1005
QY 162 ThrArgValHisGlyArg--CysProArgTyrPheAspGlyProLeuGlyValLeuGly 180
DB 1006 ATTAGGACCATGGGACTTACCCA-----TTTGATGGGCCCTCTGGCCTGTGGCT 1059
QY 181 HisAlaPheProGlyProGlyLeuGlyGlyAspThrHisPheAspGluAspGluAsn 200
DB 1060 CATGCTTTTCTCTCTGGGCCAAATTTATGGAGGAGATGCCCAATTTTGATGATGATGAACC 1119
QY 201 TrrThrLysAspGlyAlaGlyPheAsnLeuPheLeuValAlaAlaHisGluPheGlyHis 220
DB 1120 TGGCAAGTAGTTCACAAAGGCTACAACTTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 1179
QY 221 AlaLeuGlyLeuSerHisSerAsnAspGlnThrAlaLeuMetPheProAsnTyrValSer 240
DB 1180 TCCTTAGGCTTTGACCACTCCAGGACCTCGAGCACTCATGTTTCTTATCTACACCTAC 1239
QY 241 LeuAspProArgLysTyrProLeuSerGlnAspIleAsnGlyIleGlnSerIleTyr 260
DB 1240 ACCGGCAAAAGCCACTTTATGCTTCTGTATGACGATGTACAAGGGATCCAGTCTCTCTAT 1299
QY 261 GlyGlyLeuProLysValProAlaLysProLysGluProThrIleProHisAlaCysAsp 280
DB 1300 GGTCCAGGAGATGAGACACCC---AACCTAAACATCCAAAAACGCCAGACAAATGTGAC 1356
QY 281 ProAspLeuThrPheAspAlaIleThrPheArgArgGluValMetPhePheLysGly 300
DB 1357 CTTCTCTTATCCTTGTAGCCATTACCACTCTCCGAGGAGAAACATGATCTTTAAAGAC 1416
QY 301 ArgHisLeuTrrArgIleTyrTyrAspIleThrAspValGluPheGluLeuIleAlaSer 320

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DB 1417 AGATTCTTCTGGCGCTGCATCCTCAGCAGGTGTTATGCGGAGCTGTTTTTAACGAATCA 1476
QY 321 PheTrrProSerLeuProAlaAspLeuGlnAlaIleTyrGluAsnPro---ArgAspLys 339
DB 1477 TTTTGGCCAGAACTTCCCAACCGTATTGATGCTGCATATGAGCACCCCTTCTCATGACCTC 1536
QY 340 IleLeuValPheLysAspGluAsnPheTrrMetIleArgGlyTyrAlaValLeuProAsp 359
DB 1537 ATCTTCATCTTCAGAGGTAGAAAAATTTGGGCTCTTAATGGTTATGACATCTTGGAGGT 1596
QY 360 TyrProLysSerIleHisThrLeuGlyPheProGlyArgValLysLysIleAspAlaAla 379
DB 1597 TATCCCAAAAAAATATCTGAACCTGGGTCTTCCAAAAAGAGTTAAGAAGATAAGTGCAGCT 1656
QY 380 ValCysAspLysThrThrArgLysThrTyrPhePheValGlyIleTrrCysTrrArgPhe 399
DB 1657 GTTCACTTTGAGGATACAGCAAGACTCTCTCTGTTCTCAGGAAACCCAGGTCTGGAGATAT 1716
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DB 1717 GATGATACTACCATATTTATGATTAAGACTATCCGAGCTAATAGAAGAGACTTCCCA 1776
QY 420 GlyIleSerIleArgValAspAlaAlaPheGlnTyrLysGlyPhePhePheSerArg 439
DB 1777 GCAATTTGGTGATAAAGTAGATGCTGCTATGAGAAAAATGGTTATATCTATTTTCAAC 1836
QY 440 GlySerLysGlnPheGluTyrAsnIleLysThrLysAsnIleThrArgIleMetArgThr 459
DB 1837 GGACCCATACAGTTTGAATACAGCATCTGGAGTAACCGTATTGTTGCGCTCATGCCAGCA 1896
QY 460 AsnThrTrrPheGlnCys 465
DB 1897 AATTCATTTTGTGGTGT 1914

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Search completed: November 16, 2004, 00:33:30

Job time : 169 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: November 15, 2004, 20:53:31 ; Search time 28 Seconds
(without alignments)
1215.041 Million cell updates/sec

Title: US-10-729-807-10

Perfect score: 2763

Sequence: 1 MKRLLLCLFFITFTSSAPPL.....SLSLFIFGIVHLKNTSIYQ 513

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 478139 seqs, 66318000 residues

Total number of hits satisfying chosen parameters: 478139

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

Issued Patents AA:*

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2: /cgn2_6/ptodata/1/1aa/5B_COMB.pep:*

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Match	Length	DB	ID	Description
1	2763	100.0	513	4	US-09-862-631-4	Sequence 4, Appli
2	2752	99.6	513	4	US-10-140-002-192	Sequence 192, App
3	1254	45.4	477	3	US-08-704-711A-20	Sequence 20, Appl
4	1254	45.4	477	3	US-08-281-313-1	Sequence 9, Appli
5	1254	45.4	477	3	US-09-521-220-20	Sequence 20, Appl
6	1250	45.2	477	3	US-08-448-489-15	Sequence 15, Appl
7	1250	45.2	477	3	US-09-391-104-21	Sequence 21, Appl
8	1234	44.7	476	3	US-08-704-711A-21	Sequence 21, Appl
9	1234	44.7	476	3	US-08-448-489-14	Sequence 14, Appl
10	1234	44.7	476	3	US-09-521-220-21	Sequence 21, Appl
11	1234	44.7	476	3	US-09-391-104-22	Sequence 22, Appl
12	1161.5	42.0	469	3	US-09-391-104-23	Sequence 23, Appl
13	1161	42.0	467	1	US-09-178-002-4	Sequence 4, Appli
14	1161	42.0	467	3	US-09-391-104-24	Sequence 24, Appl
15	1161	42.0	468	3	US-08-448-489-13	Sequence 13, Appl
16	1157.5	41.9	469	3	US-08-448-489-12	Sequence 12, Appl
17	1150.5	41.6	469	3	US-08-704-711A-16	Sequence 16, Appl
18	1150.5	41.6	469	3	US-09-521-220-16	Sequence 16, Appl
19	1146.5	41.5	466	3	US-08-704-711A-17	Sequence 17, Appl
20	1146.5	41.5	466	3	US-09-521-220-17	Sequence 17, Appl
21	1141	41.3	471	3	US-09-391-104-25	Sequence 25, Appl
22	1133	41.0	470	3	US-08-068-392-2	Sequence 2, Appli
23	1133	41.0	470	3	US-08-396-988-2	Sequence 2, Appli
24	1133	41.0	470	3	US-08-396-988-2	Sequence 2, Appli
25	1132	41.0	471	4	US-08-994-689C-1	Sequence 1, Appli
26	1125	40.7	471	4	US-08-994-689C-21	Sequence 21, Appl
27	1120.5	40.6	444	1	US-09-178-002-2	Sequence 2, Appli

28	1016.5	36.8	462	3	US-08-068-392-3	Sequence 3, Appli
29	1016.5	36.8	462	3	US-08-396-988-3	Sequence 3, Appli
30	797	28.8	660	3	US-09-391-104-19	Sequence 19, Appl
31	797	28.8	660	4	US-09-917-254-89	Sequence 89, Appl
32	796	28.8	660	3	US-08-704-711A-18	Sequence 18, Appl
33	796	28.8	660	3	US-09-521-220-18	Sequence 18, Appl
34	788	28.5	631	3	US-08-448-489-17	Sequence 17, Appl
35	769.5	27.9	563	4	US-09-194-468A-30	Sequence 30, Appl
36	716	25.9	532	3	US-09-294-841-2	Sequence 2, Appli
37	715.5	25.9	669	3	US-08-704-711A-3	Sequence 3, Appli
38	715.5	25.9	669	3	US-09-521-220-3	Sequence 3, Appli
39	715.5	25.9	669	3	US-09-391-104-29	Sequence 29, Appl
40	713.5	25.8	607	3	US-09-000-041A-2	Sequence 2, Appli
41	713.5	25.8	607	3	US-09-211-704A-10	Sequence 10, Appl
42	713.5	25.8	607	4	US-09-734-002-2	Sequence 2, Appli
43	713	25.8	582	3	US-08-704-711A-2	Sequence 2, Appli
44	713	25.8	582	3	US-08-448-489-1	Sequence 1, Appli
45	713	25.8	582	3	US-09-211-704A-9	Sequence 9, Appli

ALIGNMENTS

RESULT 1
US-09-862-631-4
; Sequence 4, Application US/09862631
; Patent No. 6734005
; GENERAL INFORMATION:
; APPLICANT: Holmgren, Erik
; APPLICANT: Kihlen, Mats
; APPLICANT: Wood, Tim
; APPLICANT: Ekblom, Jonas
; TITLE OF INVENTION: No. 6734005el Matrix Metalloproteinases
; FILE REFERENCE: 00014regus
; CURRENT APPLICATION NUMBER: US/09/862,631
; PRIOR FILING DATE: 2000-05-22
; PRIOR APPLICATION NUMBER: 206119
; PRIOR FILING DATE: 2000-05-22
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: Patent in version 3.0
; SEQ ID NO 4
; LENGTH: 513
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-862-631-4

Query Match	100.0%	Score 2763;	DB 4;	Length 513;
Best Local Similarity	100.0%	Pred. No. 1e-285;		
Matches 513;	Conservative	0;	Mismatches	0; Indels
				0; Gaps
Qy	1	MKRLLLCLFFITFTSSAPPLVVRMTENEENMOLQAQYLNQFYSLETEGHNHVSQKNRSLID	60	
Db	1	MKRLLLCLFFITFTSSAPPLVVRMTENEENMOLQAQYLNQFYSLETEGHNHVSQKNRSLID	60	
Qy	61	DKIREMQAFGLTVTGKLDNSTLEIMTKPRGVPDVGQGYTLPGWRKYNLTIRIINTP	120	
Db	61	DKIREMQAFGLTVTGKLDNSTLEIMTKPRGVPDVGQGYTLPGWRKYNLTIRIINTP	120	
Qy	121	DMARAAVDEAIQEGLEVMSKVTPLKFTKISKGIADIMIAFRTRVHGRCPRYFDGPGVLG	180	
Db	121	DMARAAVDEAIQEGLEVMSKVTPLKFTKISKGIADIMIAFRTRVHGRCPRYFDGPGVLG	180	
Qy	181	HAPPPGGLGDTDFDEENWKDGAGFNLPVAAHFHGHGALSHNSDQALMPFNVS	240	
Db	181	HAPPPGGLGDTDFDEENWKDGAGFNLPVAAHFHGHGALSHNSDQALMPFNVS	240	
Qy	241	LDPRKYPLOSDDINGIQSIYGLPKVPKPKPTIPHACDPLDFTDAITTTTFRVMPFKG	300	
Db	241	LDPRKYPLOSDDINGIQSIYGLPKVPKPKPTIPHACDPLDFTDAITTTTFRVMPFKG	300	
Qy	301	RHLWRIYDITDVEFFELIASFWPSLPADLOAAVFNPRDKILVFKDENFWMIRGVAVLDPY	360	
Db	301	RHLWRIYDITDVEFFELIASFWPSLPADLOAAVFNPRDKILVFKDENFWMIRGVAVLDPY	360	

QY 361 PKSIHTLGFPPGRVKKIDAAVCDKTRTKTYFFVGIWCRFDEMTQTDKGPQVRVVKHPPG 420
 DB 361 PKSIHTLGFPPGRVKKIDAAVCDKTRTKTYFFVGIWCRFDEMTQTDKGPQVRVVKHPPG 420
 QY 421 ISIRVDAAFQYKGFPPFRSGSKQFEYNITKNTIRMTNTWFOCKEPKNSFGFDINKE 480
 DB 421 ISIRVDAAFQYKGFPPFRSGSKQFEYNITKNTIRMTNTWFOCKEPKNSFGFDINKE 480
 QY 481 KAHSGGKILYHKSLSLFIFGIHVHLLKNTSIYQ 513
 DB 481 KAHSGGKILYHKSLSLFIFGIHVHLLKNTSIYQ 513

RESULT 2

US-10-140-002-192
 ; Sequence 192, Application US/10140002
 ; Patent No. 6725730

GENERAL INFORMATION:

; APPLICANT: Baker, Kevin P.
 ; APPLICANT: Beresini, Maureen
 ; APPLICANT: DeForge, Laura
 ; APPLICANT: Desnoyers, Luc
 ; APPLICANT: Filvaroff, Ellen
 ; APPLICANT: Gao Wei-Qiang
 ; APPLICANT: Gerritsen, Mary E.
 ; APPLICANT: Goddard, Audrey
 ; APPLICANT: Godowski, Paul J.
 ; APPLICANT: Gurney, Austin L.
 ; APPLICANT: Sherwood, Steven
 ; APPLICANT: Smith, Victoria
 ; APPLICANT: Stewart, Timothy A.
 ; APPLICANT: Tumas, Daniel
 ; APPLICANT: Watanabe, Colin K
 ; APPLICANT: Wood, William
 ; APPLICANT: Zhang, Zemin
 ; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
 ; TITLE OF INVENTION: ACIDS ENCODING THE SAME
 ; FILE REFERENCE: F3330R1C59
 ; CURRENT APPLICATION NUMBER: US/10/140,002
 ; CURRENT FILING DATE: 2002-05-06
 ; Prior Application removed - See Palm or File Wrapper
 ; NUMBER OF SEQ ID NOS: 550
 ; SEQ ID NO 192
 ; LENGTH: 513
 ; TYPE: PRT
 ; ORGANISM: Homo Sapien
 US-10-140-002-192

Query Match 99.6%; Score 2752; DB 4; Length 513;
 Best Local Similarity 99.8%; Pred. No. 1.6e-284;
 Matches 512; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 MKRLLLCLEFFITFSSAPPLVRMTENEENMQLAQYLNQFYSLIEGHNHVSQKNSRLID 60
 DB 1 MKRLLLCLEFFITFSSAPPLVRMTENEENMQLAQYLNQFYSLIEGHNHVSQKNSRLID 60
 QY 61 DKIREMOAFLTLVTGKLDNTLEIMKTPRCGVPDVGQGYTLPGWRKYNLYRIINYP 120
 DB 61 DKIREMOAFLTLVTGKLDNTLEIMKTPRCGVPDVGQGYTLPGWRKYNLYRIINYP 120
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 DB 121 DMARAAVDEALQEGLEWVSKYTPKFTKISKIGIADIMAFTRVHGRCPRYFDGPGVLG 180
 QY 181 HAFPPGFLGGDTHFDEENWTKDAGFNFLVAHAHEFGHALGSHSNDQTALMFPNYS 240
 DB 181 HAFPPGFLGGDTHFDEENWTKDAGFNFLVAHAHEFGHALGSHSNDQTALMFPNYS 240
 QY 241 LDPKYPILSQDDINGIQSIYGLGPKVPKPKPEPTIPACDDPLDFDAITTFRRVMPFKG 300
 DB 241 LDPKYPILSQDDINGIQSIYGLGPKVPKPKPEPTIPACDDPLDFDAITTFRRVMPFKG 300

QY 301 RHLWRYYIDTVEFELIASFWPSLPADLQAAYENPRDKILVFKDENFWMIRGVAVLPDY 360
 DB 301 RHLWRYYIDTVEFELIASFWPSLPADLQAAYENPRDKILVFKDENFWMIRGVAVLPDY 360
 QY 361 PKSIHTLGFPPGRVKKIDAAVCDKTRTKTYFFVGIWCRFDEMTQTDKGPQVRVVKHPPG 420
 DB 361 PKSIHTLGFPPGRVKKIDAAVCDKTRTKTYFFVGIWCRFDEMTQTDKGPQVRVVKHPPG 420
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 DB 421 ISIRVDAAFQYKGFPPFRSGSKQFEYNITKNTIRMTNTWFOCKEPKNSFGFDINKE 480
 QY 481 KAHSGGKILYHKSLSLFIFGIHVHLLKNTSIYQ 513
 DB 481 KAHSGGKILYHKSLSLFIFGIHVHLLKNTSIYQ 513

RESULT 3

US-08-704-711A-20
 ; Sequence 20, Application US/08704711A
 ; Patent No. 6114159

GENERAL INFORMATION:

; APPLICANT: WILL, Horst
 ; APPLICANT: HINZMANN, Bernd
 ; TITLE OF INVENTION: DNA SEQUENCES FOR MATRIX
 ; TITLE OF INVENTION: METALLOPROTEASES, THEIR PRODUCTION AND USE
 ; NUMBER OF SEQUENCES: 22
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Foley & Lardner
 ; STREET: 3000 K Street, N.W., Suite 500
 ; CITY: Washington
 ; STATE: D.C.
 ; COUNTRY: USA
 ; ZIP: 20007-5109

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: PatentIn Release #1.0, Version #1.30
 CURRENT APPLICATION DATA: US/08/704,711A
 APPLICATION NUMBER: US/08/704,711A
 FILING DATE: 20-NOV-1996
 CLASSIFICATION: 435
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: WO PCT/DE95/00357
 FILING DATE: 17-MAR-1995
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: DE 4438838.1
 FILING DATE: 21-OCT-1994
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: DE 4409663.1
 FILING DATE: 17-MAR-1994

ATTORNEY/AGENT INFORMATION:
 NAME: GRANADOS, Patricia D.
 REGISTRATION NUMBER: 33,683
 REFERENCE/DOCKET NUMBER: 26083/124

TELECOMMUNICATION INFORMATION:
 TELEPHONE: (202)672-5300
 TELEFAX: (202)672-5399
 TELEX: 904136

INFORMATION FOR SEQ ID NO: 20:

SEQUENCE CHARACTERISTICS:
 LENGTH: 477 amino acids
 TYPE: amino acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 US-08-704-711A-20

Query Match 45.4%; Score 1254; DB 3; Length 477;

Best Local Similarity 51.5%; Pred. No. 9.9e-125;

Matches 247; Conservative 70; Mismatches 145; Indels 18; Gaps 9;

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61 VKKIREMOKFLGLEVTGKLDSDTLEVMRKPRGVDPVGHF-RTFFGIPKWRKTHLYTIV 119
117 NYTPDMARAAVDIAOEGLVWVKVTLKFTKISKGIADIMIAERTRVHGRCPRY-FDGP 175
120 NYTPDLPKADVASVEKALKWEEVTPFTSKLYEGEADIMISFAVREHG--DFTFFDGP 177
176 LGVLGHAFPPGGLGGDTHFEDENWTKDGAFNFLVAAEHFGHALGSHNSDQATLMF 235
178 GNVLAHAYAPGGINGDAHEDDQWTKDGTGTLFLVAHEIGHSLGLFHSANTEALMY 237
236 PNYVSL-PRKVPYLSQDDINGIQSYG-----GLPKVPK--PKEPTIPHACDPLDFTD 286
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287 AITTFRRVVRPKGRHLRIYVDITDVEFLIASWPISLPADLQAAVE-NPRDKLIVK 345
298 AVSTLURGILFVKRHRKSLRKLPELHLISSFWPSLPDGAAYEVTSKDLVFIK 357
346 ENFMIRGYAVLPDYPKSIHTLGFPRGVKKIDAAVCDKTRTKTYFFVGIVCWRFDEM 405
358 NQFWAIRGNEVRAGYPRGHTLGFPTVKIDAAISDKENKTYFFVEDKYWRFDKENS 417
406 MDKGPPQVRVHFGPISIRVDAFOYKGFPPFSRSGSKFQFENIKYNTIRMTNTWFOC 465
418 MEGPFGQIAEDFPFGIDSKIDAVFEFGFFFTGSSQLEFDPNAKVTHTLKSNWLN 477

RESULT 4

US-08-281-313-1
Sequence 9, Application US/09368169
Patent No. 6284511
GENERAL INFORMATION:
APPLICANT: Tetsuya INAKA et al.
TITLE OF INVENTION: HEAT-STABLE PROLYENDOPREPTIDASE
NUMBER OF SEQUENCES: 9
CORRESPONDENCE ADDRESS:
ADDRESSEE: Wenderoth, Lind & Ponack, L.L.P.
STREET: 2033 K Street, N.W., Suite 800
CITY: Washington
STATE: D.C.
COUNTRY: U.S.A.
ZIP: 20006
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.5 inch, 1.44 mb
COMPUTER: IBM Compatible
OPERATING SYSTEM: MS-DOS
SOFTWARE: Wordperfect 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/368,169
FILING DATE: August 5, 1999
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/750,816
FILING DATE: January 8, 1997
ATTORNEY/AGENT INFORMATION:
NAME: Lee Cheng
REGISTRATION NUMBER: 40,949
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-721-8200
TELEFAX: 202-721-8250
TELEX:
INFORMATION FOR SEQ ID NO: 9:
SEQUENCE CHARACTERISTICS:
LENGTH: 19 amino acid residues
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear

MOLECULE TYPE: Protein
ORIGINAL SOURCE:
ORGANISM: Flavobacterium meningosepticum
ORGANISM: Met Lys Tyr Asn Lys Leu Ser Val Ala Val Ala Phe Ala Phe Ala Ala Val 15
ORGANISM: 1 5 10
Sequence 1, Application US/08281313
Patent No. 6284513
GENERAL INFORMATION:
APPLICANT: Ye, Qi-Zhuang
APPLICANT: Johnson, Linda L.
APPLICANT: Hupe, Donald J.
APPLICANT: Baragi, Vijaykumar
TITLE OF INVENTION: Process for the Production of
TITLE OF INVENTION: Stromelysin Catalytic Domain Protein
NUMBER OF SEQUENCES: 8
CORRESPONDENCE ADDRESS:
ADDRESSEE: Warner-Lambert Company
STREET: 2800 Plymouth Rd.
CITY: Ann Arbor
STATE: MI
COUNTRY: US
ZIP: 48105
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/281,313
FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/012,705
FILING DATE: 03-FEB-1993
ATTORNEY/AGENT INFORMATION:
NAME: Timney, Francis J.
REGISTRATION NUMBER: 33,069
REFERENCE/DOCKET NUMBER: 4415-01-PJT
TELECOMMUNICATION INFORMATION:
TELEPHONE: 313 996-7295
TELEFAX: 313 996-1553
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 477 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
FEATURE:
NAME/KEY: Protein
LOCATION: 100..273
OTHER INFORMATION: /note= "Mature stromelysin
OTHER INFORMATION: catalytic domain protein"
FEATURE:
NAME/KEY: Region
LOCATION: 1..17
OTHER INFORMATION: /note= "Signal peptide"
FEATURE:
NAME/KEY: Region
LOCATION: 18..99
OTHER INFORMATION: /note= "Propeptide"
US-08-281-313-1

Query Match 45.4%; Score 1254; DB 3; Length 477;
Best Local Similarity 51.5%; Pred. No. 9.9e-125;
Matches 247; Conservative 70; Mismatches 145; Indels 18; Gaps 9;

Qy 1 MKRLLILLCLFFITFSSAPPLVMTENEENMQLAQAVLNQFYSLEIGNHLVQSKNRSLI 59
Db 1 MKSLPILLLCVAVCSAYPLDGAAGEDTSMNLVKYLENYDLEKDVQKQFVRKDSGPV 60
Qy 60 DDKIREMOAFLGLTVTGKLDNTLEIMKTPRCGVDPVGVGYGVTLPG---WRKYNITYRII 116

Db 61 VKKIREMQKFLGLEVTGKLDSDTLEVMKPRCGVPDVGHF--RTFPGIPKWRKTHLYRIV 119
QY 117 NYTPOMARAADVBAIOEGLEWMSKVTPKFTKISKIGIADIIMIAFRTRVRHGRCPRY--FDGP 175
Db 120 NYTPDLPKDAVDSAVEKALKVWEVTPLTFSRLYEAGEADIMISFAVREHG--DFYFPDGP 177
QY 176 LGVLGHAFPPGGLGSDTHFEDENWTKDAGNLFVAHAEFGHALGSHSNDQTALMF 235
Db 178 GNVLAHAYAPGPGINGDAHFDDDEQWTKDTTGNLFLVAHAEIGHSLGLFHSANTALMY 237
QY 236 PNYVSL--DPRKYPLSQDDINGIOSIYG-----GLPKVPAK--PKEPTIPHACDPLTFD 286
Db 238 PLYHSLTDLTRFLSQDDINGIOSLYGPPDPSPETPLVTEPVPPEPGTPANCDPALSPD 297
QY 287 AITTFRRVWFFKGRHLWRIYYDITDVEFELIASFWPSLPADLQAAVE--NPRDKILVFKD 345
Db 298 AVSTLRGEILIFKDRHFWKSLRKLPELHLISSFWPSLPSGVDAAAEVTSKDLVFIK 357
QY 346 ENFMWIRGVAVLPDYPKSIHTLGFGRVVKIDAAVCDKTKTKTYFFVGVICWRFDEMTOT 405
Db 358 NQFWAIRGNEVRAGYPRGIHTLGFPTVRKIDAAISDKENKTYFFVEDKYWRFDEKRN 417
QY 406 MDKGFQORVVVKKHPPGISIRVDAAFQYKGFSSGSKQFEYNKTKNITRIMETNTWFOC 465
Db 418 MEGFPKQIAEDPFGIDSKIDAVFEEFGFFYFTGSSQLEFFDPAKKNVTHLKSNSWLNC 477

RESULT 5

US-09-521-220-20
; Sequence 20, Application US/09521220
; Patent No. 639348
; GENERAL INFORMATION:
; APPLICANT: WILL, Horst
; HINZMANN, Bernd
; TITLE OF INVENTION: DNA SEQUENCES FOR MATRIX
; METALLOPROTEASES, THEIR PRODUCTION AND USE
; NUMBER OF SEQUENCES: 22
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Foley & Lardner
; STREET: 3000 K Street, N.W., Suite 500
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20007-5109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/521,220
; FILING DATE: 08-Mar-2000
; CLASSIFICATION: <Unknown>
; 21-OCT-1994
; 17-MAR-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/704,711
; FILING DATE: <Unknown>
; APPLICATION NUMBER: DE 4438838.1
; FILING DATE: 21-OCT-1994
; APPLICATION NUMBER: DE 4409663.1
; FILING DATE: 17-MAR-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: GRANADOS, Patricia D.
; REGISTRATION NUMBER: 33,683
; REFERENCE/DOCKET NUMBER: 26083/124
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202)672-5300
; TELEFAX: (202)672-5399
; TELEX: 904136
; INFORMATION FOR SEQ ID NO: 20:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 477 amino acids

; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; SEQUENCE DESCRIPTION: SEQ ID NO: 20:
US-09-521-220-20
Query Match 45.4%; Score 1254; DB 3; Length 477;
Best Local Similarity 51.5%; Pred. No. 9.9e-125; Indels 18; Gaps 9;
Matches 247; Conservative 70; Mismatches 145;
QY 1 MKRLLLCLLFFITFSAPFLVRMTENEE--NQMLAQAYLNOFYSLIEGHNHLVQSKNLSLI 59
Db 1 MKSLPILLLLCVAVCSAYPLDGAARGEDTSMNLVQKYLENYDYDLEKDVQKOFVRRKDSGPV 60
QY 60 DKIRMQAFAFGTLVTGKLDSDNTLEIMKTGRGVPDVGVQGYTLPG---WRKNLYRII 116
Db 61 VKKIREMQKFLGLEVTGKLDSDTLEVMKPRCGVPDVGHF--RTFPGIPKWRKTHLYRIV 119
QY 117 NYTPDMARAADVBAIOEGLEWMSKVTPKFTKISKIGIADIIMIAFRTRVRHGRCPRY--FDGP 175
Db 120 NYTPDLPKDAVDSAVEKALKVWEVTPLTFSRLYEAGEADIMISFAVREHG--DFYFPDGP 177
QY 176 LGVLGHAFPPGGLGSDTHFEDENWTKDAGNLFVAHAEFGHALGSHSNDQTALMF 235
Db 178 GNVLAHAYAPGPGINGDAHFDDDEQWTKDTTGNLFLVAHAEIGHSLGLFHSANTALMY 237
QY 236 PNYVSL--DPRKYPLSQDDINGIOSIYG-----GLPKVPAK--PKEPTIPHACDPLTFD 286
Db 238 PLYHSLTDLTRFLSQDDINGIOSLYGPPDPSPETPLVTEPVPPEPGTPANCDPALSPD 297
QY 287 AITTFRRVWFFKGRHLWRIYYDITDVEFELIASFWPSLPADLQAAVE--NPRDKILVFKD 345
Db 298 AVSTLRGEILIFKDRHFWKSLRKLPELHLISSFWPSLPSGVDAAAEVTSKDLVFIK 357
QY 346 ENFMWIRGVAVLPDYPKSIHTLGFGRVVKIDAAVCDKTKTKTYFFVGVICWRFDEMTOT 405
Db 358 NQFWAIRGNEVRAGYPRGIHTLGFPTVRKIDAAISDKENKTYFFVEDKYWRFDEKRN 417
QY 406 MDKGFQORVVVKKHPPGISIRVDAAFQYKGFSSGSKQFEYNKTKNITRIMETNTWFOC 465
Db 418 MEGFPKQIAEDPFGIDSKIDAVFEEFGFFYFTGSSQLEFFDPAKKNVTHLKSNSWLNC 477
RESULT 6
US-08-448-489-15
; Sequence 15, Application US/08448489
; Patent No. 6184022
; GENERAL INFORMATION:
; APPLICANT: SEIKI, Motoharu
; APPLICANT: SATO, Hiroshi
; APPLICANT: SHINAGAWA, Akira
; TITLE OF INVENTION: NOVEL METALLOPROTEINASE AND ENCODING DNA THEREFOR
; FILE REFERENCE: 55-290P
; CURRENT APPLICATION NUMBER: US/08/448,489
; CURRENT FILING DATE: 1995-06-07
; NUMBER OF SEQ ID NOS: 19
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 15
; LENGTH: 477
; TYPE: PRT
; ORGANISM: Unknown
; FEATURE:
; OTHER INFORMATION: Description of Unknown Organism: Known Member of
; OTHER INFORMATION: Matrix Metalloproteinase Family
US-08-448-489-15
Query Match 45.2%; Score 1250; DB 3; Length 477;
Best Local Similarity 51.2%; Pred. No. 2.6e-124;
Matches 246; Conservative 71; Mismatches 145; Indels 18; Gaps 9;
QY 1 MKRLLLCLLFFITFSAPFLVRMTENEE--NQMLAQAYLNOFYSLIEGHNHLVQSKNLSLI 59
Db 1 MKSLPILLLLCVAVCSAYPLDGAARGEDTSMNLVQKYLENYDYDLEKDVQKOFVRRKDSGPV 60

Qy	60	DDKIREMQAFGLVTGKLDNSTLEIMKTPRCGVDVGQGYTLPG---WRKYNLTYYRII	116
Db	61	VKKIREMQKFLGVTGKLDSDTLEVMRKPRCGVDVGHF-RTFPGIPKWRKTHLTYRIV	119
Qy	117	NYTPDMARAAVDEAIOEGLEVWSKVYTLKFTKISKGIADIMIAFRTVRHGCPRY-FDGP	175
Db	120	NYTPDLPKDAVSAVEKALKWVEEVTPTFSRLYEGEADIMISFAVREHG--DFVPFDGP	177
Qy	176	LGVLGHAFPPGGLGGDTHFDENWTKDGAGNLFVAAHEFGHALGSHNSDOTALMF	235
Db	178	GNVLHAHAPGPGINGDAHFDDDEQWTKDTCGTNLFVAAHGIHSLGLFHSANTEALMY	237
Qy	236	PNVYSL-DPRKYPSLQDDINGIQSIYG-----GLPKYPAK--PKRPTIPHACDOLDTPD	286
Db	238	PLYHSLTDLTTPRISQDDINGIQSLYGGPPDSPETPLVPTPEVPPGTPANCDPALSFD	297
Qy	287	AITFRREVMEFFKGRHLWRIYYDITDVDFELIASFWPSLPADLQAAYE-NPRDKILVFKD	345
Db	298	AVSLRGEILIFKORHFWKRSRKLEPELHLISSFWPSLPSCVDAAYEVTSKDLVFIKRG	357
Qy	346	ENFWIRGYAVLPDPYKSIHITLGPGRVKKIDAAVCDKTKTKTYFVFGIWCWRFDGMTQT	405
Db	358	NQFWAIRGNEVRAGYPRGIHTLGFPPTVRKIDAAISDKENKNTYFVEDKYWRFDEKRS	417
Qy	406	MDKGFPORVWHFPGCISIRVDAAFYKGFPEFSRGSKQFENIKTKNITRIMRTNWTWQC	465
Db	418	MEGFPKQIAEDFPGLDSDKIDAVFEFGFFYFTGSSQLFEDPNNAKKVTHILUKNSWLNC	477
RESULT 7			
US-09-391-104-21			
; Sequence 21, Application US/09391104			
; Patent No. 6399371			
; GENERAL INFORMATION:			
; APPLICANT: Abbott Laboratories			
; APPLICANT: Falduto, Michael T.			
; APPLICANT: Magnuson, Scott R.			
; APPLICANT: Morgan, Douglas W.			
; TITLE OF INVENTION: HUMAN MATRIX METALLOPROTEASE GENE,			
; TITLE OF INVENTION: PROTEINS ENCODED THEREFROM AND METHODS			
; FILE REFERENCE: 6073-US.P1			
; CURRENT APPLICATION NUMBER: US/09/391,104			
; CURRENT FILING DATE: 1999-09-07			
; PRIOR APPLICATION NUMBER: US 08/814,394			
; PRIOR FILING DATE: 1997-03-11			
; NUMBER OF SEQ ID NOS: 35			
; SOFTWARE: FastSeq for Windows Version 3.0			
; SEQ ID NO 21			
; LENGTH: 477			
; TYPE: prt			
; ORGANISM: Homo sapiens			
US-09-391-104-21			
Query Match 45.2%; Score 1250; DB 3; Length 477;			
Best Local Similarity 51.2%; Pred. No. 2.6e-124;			
Matches 246; Conservative 71; Mismatches 145; Indels 18; Gaps 9			
Qy	1	MKSLLLCLFFITSSAPPLVRMTNEEE-NMQLAQAYLNQFYSLEIEGNHLVQSKNRSLI	59
Db	1	MKSUPIILLLCVACSYAPLDGAARGEDTSNNLQKYLENYIDLKQVKQFVRKDSQGV	60
Qy	60	DDKIREMQAFGLVTGKLDNSTLEIMKTPRCGVDVGQGYTLPG---WRKYNLTYYRII	116
Db	61	VKKIREMQKFLGVTGKLDSDTLEVMRKPRCGVDVGHF-RTFPGIPKWRKTHLTYRIV	119
Qy	117	NYTPDMARAAVDEAIOEGLEVWSKVYTLKFTKISKGIADIMIAFRTVRHGCPRY-FDGP	175
Db	120	NYTPDLPKDAVSAVEKALKWVEEVTPTFSRLYEGEADIMISFAVREHG--DFVPFDGP	177
Qy	176	LGVLGHAFPPGGLGGDTHFDENWTKDGAGNLFVAAHEFGHALGSHNSDOTALMF	235

QY 4 LLLLCLEFFITFSSAPPLVMTENEE-NMQLAQAYLNQFYSLEIEGHLVQSKNRLIDDK 62
Db 7 LVLLCL---PVC SAYPLSGAAKEEDSKDLAQOYLEKYINLEKDVQKF-RRKDSNLIIVKK 62
QY 63 IREMQAFFGLTWTGKLDNTLEIMKTPRCGVPDVGQYGY--TLPGWRKYNLTTRIINYTP 120
Db 63 IQOMQKFLGLEVTGKLDNTLEIMKTPRCGVPDVGHFSFPQKWKTKHLYRIYVNYTP 122
QY 121 DMARAAVDEAIQEGLEWVSKVTPLEKTKISKIADIIMIAFTRVHGRCPRYFDGPIGLVIG 180
Db 123 DLPRADVDSAEKALKVWEVETPLTFSRLYEGEADIMISFAVKEHGF-YSFDPGPHSLA 181
QY 181 HAPFPGLGGDTHFEDENWTKDAGFNLFLVAHEFGHALGSLHSDQTMFPNYYS 240
Db 182 HAYPPGGLYGIHFDDEDEKWTEDASGTNLFVAHELHSLGLPHSANTALMYPLYS 241
QY 241 L-DPRKYPLOSDDINGIOSIYGLPKVPAKPKPT-----IPHACDPLTDFDAITTF 291
Db 242 FTLEAQFRLSQDDVNGIQSLYGPDPASTEPLVPTKSPVSGSEMPAKCDPALSFDAISTL 301
QY 292 RREVMFFKGRHLWRIYDITDVEFELIASFWPSLPADLQAAVE-NPRDKILVFKDENFW 350
Db 302 RGEYLFKDRYFWRSHWNPEPEFHLISAFWPSLYDAAYEVNSRDVTFIKGNEFWA 361
QY 351 IRGYAVLPDYPKSIHTLGFGRVKKIDAAVCDKTKTKTYFFVGIWCRWDEMTQTMKGF 410
Db 362 IRGNEVQAGYPRGIHTLGFPTIRKIDAAVSDKKEKTKTYFFAADKYWRFDENSQSMQGF 421
QY 411 PORVVKHFGPISIRVDAAFQYKGFYFFSRSQKQFVFNKTKNITRIMRTNFWQC 465
Db 422 PRLIADDFGVEPKVDALQAFGFFYFFSSQSFEDFPNARMVTHILKNSWLHC 476

RESULT 9

US-08-448-489-14
; Sequence 14, Application US/08448489
; Patent No. 6184022
; GENERAL INFORMATION:
; APPLICANT: SEIKI, Motoharu
; APPLICANT: SATO, Hiroshi
; APPLICANT: SHINAGAWA, Akira
; TITLE OF INVENTION: NOVEL METALLOPROTEINASE AND ENCODING DNA THEREFOR
; FILE REFERENCE: 55-230P
; CURRENT APPLICATION NUMBER: US/08/448,489
; CURRENT FILING DATE: 1995-06-07
; NUMBER OF SEQ ID NOS: 19
; SOFTWARE: Patent In Ver. 2.0
; SEQ ID NO 14
; LENGTH: 476
; TYPE: PRT
; ORGANISM: Unknown
; FEATURE:
; OTHER INFORMATION: Description of Unknown Organism: Known Member of
; OTHER INFORMATION: Matrix Metalloproteinase Family
US-08-448-489-14

Query Match 44.7%; Score 1234; DB 3; Length 476;
Best Local Similarity 51.4%; Pred. No. 1.3e-122;
Matches 244; Conservative 77; Mismatches 136; Indels 18; Gaps 8;

QY 4 LLLLCLEFFITFSSAPPLVMTENEE-NMQLAQAYLNQFYSLEIEGHLVQSKNRLIDDK 62
Db 7 LVLLCL---PVC SAYPLSGAAKEEDSKDLAQOYLEKYINLEKDVQKF-RRKDSNLIIVKK 62
QY 63 IREMQAFFGLTWTGKLDNTLEIMKTPRCGVPDVGQYGY--TLPGWRKYNLTTRIINYTP 120
Db 63 IQOMQKFLGLEVTGKLDNTLEIMKTPRCGVPDVGHFSFPQKWKTKHLYRIYVNYTP 122
QY 121 DMARAAVDEAIQEGLEWVSKVTPLEKTKISKIADIIMIAFTRVHGRCPRYFDGPIGLVIG 180
Db 123 DLPRADVDSAEKALKVWEVETPLTFSRLYEGEADIMISFAVKEHGF-YSFDPGPHSLA 181

QY 181 HAPFPGLGGDTHFEDENWTKDAGFNLFLVAHEFGHALGSLHSDQTMFPNYYS 240
Db 182 HAYPPGGLYGIHFDDEDEKWTEDASGTNLFVAHELHSLGLPHSANTALMYPLYS 241
QY 241 L-DPRKYPLOSDDINGIOSIYGLPKVPAKPKPT-----IPHACDPLTDFDAITTF 291
Db 242 FTLEAQFRLSQDDVNGIQSLYGPDPASTEPLVPTKSPVSGSEMPAKCDPALSFDAISTL 301
QY 292 RREVMFFKGRHLWRIYDITDVEFELIASFWPSLPADLQAAVE-NPRDKILVFKDENFW 350
Db 302 RGEYLFKDRYFWRSHWNPEPEFHLISAFWPSLYDAAYEVNSRDVTFIKGNEFWA 361
QY 351 IRGYAVLPDYPKSIHTLGFGRVKKIDAAVCDKTKTKTYFFVGIWCRWDEMTQTMKGF 410
Db 362 IRGNEVQAGYPRGIHTLGFPTIRKIDAAVSDKKEKTKTYFFAADKYWRFDENSQSMQGF 421
QY 411 PORVVKHFGPISIRVDAAFQYKGFYFFSRSQKQFVFNKTKNITRIMRTNFWQC 465
Db 422 PRLIADDFGVEPKVDALQAFGFFYFFSSQSFEDFPNARMVTHILKNSWLHC 476

RESULT 10

US-09-521-220-21
; Sequence 21, Application US/09521220
; Patent No. 6399348
; GENERAL INFORMATION:
; APPLICANT: WILL, Horst
; TITLE OF INVENTION: DNA SEQUENCES FOR MATRIX
; NUMBER OF SEQUENCES: 22
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Coley & Lardner
; STREET: 3000 K Street, N.W., Suite 500
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20007-5109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/521,220
; FILING DATE: 08-Mar-2000
; CLASSIFICATION: <Unknown>
; 21-OCT-1994
; 17-MAR-1994

PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/704,711
; FILING DATE: <Unknown>
; APPLICATION NUMBER: DE 4438838.1
; FILING DATE: 21-OCT-1994
; APPLICATION NUMBER: DE 4409663.1
; FILING DATE: 17-MAR-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: GRANADOS, Patricia D.
; REGISTRATION NUMBER: 33,683
; REFERENCE/DOCKET NUMBER: 26083/124
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202) 672-5300
; TELEFAX: (202) 672-5399
; TELEX: 904136
; INFORMATION FOR SEQ ID NO: 21:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 476 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; SEQUENCE DESCRIPTION: SEQ ID NO: 21:
US-09-521-220-21

Db 245 DVQ---LAQDDIDIGIAIY-GRSQNPVQPIGPQTPKACDSKLTDFDAITTRGVEMFFKDR 300
QY 302 HLMRIYDITDVEFELIASFWSLPADLQAAVE-NPRDKILVPKDNFWMIRGYAVLPDY 360
Db 301 FYMRTNPFYPEVLELNFISVFWPLNGLEAAVEFADRDEVRFPKNGKYWAVQSQNVLHG 360
QY 361 PXSIIH-TLGFPGRVKKIDAACVCKTKTKYFFVGIWCFRDEMTQMDKGFPPORVVKHFP 419
Db 361 PKDIYSFGFPRTVKHIDAALSEENTGKTYFFVANKYRYDEKRSMDPGYKMIADHP 420
QY 420 GISIRVDAAFQYKGFPPFSGRSKQFEYNKTKNITRMTNTWFOCKE 467
Db 421 GICHKVDVEMKDGFFYFFHGTQYKFDKPKTRILLTLQKANSWFNCRK 468

RESULT 13

US-09-178-002-4
; Sequence 4, Application US/09178002
; Patent No. H001973
; GENERAL INFORMATION:
; APPLICANT: Hu, Shou-Ih
; TITLE OF INVENTION: Human Neutrophil Collagenase Splice Variant
; FILE REFERENCE: CGC 2048
; CURRENT APPLICATION NUMBER: US/09/178,002
; CURRENT FILING DATE: 1998-10-22
; NUMBER OF SEQ ID NOS: 9
; SOFTWARE: Patent In Ver. 2.0
; SEQ ID NO 4
; LENGTH: 467
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-178-002-4

Query Match 42.0%; Score 1161; DB 1; Length 467;
Best Local Similarity 48.3%; Pred. No. 8e-115;
Matches 228; Conservative 71; Mismatches 157; Indels 16; Gaps 8;

QY 1 MKRLLLLCLFFITFSSAFPLVMTENEENMOLAQAVLNQFYSLEIEGNHLVQSKNLSLD 60
Db 4 LKTLPELLLLHVOISKAFF---VSSKEKNTKVQDYLEKPYQLPSNQYOSTRKNGTNIV 60
QY 61 DKIREMAQFFGLTVTKLDSNTLEIMKTPRCGVPDVGQYGYTL----PQWRKYNLTYYRII 116
Db 61 EKLKEMQRFGLNVTGKPNKEETLDMKKPCRCGVPDSG--GFMLTPCNPXWERTNLTYYRI 118
QY 117 NTPDMARAADVEAIOEGLEVSKVTPPLKFTKISKIADIIMIAFRTRVIG-RCPRYFDGP 175
Db 119 NTPQLSEAEVERAIKDAFELMSVASPLIFTRISQGEADINIAFYQRDHGDNSP--FDGP 176
QY 176 LGVLGHAFPPGGLGSDTHFDEENWTKDAGFNLFVAAREFGHALGSHNSNDQTALMF 235
Db 177 NGLIAHAFQGGIGGDAHFDAEETWNTSANYNLFVAAREFGHSLGLAHSSDGPALMY 236
QY 236 PNVSLDPRKYPPLSQDDINGIQSIYGLPKVPKPKKEPTIPHACDPLDFTDAITTPRREV 295
Db 237 PNVAFRETNSYSLPQDDIDIGIAIY-GLSSNPQTPGTPKPCDPSLFTDAITTLRGEI 295
QY 296 MFPGKRLHRIYYDITDVEFELIASFWPSLPADLQAAVEN-PRDKILVPKDNFWMIRGY 354
Db 296 LFFKDRYFRRHPQLQRVEMNFIISLFWPSLPTGIAAYEDFDRDLIFLFGKQYWALS 355
QY 355 AVLDPYKPSIHTLGPGRVKKIDAACVCKTKTKYFFVGIWCFRDEMTQMDKGFPPORV 414
Db 356 DILQGVFKDISNYGPFSSVQAIDAAVYRS--KTYFFVNDQFWRYDNQRFMEPGPKSI 413
QY 415 VKHFGGISIRVDAAFQYKGFPPFSGRSKQFEYNKTKNITRMTNTWFOCK 466
Db 414 SGAFFGIESKVDVAFQOEHHFHFVSGPRYVAFDLIAQRTVRVARGNKWLNCR 465

RESULT 14

US-09-391-104-24
; Sequence 24, Application US/09391104

; Patent No. 6399371
; GENERAL INFORMATION:
; APPLICANT: Abbott Laboratories
; APPLICANT: Falduto, Michael T.
; APPLICANT: Magnuson, Scott R.
; APPLICANT: Morgan, Douglas W.
; TITLE OF INVENTION: HUMAN MATRIX METALLOPROTEINASE GENE,
; TITLE OF INVENTION: OF USING SAME
; FILE REFERENCE: 6073.US.PI
; CURRENT APPLICATION NUMBER: US/09/391,104
; CURRENT FILING DATE: 1999-09-07
; PRIOR APPLICATION NUMBER: US 08/814,394
; PRIOR FILING DATE: 1997-03-11
; NUMBER OF SEQ ID NOS: 35
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 24
; LENGTH: 467
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-391-104-24

Query Match 42.0%; Score 1161; DB 3; Length 467;
Best Local Similarity 48.3%; Pred. No. 8e-115;
Matches 228; Conservative 71; Mismatches 157; Indels 16; Gaps 8;

QY 1 MKRLLLLCLFFITFSSAFPLVMTENEENMOLAQAVLNQFYSLEIEGNHLVQSKNLSLD 60
Db 4 LKTLPELLLLHVOISKAFF---VSSKEKNTKVQDYLEKPYQLPSNQYOSTRKNGTNIV 60
QY 61 DKIREMAQFFGLTVTKLDSNTLEIMKTPRCGVPDVGQYGYTL----PQWRKYNLTYYRII 116
Db 61 EKLKEMQRFGLNVTGKPNKEETLDMKKPCRCGVPDSG--GFMLTPCNPXWERTNLTYYRI 118
QY 117 NTPDMARAADVEAIOEGLEVSKVTPPLKFTKISKIADIIMIAFRTRVIG-RCPRYFDGP 175
Db 119 NTPQLSEAEVERAIKDAFELMSVASPLIFTRISQGEADINIAFYQRDHGDNSP--FDGP 176
QY 176 LGVLGHAFPPGGLGSDTHFDEENWTKDAGFNLFVAAREFGHALGSHNSNDQTALMF 235
Db 177 NGLIAHAFQGGIGGDAHFDAEETWNTSANYNLFVAAREFGHSLGLAHSSDGPALMY 236
QY 236 PNVSLDPRKYPPLSQDDINGIQSIYGLPKVPKPKKEPTIPHACDPLDFTDAITTPRREV 295
Db 237 PNVAFRETNSYSLPQDDIDIGIAIY-GLSSNPQTPGTPKPCDPSLFTDAITTLRGEI 295
QY 296 MFPGKRLHRIYYDITDVEFELIASFWPSLPADLQAAVEN-PRDKILVPKDNFWMIRGY 354
Db 296 LFFKDRYFRRHPQLQRVEMNFIISLFWPSLPTGIAAYEDFDRDLIFLFGKQYWALS 355
QY 355 AVLDPYKPSIHTLGPGRVKKIDAACVCKTKTKYFFVGIWCFRDEMTQMDKGFPPORV 414
Db 356 DILQGVFKDISNYGPFSSVQAIDAAVYRS--KTYFFVNDQFWRYDNQRFMEPGPKSI 413
QY 415 VKHFGGISIRVDAAFQYKGFPPFSGRSKQFEYNKTKNITRMTNTWFOCK 466
Db 414 SGAFFGIESKVDVAFQOEHHFHFVSGPRYVAFDLIAQRTVRVARGNKWLNCR 465

RESULT 15

US-08-448-489-13
; Sequence 13, Application US/08448489
; Patent No. 6184022
; GENERAL INFORMATION:
; APPLICANT: SEIKI, Motoharu
; APPLICANT: SATO, Hiroshi
; APPLICANT: SHINAGAWA, Akira
; TITLE OF INVENTION: NOVEL METALLOPROTEINASE AND ENCODING DNA THEREFOR
; FILE REFERENCE: 55-290P
; CURRENT APPLICATION NUMBER: US/08/448,489
; CURRENT FILING DATE: 1995-06-07
; NUMBER OF SEQ ID NOS: 19
; SOFTWARE: Patent In Ver. 2.0

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; SEQ ID NO 13
; LENGTH: 468
; TYPE: PRT
; ORGANISM: Unknown
; FEATURE:
; OTHER INFORMATION: X = UNKNOWN
;
; INFORMATION: Description of Unknown Organism: Known Member of
; OTHER INFORMATION: Matrix Metalloproteinase Family
US-08-448-489-13

Query Match      42.0%; Score 1161; DB 3; Length 468;
Best Local Similarity 48.3%; Pred. No. 8.1e-115;
Matches 228; Conservative 71; Mismatches 157; Indels 16; Gaps 8;

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4 LKTLFLLLLHVQISKAPP--VSSKEKNTKTVDYLEKFYQLPSNQYQSTRKNGTNVIV 60
QY 61 DKIREMQAFFGLTVTGKLDNSTLEIMKTPRCGVPDVGQGYTL---PGWRKYNLTYYRI 116
Db : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
61 EKLKMQRFGLNVTGKNEETLDMKPRCGVPDSG--GFMLTPGNPKWERTNLTYYRI 118
QY 117 NYTPDMARAANDVAIQEGLEVMSKVTPLKFTKISKGIADIMIAFRTRVHG-RCPRYFDGP 175
Db : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
119 NYTPQSEAEVERAIKDAFELMSVASPLIFTRISQGEADINIAFYQRDHGDNSP--FDGP 176
QY 176 LGVLGHAPPGPLCGDTHFDEDEENWTKDAGFNFLVAAHEFHGALGSHSNDOTALMF 235
Db : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
177 NGILAHAFQPGQGGIGDAHFAEETWTNTSANYNLFVAAHEFHGSLGSHSSDPGALMY 236
QY 236 PNYVSLDRPKYPLSDDDINGIOSIYGLPKVPKPKETIPHACDPDLTDAITTFREBV 295
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237 PNYAFRETSNYSLPDDIDGIAIY-GLSSNPIQTGSTPKPCDPSLTFDAITTLRGEI 295
QY 296 MFFKGRHLWRIYYDITDVEFELIASFWPSLPADLOAAYEN-PRDKILVFKDENFWMIRGY 354
Db : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
296 LFFKDRYFWRHRPQLQRVEMNFISLFWPSLPTGIQAAYEDFDRDLIFLFGNQYWALSGY 355
QY 355 AVLDPYPKSIHTLGPGRVKKIDAAVCDKTRKTYFFVGICWRPEDEMTQTMDKGPORV 414
Db : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
356 DILQGYPKDISNYGPFSSVQAIDAAVYRS--KTYFFVNDQFWRYDNQRQFMFPGYPKSI 413
QY 415 VKHPPGISIRVDAAFQYKGFPPFSRSGSKOFEYNIKTKNITRIMRTNTWFOCK 466
Db : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
414 SCAPFGIESKVDVAFQEHFFHVFSGPRYAFDLIAQRVTRVARGNKWLNCR 465
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Search completed: November 15, 2004, 21:02:23
Job time : 29 secs

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OM nucleic - nucleic search, using sw model

Run on: November 15, 2004, 13:11:05 ; Search time 1645 Seconds
(without alignments)
5341.888 Million cell updates/sec

Title: US-10-729-807-28

Perfect score: 1627

Sequence: 1 gcttcagctgaagaagaga.....aattcgtctcaaatagaa 1627

Scoring table: IDENTITY NUC

Gapop 10.0 , Gapext 1.0

Searched: 3625171 seqs, 2700493622 residues

Total number of hits satisfying chosen parameters: 7250342

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications NA:*

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2: /cgn2_6/ptodata/1/pubpna/PCT_NEW_PUB.seq:*

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21: /cgn2_6/ptodata/1/pubpna/US60_PUBCOMB.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1627	100.0	1627	17	US-10-729-807-28
2	1627	100.0	1647	10	Sequence 28, Appl
3	1625.4	99.9	1647	14	Sequence 1, Appl
4	1625.4	99.9	1647	14	Sequence 191, Appl
5	1625.4	99.9	1647	14	Sequence 191, Appl
6	1625.4	99.9	1647	14	Sequence 191, Appl
7	1625.4	99.9	1647	14	Sequence 191, Appl
8	1625.4	99.9	1647	14	Sequence 191, Appl
9	1625.4	99.9	1647	14	Sequence 191, Appl
10	1625.4	99.9	1647	14	Sequence 191, Appl
11	1625.4	99.9	1647	14	Sequence 191, Appl
12	1625.4	99.9	1647	14	Sequence 191, Appl

13	1625.4	99.9	1647	14	US-10-142-431-191	Sequence 191, App
14	1625.4	99.9	1647	14	US-10-143-114-191	Sequence 191, App
15	1625.4	99.9	1647	14	US-10-140-002-191	Sequence 191, App
16	1625.4	99.9	1647	14	US-10-142-419-191	Sequence 191, App
17	1625.4	99.9	1647	14	US-10-123-262-191	Sequence 191, App
18	1625.4	99.9	1647	14	US-10-142-423-191	Sequence 191, App
19	1625.4	99.9	1647	14	US-10-121-050-191	Sequence 191, App
20	1625.4	99.9	1647	14	US-10-141-755-191	Sequence 191, App
21	1625.4	99.9	1647	14	US-10-143-032-191	Sequence 191, App
22	1625.4	99.9	1647	14	US-10-123-108-191	Sequence 191, App
23	1625.4	99.9	1647	14	US-10-123-236-191	Sequence 191, App
24	1625.4	99.9	1647	14	US-10-123-261-191	Sequence 191, App
25	1625.4	99.9	1647	14	US-10-140-921-191	Sequence 191, App
26	1625.4	99.9	1647	14	US-10-140-928-191	Sequence 191, App
27	1625.4	99.9	1647	14	US-10-121-045-191	Sequence 191, App
28	1625.4	99.9	1647	14	US-10-123-292-191	Sequence 191, App
29	1625.4	99.9	1647	14	US-10-123-903-191	Sequence 191, App
30	1625.4	99.9	1647	14	US-10-124-819-191	Sequence 191, App
31	1625.4	99.9	1647	14	US-10-124-822-191	Sequence 191, App
32	1625.4	99.9	1647	14	US-10-140-925-191	Sequence 191, App
33	1625.4	99.9	1647	14	US-10-160-498-191	Sequence 191, App
34	1625.4	99.9	1647	14	US-10-124-824-191	Sequence 191, App
35	1625.4	99.9	1647	14	US-10-127-825A-191	Sequence 191, App
36	1625.4	99.9	1647	14	US-10-127-828A-191	Sequence 191, App
37	1625.4	99.9	1647	14	US-10-127-835A-191	Sequence 191, App
38	1625.4	99.9	1647	14	US-10-127-839A-191	Sequence 191, App
39	1625.4	99.9	1647	14	US-10-127-901A-191	Sequence 191, App
40	1625.4	99.9	1647	14	US-10-128-693A-191	Sequence 191, App
41	1625.4	99.9	1647	14	US-10-131-813A-191	Sequence 191, App
42	1625.4	99.9	1647	14	US-10-131-818A-191	Sequence 191, App
43	1625.4	99.9	1647	14	US-10-131-823A-191	Sequence 191, App
44	1625.4	99.9	1647	14	US-10-131-824A-191	Sequence 191, App
45	1625.4	99.9	1647	14	US-10-131-830A-191	Sequence 191, App

ALIGNMENTS

RESULT 1

US-10-729-807-28

; Sequence 28, Application US/10729807

; Publication No. US20040132158A1

; GENERAL INFORMATION:

; APPLICANT: BANDMAN, Olga; HILLMAN, Jennifer L.

; APPLICANT: TANG, Y. Tom; LAL, Preeti G.

; APPLICANT: YUE, Henry; AZIMZAI, Yalda

; APPLICANT: BAUGHN, Mariah R.; LU, Dyoung Aina M.

; TITLE OF INVENTION: HUMAN PEPTIDASES

; FILE REFERENCE: PF-0651-1 DIV

; CURRENT APPLICATION NUMBER: US/10/729,807

; CURRENT FILING DATE: 2003-12-05

; PRIOR APPLICATION NUMBER: US 09/889,238

; PRIOR FILING DATE: 2002-01-24

; PRIOR APPLICATION NUMBER: PCT/US00/00641

; PRIOR FILING DATE: 2000-01-11

; PRIOR APPLICATION NUMBER: US 60/172,247

; PRIOR FILING DATE: 1999-01-11

; PRIOR APPLICATION NUMBER: US 60/132,253

; PRIOR FILING DATE: 1999-05-03

; PRIOR APPLICATION NUMBER: US 60/136,653

; PRIOR FILING DATE: 1999-05-27

; NUMBER OF SEQ ID NOS: 39

; SOFTWARE: PERL Program

; SEQ ID NO 28

; LENGTH: 1627

; TYPE: DNA

; ORGANISM: Homo sapiens

; FEATURE:

; NAME/KEY: misc feature

; OTHER INFORMATION: Incyte ID No: 3772696CB1

US-10-729-807-28

Query Match

100.0%; Score 1627; DB 17; Length 1627;

1021	ACGAAACCCCGACGAGATAAGATTCTGGTGTTTTAAAGATGAACACTTCGTGGATGATCAGAG	1080
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1081	GATATGCTGCTCTGGCAGATTATCCAAATCATCCATACATAGTGGTTTCCAGGACGTG	1140
1141	TGAAGAAATATAGATGCAGCCGCTCTGTGATAGACCAAGAAAAACCTACTTCTTTGTGG	1200
1141	TGAAGAAATATAGATGCAGCCGCTCTGTGATAGACCAAGAAAAACCTACTTCTTTGTGG	1200
1201	GCATTTGGTGTGGAGGTTTGATGAAATGACCCAAACCATGACAAGATTCCTGGCGAGA	1260
1201	GCATTTGGTGTGGAGGTTTGATGAAATGACCCAAACCATGACAAGATTCCTGGCGAGA	1260
1261	GAGTGGTAAAAACACATTCCTCGAAATCAGTATCCGTTGTGANGCTGCTTTCCAGTCAAAAG	1320
1261	GAGTGGTAAAAACATTCCTCGAAATCAGTATCCGTTGTGANGCTGCTTTCCAGTCAAAAG	1320
1321	GATTCTTCTTTTTCAGCCGTGGATCAAGCAATTTTGAATACAACTTAAGACAAAGAATA	1380
1321	GATTCTTCTTTTTCAGCCGTGGATCAAGCAATTTTGAATACAACTTAAGACAAAGAATA	1380
1381	TTACCCGAATCATGAACTAATACTTGGTTTCAATGCAAGAAACCAAGAACTCCTCAT	1440
1381	TTACCCGAATCATGAACTAATACTTGGTTTCAATGCAAGAAACCAAGAACTCCTCAT	1440
1441	TTGGTTTTGATATCAACAGGAAAAAGCAATTCAGGAGGCATTAAGATATTGTATCATTA	1500
1441	TTGGTTTTGATATCAACAGGAAAAAGCAATTCAGGAGGCATTAAGATATTGTATCATTA	1500
1501	AGAGTTTAAGCTGTATTATTTTGGTATTGTTTCATTTGCTGAAAAACACTTCTATTATTATC	1560
1501	AGAGTTTAAGCTGTATTATTTTGGTATTGTTTCATTTGCTGAAAAACACTTCTATTATTATC	1560
1561	AATAAATTCATAGACCTAAAAATAAACCTCAACAGGCTTTTTTAATAATAAATTCGTGTTCAA	1620
1561	AATAAATTCATAGACCTAAAAATAAACCTCAACAGGCTTTTTTAATAATAAATTCGTGTTCAA	1620
1621	AATAGAA 1627	QY
1621	AATAGAA 1627	Db

RESULT 2

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US-09-862-631-1
; Sequence 1, Application US/09862631
; Publication No. US200300321641
; GENERAL INFORMATION:
; APPLICANT: Holmgren, Erik
; APPLICANT: Kihlen, Mats
; APPLICANT: Wood, Tim
; APPLICANT: Ekblom, Jonas
; TITLE OF INVENTION: No. US200300321641
; FILE REFERENCE: 0001489US
; CURRENT APPLICATION NUMBER: US/09/09/0001489US
; CURRENT FILING DATE: 2001-05-22
; PRIOR APPLICATION NUMBER: 206119
; PRIOR FILING DATE: 2000-05-22
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: Patentin version 3.0
; SEQ ID NO 1
; LENGTH: 1845
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-862-631-1

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Best Local Similarity 100.0%; Pred. No 0;
Matches 1627; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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	Best Local Similarity	100.0%;	Pred. No. 0;	Mismatches	0;	Indels	0;	Gaps	0;
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1	b	GCTTCAGCTGAAGAAAGAGAGGAATGAAGCGCTTCGTCTTGTGTGTTTCTTTATAA	60						
61	Y	CAITTTCTTCGTATTTCCCTTAGTCGGATGAGGNAATGAGAAATATCAACATGG	120						
61	b	CAITTTCTTCGTATTTCCCTTAGTCGGATGAGGNAATGAGAAATATCAACATGG	120						
121	Y	CTCAGGCATATCTCAACAGCTTTACTCTCTTGAAATAGAGGGAATCATCTTTTCAAA	180						
121	b	CTCAGGCATATCTCAACAGCTTTACTCTCTTGAAATAGAGGGAATCATCTTTTCAAA	180						
181	Y	GCAAGATAGAGGTCTCATAGATGCAAAATTCGGGAAATGCAAGCAATTTTGGATTGA	240						
181	b	GCAAGATAGAGGTCTCATAGATGCAAAATTCGGGAAATGCAAGCAATTTTGGATTGA	240						
241	Y	CAGTGACTGGAAAACCTCGACTCAACACCCCTTGAGATCATGAAGACACCCAGGTGTGGG	300						
241	b	CAGTGACTGGAAAACCTCGACTCAACACCCCTTGAGATCATGAAGACACCCAGGTGTGGG	300						
301	Y	TGCTGTATGTGGGCCAGTATGGCTACACCTCCCTGGGTGAGAAATATCAACCTCACCT	360						
301	b	TGCTGTATGTGGGCCAGTATGGCTACACCTCCCTGGGTGAGAAATATCAACCTCACCT	360						
361	Y	ACAGAAATATATACTATFACTCGGATATGGACAGCTGCTGGATGAGGCTATCCAAG	420						
361	b	ACAGAAATATATACTATFACTCGGATATGGACAGCTGCTGGATGAGGCTATCCAAG	420						
421	Y	AAGGTTTAGAAGTGTGGAGCAAGTCACTCCACTAAAAATTCACCAAGATTTCAAAGGGGA	480						
421	b	AAGGTTTAGAAGTGTGGAGCAAGTCACTCCACTAAAAATTCACCAAGATTTCAAAGGGGA	480						
481	Y	TTGCAGACATCATGATTCCTTTAGGACTCGAGTCCATGGTCGTCTCTCGCTATTTTG	540						
481	b	TTGCAGACATCATGATTCCTTTAGGACTCGAGTCCATGGTCGTCTCTCGCTATTTTG	540						
541	Y	ATGTTCCCTTTGGAGTGTCTGCCATGCTTTCTCTGGTCCGGTCTGGGTGTGTGACA	600						
541	b	ATGTTCCCTTTGGAGTGTCTGCCATGCTTTCTCTGGTCCGGTCTGGGTGTGTGACA	600						
601	Y	CTCATTTTATGAGGATGAAACTGGAACCAAGGATGGAGCAGGATTCACCTTTGTTCTTG	660						
601	b	CTCATTTTATGAGGATGAAACTGGAACCAAGGATGGAGCAGGATTCACCTTTGTTCTTG	660						
661	Y	TGGCTGCTCATGAAATTTGCTCATGACTGGGCTCTCTCCTCCATGATCAAAAGCCT	720						
661	b	TGGCTGCTCATGAAATTTGCTCATGACTGGGCTCTCTCCTCCATGATCAAAAGCCT	720						
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781	b	TCAATGGAATCCAGTCCATCTATGAGGCTGCTGCTAGGTAAGGTAAGGTAAGGTAAG	840						
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841	b	CCACTATACCCCATGCTGTGACCTTGTGACTTTTGAACGCTATCAAACTTTCCGCA	900						
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901	b	GAGAAGTAATGTTCTTTAAAGGAGGACCTATGAGGATCTATTAATGATATCACGGATG	960						
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1021	Y	ACCAGAACCCAGAGATAAGATTCGTGTTTTTAAAGTGAATCACTCTGGATGATCAGAG	1080						

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QY 121 CTCAGCATATCTCAACCAAGTTCTTACTCTCTGAAATAGAGGGAATCATCTTTTCAAA 180
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Db 481 TTGAGACATCATGATGCTTTAGGACTCGAGTCCATGCTCGGTGCTGCTGCTATTTTG 540
QY 541 ATGGTCCCTTGGGAGTGTGGCCATGCTTTCCCTGCTGCTCGGTGCTGCTGCTGACA 600
Db 541 ATGGTCCCTTGGGAGTGTGGCCATGCTTTCCCTGCTGCTCGGTGCTGCTGCTGACA 600
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QY 661 TGGCTGCTCATGATTTGGTCTATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 720
Db 661 TGGCTGCTCATGATTTGGTCTATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 720
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Db 721 TGATGTTCCCAATATGCTCTCCCTGAGTCCAGAAATACCCACTTTCTCAGGATGATA 780
QY 781 TCAATGGAAATCCAGTCCATCTATGGAGTCTGCTTAAGGTACCTGCTAAGCCAAAGGAAC 840
Db 781 TCAATGGAAATCCAGTCCATCTATGGAGTCTGCTTAAGGTACCTGCTAAGCCAAAGGAAC 840
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QY 1021 ACAGAAACCCAGAGATGAAGATTTGTTTTTAAAGATGAAAATCTTGGATGATCAGAG 1080
Db 1021 ACAGAAACCCAGAGATGAAGATTTGTTTTTAAAGATGAAAATCTTGGATGATCAGAG 1080
QY 1081 GATATGCTGCTTCCAGATATATCCCAATCCATCCATACATATAGGTTTTCCAGAGCTG 1140
Db 1081 GATATGCTGCTTCCAGATATATCCCAATCCATCCATACATATAGGTTTTCCAGAGCTG 1140

QY 1141 TGAAGAAATAGATGACGCGTCTGTGATAGACCAAGAAACCACTACTTCTTTGTGG 1200
Db 1141 TGAAGAAATAGATGACGCGTCTGTGATAGACCAAGAAACCACTACTTCTTTGTGG 1200
QY 1201 GCATTTGGTGTCTGAGGTTTGAATGACCCCAACCAAGGATTCGCCGAGA 1260
Db 1201 GCATTTGGTGTCTGAGGTTTGAATGACCCCAACCAAGGATTCGCCGAGA 1260
QY 1261 GAGTGTTAAACACATTTCTCGGATCAGTATCGGTGCTGCTTTCCAGTACAAAG 1320
Db 1261 GAGTGTTAAACACATTTCTCGGATCAGTATCGGTGCTGCTTTCCAGTACAAAG 1320
QY 1321 GATTTCTTTTTCAGCGTGGATCAAGCAATTTGAATACACATTAAGACAAAGATA 1380
Db 1321 GATTTCTTTTTCAGCGTGGATCAAGCAATTTGAATACACATTAAGACAAAGATA 1380
QY 1381 TTACCCGAATCATGAGAACTAATACTTGGTTTCAATGCAAGAACCAAGAACTCTCTAT 1440
Db 1381 TTACCCGAATCATGAGAACTAATACTTGGTTTCAATGCAAGAACCAAGAACTCTCTAT 1440
QY 1441 TTGGTTTTGATATCAACAGGAAAGACATTCAGGAGGCATAAAGATATTGTATCAT 1500
Db 1441 TTGGTTTTGATATCAACAGGAAAGACATTCAGGAGGCATAAAGATATTGTATCAT 1500
QY 1501 AGAGTTTAAAGCTTGTATTTTGGTATTTGTTTCAATTTGCTGAAACACCTTATTATC 1560
Db 1501 AGAGTTTAAAGCTTGTATTTTGGTATTTGTTTCAATTTGCTGAAACACCTTATTATC 1560
QY 1561 AATAAATTCATAGACCTAAATATAACCTCAACAGTCTTTTAAATATAATTCGTTCAA 1620
Db 1561 AATAAATTCATAGACCTAAATATAACCTCAACAGTCTTTTAAATATAATTCGTTCAA 1620
QY 1621 AATAGAA 1627
Db 1621 AATAGAA 1627

RESULT 3

US-10-028-072-191
; Sequence 191, Application US/10028072
; Publication No. US20030004311A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Beresini, Maureen
; APPLICANT: DeForge, Laura
; APPLICANT: Desnoyers, Luc
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Sherwood, Steven
; APPLICANT: Smith, Victoria
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Watanabe, Colin K
; APPLICANT: Wood, William
; APPLICANT: Zhang
; TITLE OF INVENTION:
; FILE REFERENCE:
; CURRENT APPLICATION NUMBER: US/10/028,072
; CURRENT FILING DATE: 2001-12-19
; PRIOR APPLICATION NUMBER: 60/049911
; PRIOR FILING DATE: 1997-06-18
; PRIOR APPLICATION NUMBER: 60/056974
; PRIOR FILING DATE: 1997-08-26
; PRIOR APPLICATION NUMBER: 60/059113
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/059115
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/059117
; PRIOR FILING DATE: 1997-09-17

PRIOR APPLICATION NUMBER: 60/059122
 PRIOR FILING DATE: 1997-09-17
 PRIOR APPLICATION NUMBER: 60/059184
 PRIOR FILING DATE: 1997-09-17
 PRIOR APPLICATION NUMBER: 60/059263
 PRIOR FILING DATE: 1997-09-18
 PRIOR APPLICATION NUMBER: 60/059352
 PRIOR FILING DATE: 1997-09-19
 PRIOR APPLICATION NUMBER: 60/059588
 PRIOR FILING DATE: 1997-09-19
 PRIOR APPLICATION NUMBER: 60/059836
 PRIOR FILING DATE: 1997-09-24
 PRIOR APPLICATION NUMBER: 60/062250
 PRIOR FILING DATE: 1997-10-17
 PRIOR APPLICATION NUMBER: 60/062285
 PRIOR FILING DATE: 1997-10-17
 PRIOR APPLICATION NUMBER: 60/062287
 PRIOR FILING DATE: 1997-10-17
 PRIOR APPLICATION NUMBER: 60/062814
 PRIOR FILING DATE: 1997-10-24
 PRIOR APPLICATION NUMBER: 60/062816
 PRIOR FILING DATE: 1997-10-24
 PRIOR APPLICATION NUMBER: 60/063045
 PRIOR FILING DATE: 1997-10-24
 PRIOR APPLICATION NUMBER: 60/063082
 PRIOR FILING DATE: 1997-10-31
 PRIOR APPLICATION NUMBER: 60/063127
 PRIOR FILING DATE: 1997-10-24
 PRIOR APPLICATION NUMBER: 60/063327
 PRIOR FILING DATE: 1997-10-27
 PRIOR APPLICATION NUMBER: 60/063329
 PRIOR FILING DATE: 1997-10-27
 PRIOR APPLICATION NUMBER: 60/063550
 PRIOR FILING DATE: 1997-10-28
 PRIOR APPLICATION NUMBER: 60/063561
 PRIOR FILING DATE: 1997-10-28
 PRIOR APPLICATION NUMBER: 60/063704
 PRIOR FILING DATE: 1997-10-29
 PRIOR APPLICATION NUMBER: 60/063733
 PRIOR FILING DATE: 1997-10-29
 PRIOR APPLICATION NUMBER: 60/063735
 PRIOR FILING DATE: 1997-10-29
 PRIOR APPLICATION NUMBER: 60/063738
 PRIOR FILING DATE: 1997-10-29
 PRIOR APPLICATION NUMBER: 60/063755
 PRIOR FILING DATE: 1997-10-17
 PRIOR APPLICATION NUMBER: 60/064248
 PRIOR FILING DATE: 1997-11-03
 PRIOR APPLICATION NUMBER: 60/064809
 PRIOR FILING DATE: 1997-11-07
 PRIOR APPLICATION NUMBER: 60/065186
 PRIOR FILING DATE: 1997-11-12
 PRIOR APPLICATION NUMBER: 60/065846
 PRIOR FILING DATE: 1997-11-17
 PRIOR APPLICATION NUMBER: 60/066364
 PRIOR FILING DATE: 1997-11-21
 PRIOR APPLICATION NUMBER: 60/066453
 PRIOR FILING DATE: 1997-11-24
 PRIOR APPLICATION NUMBER: 60/066511
 PRIOR FILING DATE: 1997-11-24
 PRIOR APPLICATION NUMBER: 60/066770
 PRIOR FILING DATE: 1997-11-24
 PRIOR APPLICATION NUMBER: 60/069212
 PRIOR FILING DATE: 1997-12-11
 PRIOR APPLICATION NUMBER: 60/069278
 PRIOR FILING DATE: 1997-12-11
 PRIOR APPLICATION NUMBER: 60/069334
 PRIOR FILING DATE: 1997-12-11
 PRIOR APPLICATION NUMBER: 60/069694
 PRIOR FILING DATE: 1997-12-16
 PRIOR APPLICATION NUMBER: 60/072320
 PRIOR FILING DATE: 1998-01-23
 PRIOR APPLICATION NUMBER: 60/073612

		Query Match		99.9%; Score 1625.4; DB 14; Length 1647;	
		Best Local Similarity		99.9%; Pred. No. 0;	
		Matches 1626; Conservative 0; Mismatches 1; Indels 0; Gaps 0;			
QY	1	GCTTCAGCTGAAAGAGAGAGGAATGAAGCGCTTCTGCTCTCTGCTTGGTCTTTTATAA	60	Db	721
	1	GCTTCAGCTGAAAGAGAGAGGAATGAAGCGCTTCTGCTCTCTGCTTGGTCTTTTATAA	60		721
QY	61	GATTTTCTTCTGCATTTCCCTTAGTCGCGATGACGGAAATGAAGAAATATGCAACTGG	120	Db	781
	61	CATTTTCTTCTGCATTTCCCTTAGTCGCGATGACGGAAATGAAGAAATATGCAACTGG	120		781
QY	121	CTCAGGCATATCTCAACAGTTCTACTCTCTTGAATAGAAGGAATCATCTTGTTCAAA	180	Db	841
	121	CTCAGGCATATCTCAACAGTTCTACTCTCTTGAATAGAAGGAATCATCTTGTTCAAA	180		841
QY	181	GCAAGAAATAGGAGTCTCATAGATGACAAATTCGGGAAATGAAGCAATTTTGGATTTGA	240	Db	901
	181	GCAAGAAATAGGAGTCTCATAGATGACAAATTCGGGAAATGAAGCAATTTTGGATTTGA	240		901
QY	241	CAGTGACTGGAAAACCTGGACTCAACACCTTGAGATCATGAAGACACCCAGGTGGGG	300	Db	961
	241	CAGTGACTGGAAAACCTGGACTCAACACCTTGAGATCATGAAGACACCCAGGTGGGG	300		961
QY	301	TGCTGATGTGGCCAGTATGCTACACCTCCCTGGGTGGAGAAATACAACTCACT	360	Db	1021
	301	TGCTGATGTGGCCAGTATGCTACACCTCCCTGGGTGGAGAAATACAACTCACT	360		1021
QY	361	ACAGAAATATAACTATCTCCGATATGCGACGAGCTGCTGTGGATGAGGCTATCCAA	420	Db	1081
	361	ACAGAAATATAACTATCTCCGATATGCGACGAGCTGCTGTGGATGAGGCTATCCAA	420		1081
QY	421	AAGGTTTAGAGTGTGGAGAAAGTCACTCACTAAATTCACCAAGATTTCAAAGGGGA	480	Db	1141
	421	AAGGTTTAGAGTGTGGAGAAAGTCACTCACTAAATTCACCAAGATTTCAAAGGGGA	480		1141
QY	481	TTGAGACATCATGATGCTTTAGGACTCGAGTCCATGCTGCTGCTGCTGCTGCTGCT	540	Db	1201
	481	TTGAGACATCATGATGCTTTAGGACTCGAGTCCATGCTGCTGCTGCTGCTGCTGCT	540		1201
QY	541	ATGGTCCCTTGGAGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT	600	Db	1261
	541	ATGGTCCCTTGGAGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT	600		1261
QY	601	CTCATTTTATGAGGATGAAATCTGGACCAAGATGGAGGAGGATTCAACTTGTTCCTG	660	Db	1321
	601	CTCATTTTATGAGGATGAAATCTGGACCAAGATGGAGGAGGATTCAACTTGTTCCTG	660		1321
QY	661	TGGCTGCTCATGATTTGGTTCATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT	720	Db	1381
	661	TGGCTGCTCATGATTTGGTTCATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT	720		1381

RESULT 4
US-10-140-808-191
; Sequence 191, Application US/10140808
; Publication No. US20030017563A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Beresini, Maureen
; APPLICANT: DeForge, Laura


```

: Sequence 191, Application US/10121049
: Publication No. US2003002239A1
: GENERAL INFORMATION:
: APPLICANT: Baker, Kevin P.
: APPLICANT: Beresini, Maureen
: APPLICANT: DeForge, Laura
: APPLICANT: Desnoyers, Luc
: APPLICANT: Filvaroff, Ellen
: APPLICANT: Gao, Wei-Qiang
: APPLICANT: Gerritsen, Mary E.
: APPLICANT: Goddard, Audrey
: APPLICANT: Godowski, Paul J.
: APPLICANT: Gurney, Austin L.
: APPLICANT: Sherwood, Steven
: APPLICANT: Smith, Victoria
: APPLICANT: Stewart, Timothy A.
: APPLICANT: Tumas, Daniel
: APPLICANT: Watanabe, Colin K
: APPLICANT: Wood, William
: APPLICANT: Zhang, Zemin
: TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
: TITLE OF INVENTION: ACIDS ENCODING THE SAME
: FILE REFERENCE: P3330R1C17
: CURRENT APPLICATION NUMBER: US/10/121,049
: CURRENT FILING DATE: 2002-04-12
: Prior Application removed - See File Wrapper or Palm
: NUMBER OF SEQ ID NOS: 550
: SEQ ID NO 191
: LENGTH: 1647
: TYPE: DNA
: ORGANISM: Homo Sapien
: US-10-121-049-191

```

Query Match	99.9%;	Score 1625.4;	DB 14;	Length 1647;
Best Local Similarity	99.9%;	Pred. No. 0;		
Matches 1626;	Conservative 0;	Mismatches 1;	Indels 0;	Gaps 0;
QY 1	GCTTCAGCTGAAGAAGAGAGGAATGAAGCGGCTTCTGCTTCTGTTGTTTGTCTTTATAA	60		
DB				
QY 1	GCTTCAGCTGAAGAAGAGAGGAATGAAGCGGCTTCTGCTTCTGTTTGTCTTTATAA	60		
DB				
QY 61	CAITTTCTTCTGCATTTCCCTTAGTCCGGATGACGGAATAATGAAGAAATATGCAACTGG	120		
DB				
QY 61	CAITTTCTTCTGCATTTCCCTTAGTCCGGATGACGGAATAATGAAGAAATATGCAACTGG	120		
DB				
QY 121	CTCAGGCATATCTCAACAGATTCTACTCTCTGAAATAGAAGGAATCATCTGTTCAAA	180		
DB				
QY 121	CTCAGGCATATCTCAACAGATTCTACTCTCTGAAATAGAAGGAATCATCTGTTCAAA	180		
DB				
QY 181	GCAAGAAATAGGAGTCTCATAGATGACAAAAATTCGGGAATGCAAGCATTTTTTGGATTGA	240		
DB				
QY 181	GCAAGAAATAGGAGTCTCATAGATGACAAAAATTCGGGAATGCAAGCATTTTTTGGATTGA	240		
DB				
QY 241	CAGTGACTGGAATACTGGACTCAAACACCCTTGAGATCATGAAGACACCCAGGTGTGGG	300		
DB				
QY 241	CAGTGACTGGAATACTGGACTCAAACACCCTTGAGATCATGAAGACACCCAGGTGTGGG	300		
DB				
QY 301	TGCCTGATGTGGGCCAGTATGGCTACACCTCCCTGGGTGAGAAAAATPACAACCTCACCT	360		
DB				
QY 301	TGCCTGATGTGGGCCAGTATGGCTACACCTCCCTGGGTGAGAAAAATPACAACCTCACCT	360		
DB				
QY 361	ACAGAAATAAATAACTATACTCCGGATATGGACAGCTGCTGCGATGAGGCTATCCAAAG	420		
DB				
QY 361	ACAGAAATAAATAACTATACTCCGGATATGGACAGCTGCTGCGATGAGGCTATCCAAAG	420		
DB				
QY 421	AAGTTTGAAGTGTGGAGCAAAAGTCACTCCACTAAAATTCAACAAAGATTTCAAAGGGA	480		
DB				
QY 421	AAGTTTGAAGTGTGGAGCAAAAGTCACTCCACTAAAATTCAACAAAGATTTCAAAGGGA	480		
DB				
QY 481	TTGCAGACATCATGATTCCTTTTAGGACTCGAGTCCATGGTGGTGCTCGCTATTTTG	540		
DB				
QY 481	TTGCAGACATCATGATTCCTTTTAGGACTCGAGTCCATGGTGGTGCTCGCTATTTTG	540		
DB				

QY 1561 AATAAATTCATAGACCTAAATAAATAAATCTCAACAGGCTCTTTTAATATAAATTTCTGCTTCAA 1620
Db |||||
QY 1561 AATAAATTCATAGACCTAAATAAATAAATCTCAACAGGCTCTTTTAATATAAATTTCTGCTTCAA 1620
Db |||||
QY 1621 AATAGAA 1627
Db |||||
QY 1621 AATAGAA 1627

RESULT 7

US-10-140-470-191
; Sequence 191, Application US/10140470
; Publication No. US20030022331A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Beresini, Maureen
; APPLICANT: Deforge, Laura
; APPLICANT: Desnoyers, Luc
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Sherwood, Steven
; APPLICANT: Smith, Victoria
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Watanabe, Colin K
; APPLICANT: Wood, William
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P3330RIC160
; CURRENT APPLICATION NUMBER: US/10/140,470
; CURRENT FILING DATE: 2002-05-06
; Prior Application removed - See Palm or File Wrapper
; NUMBER OF SEQ ID NOS: 550
; SEQ ID NO 191
; LENGTH: 1647
; TYPE: DNA
; ORGANISM: Homo Sapien
US-10-140-470-191

Query Match 99.9%; Score 1625.4; DB 14; Length 1647;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 1626; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GCTTCAGCTGAAGAAAGAGAGGAATGAAGCGCCTTCTGCTCTCTGTGTGTTGTTCTTTTATAA 60
Db 1 GCTTCAGCTGAAGAAAGAGAGGAATGAAGCGCCTTCTGCTCTCTGTGTGTTGTTCTTTTATAA 60
QY 61 CATTTTCTTCGATTTCCCTTAGTCCCGATGACGGAAATCAAGAAAATATGCAACTGG 120
Db 61 CATTTTCTTCGATTTCCCTTAGTCCCGATGACGGAAATCAAGAAAATATGCAACTGG 120
QY 121 CTCAGGCATATCTCAACAGTTCTACTCTCTTGAATAGAGGGAATCATCTGTGTTCAA 180
Db 121 CTCAGGCATATCTCAACAGTTCTACTCTCTTGAATAGAGGGAATCATCTGTGTTCAA 180
QY 181 GCAAGAAATAGGAGTCTCATAGATGACAAAATTCGGGAATGCAAGCATTTTTCGATTGA 240
Db 181 GCAAGAAATAGGAGTCTCATAGATGACAAAATTCGGGAATGCAAGCATTTTTCGATTGA 240
QY 241 CAGTGACTGGAAAACTGGACTCAAAACCTTGGAGATCATGAAGACACCCAGGTGTGGGG 300
Db 241 CAGTGACTGGAAAACTGGACTCAAAACCTTGGAGATCATGAAGACACCCAGGTGTGGGG 300
QY 301 TGCCTGATGTGGCCAGTATGGCTACACCTCCCTGGGTGGAGAAAATACAACTTCACCT 360
Db 301 TGCCTGATGTGGCCAGTATGGCTACACCTCCCTGGGTGGAGAAAATACAACTTCACCT 360

QY 361 ACAGAAATATAAATCTATATCTCCGGATATGGCAGAGCTGCTGTGGATGAGGCTATCCAAG 420
Db |||||
QY 361 ACAGAAATATAAATCTATATCTCCGGATATGGCAGAGCTGCTGTGGATGAGGCTATCCAAG 420
Db |||||
QY 421 AAGGTTTGAAGTGTGGAGCAAAAGTCACCTCCACTTAAATTCACCAAGATTTTCAAGGGGA 480
Db |||||
QY 421 AAGGTTTGAAGTGTGGAGCAAAAGTCACCTCCACTTAAATTCACCAAGATTTTCAAGGGGA 480
Db |||||
QY 481 TTGCAGACATCATGATTTGGCTTTAGGATCGAGTCCATGCTCGGTGCTCCTCGCTATTTTG 540
Db |||||
QY 481 TTGCAGACATCATGATTTGGCTTTAGGATCGAGTCCATGCTCGGTGCTCCTCGCTATTTTG 540
Db |||||
QY 541 ATGGTCCCTTGGAGTGTGCTTGGCCATGCTTCTCTCGTGGGTGCTGGGTGGTGACA 600
Db |||||
QY 541 ATGGTCCCTTGGAGTGTGCTTGGCCATGCTTCTCTCGTGGGTGCTGGGTGGTGACA 600
Db |||||
QY 601 CTCATTTTGTGAGGATGAAAACTGGACCAAGATGGAGCAGGATTCACATTTGTTCTTG 660
Db |||||
QY 601 CTCATTTTGTGAGGATGAAAACTGGACCAAGATGGAGCAGGATTCACATTTGTTCTTG 660
Db |||||
QY 661 TGGCTGCTCATGAAATTTGGTCAATGCACTGGGCTCTCTCACTCCAATGATCAACAGCCT 720
Db |||||
QY 661 TGGCTGCTCATGAAATTTGGTCAATGCACTGGGCTCTCTCACTCCAATGATCAACAGCCT 720
Db |||||
QY 721 TGATGTTCCCAATTTATGCTCTCCCTGGATCCAGAAAATACCCACTTTCTCAGGATGATA 780
Db |||||
QY 721 TGATGTTCCCAATTTATGCTCTCCCTGGATCCAGAAAATACCCACTTTCTCAGGATGATA 780
Db |||||
QY 781 TCAATGGAATCCAGTCCATCTATGAGGTCTCCCTAAAGTACTCTGTAAGCCAAAGGAAC 840
Db |||||
QY 781 TCAATGGAATCCAGTCCATCTATGAGGTCTCCCTAAAGTACTCTGTAAGCCAAAGGAAC 840
Db |||||
QY 841 CCATATATCCCCATGCTGTGACCTTGTGACCTTTTGACGCTATCAAACTTTCCGCA 900
Db |||||
QY 841 CCATATATCCCCATGCTGTGACCTTGTGACCTTTTGACGCTATCAAACTTTCCGCA 900
Db |||||
QY 901 GAGAAATATGTTCTTTAAAGCAGGACCTATGAGGATCTATTATGATATCAAGGATG 960
Db |||||
QY 901 GAGAAATATGTTCTTTAAAGCAGGACCTATGAGGATCTATTATGATATCAAGGATG 960
Db |||||
QY 961 TTGAGTTTGAATTAATTCCTTCATTTGCGCATCTCTGCCAGTCTATGCAAGCTGCAT 1020
Db |||||
QY 961 TTGAGTTTGAATTAATTCCTTCATTTGCGCATCTCTGCCAGTCTATGCAAGCTGCAT 1020
Db |||||
QY 1021 ACAGAAACCCAGAGATGAATCTGTTTAAAGATGAAAACTTCTGGATGATCAGAG 1080
Db |||||
QY 1021 ACAGAAACCCAGAGATGAATCTGTTTAAAGATGAAAACTTCTGGATGATCAGAG 1080
Db |||||
QY 1081 GATATGCTGCTTGGCAGATTTATCCCAATCCATCCATACATTAGGTTTTCAGGACGTG 1140
Db |||||
QY 1081 GATATGCTGCTTGGCAGATTTATCCCAATCCATCCATACATTAGGTTTTCAGGACGTG 1140
Db |||||
QY 1141 TGAAGAAAAATAGATGACGCGCTCTGTGATAAGACACAAAGAAAAACCTTCTTTGG 1200
Db |||||
QY 1141 TGAAGAAAAATAGATGACGCGCTCTGTGATAAGACACAAAGAAAAACCTTCTTTGG 1200
Db |||||
QY 1201 GCATTTGGTGTGAGGTTTGTGAAATGACCCAAACCATGCAAAAGGATTTCCCGCAGA 1260
Db |||||
QY 1201 GCATTTGGTGTGAGGTTTGTGAAATGACCCAAACCATGCAAAAGGATTTCCCGCAGA 1260
Db |||||
QY 1261 GAGTGGTAAACACATTTCTCGGATCAGTATCCGTGTGTGATGCTGCTTTCCAGTACAAG 1320
Db |||||
QY 1261 GAGTGGTAAACACATTTCTCGGATCAGTATCCGTGTGTGATGCTGCTTTCCAGTACAAG 1320
Db |||||
QY 1321 GATTTCTTTTTCAGCGCTGGATCAAGCAATTTTGAATCAACATTAAGCAAGGATA 1380
Db |||||
QY 1321 GATTTCTTTTTCAGCGCTGGATCAAGCAATTTTGAATCAACATTAAGCAAGGATA 1380
Db |||||
QY 1381 TTACCCGAATCATGAGAACTAATCTTGGTTTCAATGCAAAAGAACCAAGAACTTCCTCAT 1440
Db |||||
QY 1381 TTACCCGAATCATGAGAACTAATCTTGGTTTCAATGCAAAAGAACCAAGAACTTCCTCAT 1440
Db |||||
QY 1441 TTGTTTGTGATATCAACAGGAAAAAGCACTTCAGGAGGATTAAGATATTGTATCATA 1500

Db 1441 TTGGTTTTCATATCAACAGGAAACGACATTCAGAGGCATTAAGATATTTGATCATATA 1500
Qy 1501 AGAGTTTAAAGCTGTGTTTATTTTGGTATTTGTTCAATTTGCTGAAACACATTCATTTATC 1560
Db 1501 AGAGTTTAAAGCTGTGTTTATTTTGGTATTTGTTCAATTTGCTGAAACACATTCATTTATC 1560
Qy 1561 AATAAATTCATAGACCTAAATTAACCTCAACAGGCTTTTAAATATAAAATTTGCTTTCAA 1620
Db 1561 AATAAATTCATAGACCTAAATTAACCTCAACAGGCTTTTAAATATAAAATTTGCTTTCAA 1620
Qy 1621 AATAGAA 1627
Db 1621 AATAGAA 1627

RESULT 8

US-10-175-746-191
; Sequence 191, Application US/10175746
; Publication No. US20030027270A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Beresini, Maureen
; APPLICANT: DeForge, Laura
; APPLICANT: Desnoyers, Luc
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Sherwood, Steven
; APPLICANT: Smith, Victoria
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Watanabe, Colin K
; APPLICANT: Wood, William
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE OF INVENTION: ACIDS ENCODING THE SAME
; FILE REFERENCE: P3330R1C353
; CURRENT APPLICATION NUMBER: US/10/175,746
; CURRENT FILING DATE: 2002-06-19
; Prior Application removed - See File Wrapper or Palm
; NUMBER OF SEQ ID NOS: 550
; SEQ ID NO 191
; LENGTH: 1647
; TYPE: DNA
; ORGANISM: Homo Sapien
US-10-175-746-191

Query Match 99.9%; Score 1625.4; DB 14; Length 1647;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 1626; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
Qy 1 GCTTCAGCTGAAGAAGAGAGAGATGAAGCGCTCTGCTCTGTTGTTGTTCTTTATAA 60
Db 1 GCTTCAGCTGAAGAAGAGAGAGATGAAGCGCTCTGCTCTGTTGTTGTTCTTTATAA 60
Qy 61 CATTTTCTTCGTCAATTCCTTGTAGTCCGGATGACGGAATAATGAAGAAATATGCAACTGG 120
Db 61 CATTTTCTTCGTCAATTCCTTGTAGTCCGGATGACGGAATAATGAAGAAATATGCAACTGG 120
Qy 121 CTCAGGCATATCTCAACAGTTCTACTCTCTTGAATAGAGAGGGAATCATCTGTTCAA 180
Db 121 CTCAGGCATATCTCAACAGTTCTACTCTCTTGAATAGAGAGGGAATCATCTGTTCAA 180
Qy 181 GCAAGAATAGAGGCTCTCATAGATGACAAATTCGGGAATGCAAGCATTTTGGATTGA 240
Db 181 GCAAGAATAGAGGCTCTCATAGATGACAAATTCGGGAATGCAAGCATTTTGGATTGA 240
Qy 241 CAGTGACTGGAAAACTGGACTCAACACCCCTTGAGATCATGAAGACACCCAGGTGTGGG 300
Db 241 CAGTGACTGGAAAACTGGACTCAACACCCCTTGAGATCATGAAGACACCCAGGTGTGGG 300

Db 241 CAGTGACTGGAAAACTGGACTCAACACCCCTTGAGATCATGAAGACACCCAGGTGTGGG 300
Qy 301 TGCCTGATGTGGGCCAGTATGCTACACCCCTCCCTGGGTGGAGAAATACAACCTCACCT 360
Db 301 TGCCTGATGTGGGCCAGTATGCTACACCCCTCCCTGGGTGGAGAAATACAACCTCACCT 360
Qy 361 ACAGATAATAAACHATATCTCCGGATATGGCAGAGCTCTGTGGATGAGGCTATCAAG 420
Db 361 ACAGATAATAAACHATATCTCCGGATATGGCAGAGCTCTGTGGATGAGGCTATCAAG 420
Qy 421 AAGGTTTAGAGTGTGGAGCAAAAGTCACTCCACTAAATTCACCAAGATTTCAAGAGGGA 480
Db 421 AAGGTTTAGAGTGTGGAGCAAAAGTCACTCCACTAAATTCACCAAGATTTCAAGAGGGA 480
Qy 481 TTGCAGACATCATGATTGCTTTAGGACTCGAGTCCATGGTCCGCTCGCTATTTTGG 540
Db 481 TTGCAGACATCATGATTGCTTTAGGACTCGAGTCCATGGTCCGCTCGCTATTTTGG 540
Qy 541 ATGGTCCCTTTGGAGTGTCTTGGCCATGCCCTTCTCTCTGGTCCGGTCTGGGTGGTGACA 600
Db 541 ATGGTCCCTTTGGAGTGTCTTGGCCATGCCCTTCTCTCTGGTCCGGTCTGGGTGGTGACA 600
Qy 601 CTCATTTGATGAGGATGAAACTGCAACAGATGGAGCAGATTCACCTTGTTCCTG 660
Db 601 CTCATTTGATGAGGATGAAACTGCAACAGATGGAGCAGATTCACCTTGTTCCTG 660
Qy 661 TGGCTGCTCATGAATTTGGTCACTGGGCTCTCTCACTCCAATGATCAAAACAGCCT 720
Db 661 TGGCTGCTCATGAATTTGGTCACTGGGCTCTCTCACTCCAATGATCAAAACAGCCT 720
Qy 721 TGATGTTCCAAATTAATGCTCTCCCTGGATCCAGAAATACCCACTTTCTCAGGATGATA 780
Db 721 TGATGTTCCAAATTAATGCTCTCCCTGGATCCAGAAATACCCACTTTCTCAGGATGATA 780
Qy 781 TCAATGGAATCCAGTCCATCTGAGAGTCTGCCAAGGATACCTGCTAAGCAAGGAAC 840
Db 781 TCAATGGAATCCAGTCCATCTGAGAGTCTGCCAAGGATACCTGCTAAGCAAGGAAC 840
Qy 841 CCATATACCCCATGCTGACCCCTGACCTTGTGCTTTTGAAGATGAAACCTTTCGCA 900
Db 841 CCATATACCCCATGCTGACCCCTGACCTTGTGCTTTTGAAGATGAAACCTTTCGCA 900
Qy 901 GAGAAGTAATGTTCTTTAAAGGAGGACCACTATGAGGATCTATATGATATCAGGATG 960
Db 901 GAGAAGTAATGTTCTTTAAAGGAGGACCACTATGAGGATCTATATGATATCAGGATG 960
Qy 961 TTGAGTTTGAATTAATTTGCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1020
Db 961 TTGAGTTTGAATTAATTTGCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1020
Qy 1021 ACAGAAACCCAGAGATAAGATTTCTGGTTTTTAAAGATGAAACCTTCTGATGATCAGAG 1080
Db 1021 ACAGAAACCCAGAGATAAGATTTCTGGTTTTTAAAGATGAAACCTTCTGATGATCAGAG 1080
Qy 1081 GATATGCTGTTCTCCAGATTTATCCCAATCCATCCATACATATAGGTTTCCAGGACGTG 1140
Db 1081 GATATGCTGTTCTCCAGATTTATCCCAATCCATCCATACATATAGGTTTCCAGGACGTG 1140
Qy 1141 TGAAGAAATAGATGAGCGCTCTGTGATAGACCAAGAAACCACTTCTTGTGG 1200
Db 1141 TGAAGAAATAGATGAGCGCTCTGTGATAGACCAAGAAACCACTTCTTGTGG 1200
Qy 1201 GCATTTGGTGTGGAGGTTTGTATGAAATGACCCAAACCATGGAACAAAGGATTCGCGCAGA 1260
Db 1201 GCATTTGGTGTGGAGGTTTGTATGAAATGACCCAAACCATGGAACAAAGGATTCGCGCAGA 1260
Qy 1261 GAGTGGTAAACACATTTCTCGAATCAGTATCCGTTGTGATGCTGCTTCCAGTACAAG 1320
Db 1261 GAGTGGTAAACACATTTCTCGAATCAGTATCCGTTGTGATGCTGCTTCCAGTACAAG 1320
Qy 1321 GATTTCTTTTTCAGCGGTGGATCAAAAGCAATTTGAATACAACTTAAGACAAAGATA 1380
Db 1321 GATTTCTTTTTCAGCGGTGGATCAAAAGCAATTTGAATACAACTTAAGACAAAGATA 1380

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QY 1381 TTACCGAATCATGAGAACTAATCTTGGTTTCAATGCAAGAACCAAGAACTCTCTCAT 1440
Db 1381 TTACCGAATCATGAGAACTAATCTTGGTTTCAATGCAAGAACCAAGAACTCTCTCAT 1440
QY 1441 TTGGTTTGTATATCAACAGGAAAAAGACATTCAGAGGCATPAAGATATTGTATATA 1500
Db 1441 TTGGTTTGTATATCAACAGGAAAAAGACATTCAGAGGCATPAAGATATTGTATATA 1500
QY 1501 AGAGTTTAAGCTTGTTTATTTTGGTATTGTTCAATTTGCTGAAAAACACTTCTATTATC 1560
Db 1501 AGAGTTTAAGCTTGTTTATTTTGGTATTGTTCAATTTGCTGAAAAACACTTCTATTATC 1560
QY 1561 AATAAATTCATAGACCTTAAATAAACTCAACAGGCTCTTTAATATAAAATTTGCTTCAA 1620
Db 1561 AATAAATTCATAGACCTTAAATAAACTCAACAGGCTCTTTAATATAAAATTTGCTTCAA 1620
QY 1621 AATAGAA 1627
Db 1621 AATAGAA 1627

RESULT 9
US-10-176-918-191
; Sequence 191, Application US/10176918
; Publication No. US20030027275A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Bersini, Maureen
; APPLICANT: DeForge, Laura
; APPLICANT: Desnoyers, Luc
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Sherwood, Steven
; APPLICANT: Smith, Victoria
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Watanabe, Colin K
; APPLICANT: Wood, William
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P3330RIC382
; CURRENT APPLICATION NUMBER: US/10/176,918
; Prior Filing Date: 2002-06-20
; Prior Application removed - See File Wrapper or Palm
; NUMBER OF SEQ ID NOS: 550
; SEQ ID NO 191
; LENGTH: 1647
; TYPE: DNA
; ORGANISM: Homo Sapien
US-10-176-918-191

Query Match 99.9%; Score 1625.4; DB 14; Length 1647;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 1626; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GCCTTCAGCTGAAGAAAGAGAGGAATGAAGCGCCTTCTGCTTCTGTTGTTTCTTTATAA 60
Db 1 GCCTTCAGCTGAAGAAAGAGAGGAATGAAGCGCCTTCTGCTTCTGTTGTTTCTTTATAA 60
QY 61 CATTTTCTTCTGCAATTCCTTTCAGTCCGATGACGGAATAAAGAAATATGCAACTGG 120
Db 61 CATTTTCTTCTGCAATTCCTTTCAGTCCGATGACGGAATAAAGAAATATGCAACTGG 120
QY 121 CTCAGGCATATCTCAACAGTTCTACTCTCTTGAATAGAGGGAATCATCTTGTTCAAA 180
Db 121 CTCAGGCATATCTCAACAGTTCTACTCTCTTGAATAGAGGGAATCATCTTGTTCAAA 180
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QY 181 GCAAGTAATAGGAGTCTCATAGATGACAAATTCGGGAAATGCAAGCATTTTTTGGATTGA 240
Db 181 GCAAGTAATAGGAGTCTCATAGATGACAAATTCGGGAAATGCAAGCATTTTTTGGATTGA 240
QY 241 CAGTGAATCGGAAAACTGGACTCAAAACACCCCTTGAGATCATGAAGACACCCAGGTGTGGGG 300
Db 241 CAGTGAATCGGAAAACTGGACTCAAAACACCCCTTGAGATCATGAAGACACCCAGGTGTGGGG 300
QY 301 TGCCTGATGTGGGCCAGTATGAGTACACCCCTCCCTGGGTGGAGAAATACAACTCACCT 360
Db 301 TGCCTGATGTGGGCCAGTATGAGTACACCCCTCCCTGGGTGGAGAAATACAACTCACCT 360
QY 361 ACAGATAATAAATACTACTCCGGATATGCGACGAGCTGCTGTGATGAGGCTATCCAAG 420
Db 361 ACAGATAATAAATACTACTCCGGATATGCGACGAGCTGCTGTGATGAGGCTATCCAAG 420
QY 421 AAGGTTTGAAGTGTGGAGCAAAAGTCACCTCCACTTAAATTCACCAAGATTTCAAAGGGGA 480
Db 421 AAGGTTTGAAGTGTGGAGCAAAAGTCACCTCCACTTAAATTCACCAAGATTTCAAAGGGGA 480
QY 481 TTGCAGACATCATGATATGCTTTAGGACTCGAGTCCATGGTCGGTCTCTCGCTATTTTG 540
Db 481 TTGCAGACATCATGATATGCTTTAGGACTCGAGTCCATGGTCGGTCTCTCGCTATTTTG 540
QY 541 ATGCTCCCTTGGAGTGTCTTGGCCATGCTTTCTCTCTGCTGGTCCGGTCTGGGTGTGACA 600
Db 541 ATGCTCCCTTGGAGTGTCTTGGCCATGCTTTCTCTCTGCTGGTCCGGTCTGGGTGTGACA 600
QY 601 CTCATTTTATGAGGATGAAAACTGGACCAAGATGGAGCAGGATTTCAACTTGTTCCTTG 660
Db 601 CTCATTTTATGAGGATGAAAACTGGACCAAGATGGAGCAGGATTTCAACTTGTTCCTTG 660
QY 661 TGGCTGTCTCATGAATTTGGTCAATGCACTGGGCTCTCTCACTCCAATGATCAACAGCT 720
Db 661 TGGCTGTCTCATGAATTTGGTCAATGCACTGGGCTCTCTCACTCCAATGATCAACAGCT 720
QY 721 TGATGTTCCCAAAATATGCTCTCCCTGGATCCAGAAAATACCCACTTCTCAGGATGATA 780
Db 721 TGATGTTCCCAAAATATGCTCTCCCTGGATCCAGAAAATACCCACTTCTCAGGATGATA 780
QY 781 TCAATGGAATCAGTCCCATCTATGAGGTCTGCTTAAAGTACCTGTAAGCCAAAGGAC 840
Db 781 TCAATGGAATCAGTCCCATCTATGAGGTCTGCTTAAAGTACCTGTAAGCCAAAGGAC 840
QY 841 CCATATACCCCATGCTGTGACCCCTGACTTTGACGCTATCACTTTCCGCA 900
Db 841 CCATATACCCCATGCTGTGACCCCTGACTTTGACGCTATCACTTTCCGCA 900
QY 901 GAGAGTAATCTTCTTTAAAGCAGGACCTATGGAGATCTATGATGATCAAGGATG 960
Db 901 GAGAGTAATCTTCTTTAAAGCAGGACCTATGGAGATCTATGATGATCAAGGATG 960
QY 961 TTGAGTTTGAATTAATTTGCTTTCATTTGGCCATCTCTGCCAGCTGATCTGCAAGCTGAT 1020
Db 961 TTGAGTTTGAATTAATTTGCTTTCATTTGGCCATCTCTGCCAGCTGATCTGCAAGCTGAT 1020
QY 1021 ACAGAACCCAGAGATAAGATTTCTGTTTTTAAAGATGAAAACTTCTGGATGATCAGAG 1080
Db 1021 ACAGAACCCAGAGATAAGATTTCTGTTTTTAAAGATGAAAACTTCTGGATGATCAGAG 1080
QY 1081 GATATGCTGCTTCCAGATTTATCCCAATCCATCCATACATTAGGTTTTTCCAGAGCTG 1140
Db 1081 GATATGCTGCTTCCAGATTTATCCCAATCCATCCATACATTAGGTTTTTCCAGAGCTG 1140
QY 1141 TGAAGAAAAATAGATGACGCGCTGTGTATAGACCAAGAACCAAGAAAACTTCTTTCTGG 1200
Db 1141 TGAAGAAAAATAGATGACGCGCTGTGTATAGACCAAGAACCAAGAAAACTTCTTTCTGG 1200
QY 1201 GCATTTGGTGTGAGGTTTTGATGAAATGACCCAAACCATGGAACAAAGGATTTCCCGCAGA 1260
Db 1201 GCATTTGGTGTGAGGTTTTGATGAAATGACCCAAACCATGGAACAAAGGATTTCCCGCAGA 1260
QY 1261 GAGTGTAAACACTTTCTCTGGATCAGTATCCGTGTGATGCTGCTTCCAGTACAAAG 1320
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Db 1261 GAGTGGTAAACACATTTCTCGGAATCAGTATCCGTTGATGCTGCTTCCAGTACAAAG 1320
Qy 1321 GATTCTTCTTTTTCAGCCCGTGGATCAAGCAATTTGAATACAAATTAAGACAAAGATA 1380
Db 1321 GATTCTTCTTTTTCAGCCCGTGGATCAAGCAATTTGAATACAAATTAAGACAAAGATA 1380
Qy 1381 TTACCCGAATCATAGAGAACTAATACATTTGGTTTCAATGCGAAAGAACCAAGAACTCTCAT 1440
Db 1381 TTACCCGAATCATAGAGAACTAATACATTTGGTTTCAATGCGAAAGAACCAAGAACTCTCAT 1440
Qy 1441 TTGGTTTGGATATCAACAGGAAAGACATTCAGAGGACATAAAGATATTCTATCAVA 1500
Db 1441 TTGGTTTGGATATCAACAGGAAAGACATTCAGAGGACATAAAGATATTCTATCAVA 1500
Qy 1501 AGAGTTTAAGCTTGTATTTTGGTATTGTTTCATTTGGTGAAGAAACATCTTATTTATC 1560
Db 1501 AGAGTTTAAGCTTGTATTTTGGTATTGTTTCATTTGGTGAAGAAACATCTTATTTATC 1560
Qy 1561 AATAAATTCATAGACCTAAATAAACCTCAACAGGCTTTTAAATATAAATTCGCTTCAA 1620
Db 1561 AATAAATTCATAGACCTAAATAAACCTCAACAGGCTTTTAAATATAAATTCGCTTCAA 1620
Qy 1621 AATAGAA 1627
Db 1621 AATAGAA 1627

RESULT 10

US-10-176-921-191
; Sequence 191, Application US/10176921
; Publication No. US20030027276A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Beresini, Maureen
; APPLICANT: DeForge, Laura
; APPLICANT: Desnoyers, Luc
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Sherwood, Steven
; APPLICANT: Smith, Victoria
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Watanabe, Colin K
; APPLICANT: Wood, William
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; TITLE OF INVENTION: ACIDS ENCODING THE SAME
; FILE REFERENCE: P3330R1C288
; CURRENT APPLICATION NUMBER: US/10/176,921
; CURRENT FILING DATE: 2002-06-20
; Prior Application removed - See File Wrapper or Palm
; NUMBER OF SEQ ID NOS: 550
; SEQ ID NO 191
; LENGTH: 1647
; TYPE: DNA
; ORGANISM: Homo Sapien
US-10-176-921-191

Query Match 99.9%; Score 1625.4; DB 14; Length 1647;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 1626; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
Qy 1 GCTTCAGCTGAAGAAAGAGAGGAATGAGCGCCCTCTGCTCTCTGTTGTTGTTCTTTATAA 60
Db 1 GCTTCAGCTGAAGAAAGAGAGGAATGAGCGCCCTCTGCTCTCTGTTGTTGTTCTTTATAA 60
Qy 61 CATTTTCTTCTGCAATTTCCCTTAGTCCGGATGACGGAAATGAAGAAATATGCAACTGG 120

Db 61 CATTTTCTTCTGCAATTTCCCTTAGTCCGGATGACGGAAATGAAGAAATATGCAACTGG 120
Qy 121 CTCAGGCATATCTCAACCAAGTTCTACTCTCTTGAAATAGAAGGGAATCATCTTTGTTCAAA 180
Db 121 CTCAGGCATATCTCAACCAAGTTCTACTCTCTTGAAATAGAAGGGAATCATCTTTGTTCAAA 180
Qy 181 GCAAGAATAGGAGTCTCATAGATGACAAAATTCGGGAAATGCAAGCATTTTTTGGATTGA 240
Db 181 GCAAGAATAGGAGTCTCATAGATGACAAAATTCGGGAAATGCAAGCATTTTTTGGATTGA 240
Qy 241 CAGTGACTGGAAAACTGGGACTCAAAACACCCCTTGAGATCATGAAGACACCCAGGTGGGG 300
Db 241 CAGTGACTGGAAAACTGGGACTCAAAACACCCCTTGAGATCATGAAGACACCCAGGTGGGG 300
Qy 301 TGCCTGATGTCGGCCAGTATGGCTACACCTCCCTCGGTGGAGAAAATACAACTCACCT 360
Db 301 TGCCTGATGTCGGCCAGTATGGCTACACCTCCCTCGGTGGAGAAAATACAACTCACCT 360
Qy 361 ACAGAAATAATAAATACTATCTCCGGATATGCGAGCTGCTGTGGATGAGGCTATCCAAAG 420
Db 361 ACAGAAATAATAAATACTATCTCCGGATATGCGAGCTGCTGTGGATGAGGCTATCCAAAG 420
Qy 421 AAGGTTTAGAAGTGTGGAGCAAAAGTCACTCCACTAAATTCACCAAGATTTCAAGAGGGA 480
Db 421 AAGGTTTAGAAGTGTGGAGCAAAAGTCACTCCACTAAATTCACCAAGATTTCAAGAGGGA 480
Qy 481 TTGCAGACATCATGATTGGCTTTAGGACTCGAGTCCATGGTCCGTTGCTCTCGCTATTTTG 540
Db 481 TTGCAGACATCATGATTGGCTTTAGGACTCGAGTCCATGGTCCGTTGCTCTCGCTATTTTG 540
Qy 541 ATGGTCCCTTTGGGAGTGTGGCCATGCCCTTCTCTGCTCGGGTCTGGGTGGTGACA 600
Db 541 ATGGTCCCTTTGGGAGTGTGGCCATGCCCTTCTCTGCTCGGGTCTGGGTGGTGACA 600
Qy 601 CTCATTTTGTAGGAGTGAATAACTGACCAAGAGTGGAGCAGGATCAACTGTTTCTTGT 660
Db 601 CTCATTTTGTAGGAGTGAATAACTGACCAAGAGTGGAGCAGGATCAACTGTTTCTTGT 660
Qy 661 TGGCTGCTCATGAATTTGGTTCATGCACTGGGGTCTCTCACTCCAATGATCAAAAGCCT 720
Db 661 TGGCTGCTCATGAATTTGGTTCATGCACTGGGGTCTCTCACTCCAATGATCAAAAGCCT 720
Qy 721 TGATGTTTCCCAAAATTAATGCTCTCCCTGGATCCCAAGAAATACCCACTTTCTCAGGATGATA 780
Db 721 TGATGTTTCCCAAAATTAATGCTCTCCCTGGATCCCAAGAAATACCCACTTTCTCAGGATGATA 780
Qy 781 TCAATGAATCCAGTCCATCTATGGAGTCTGCTTAAGGTACCTGCTTAAGCAAGGAAC 840
Db 781 TCAATGAATCCAGTCCATCTATGGAGTCTGCTTAAGGTACCTGCTTAAGCAAGGAAC 840
Qy 841 CCATATACCCCATGCTGTGACCCCTGACCTTGACTTTTGACGCTATCACAACCTTTCCGCA 900
Db 841 CCATATACCCCATGCTGTGACCCCTGACCTTGACTTTTGACGCTATCACAACCTTTCCGCA 900
Qy 901 GAGAAGTAATGTTCTTTTAAAGGAGGACCACTATGGAGATCTATATGATATCAGGATG 960
Db 901 GAGAAGTAATGTTCTTTTAAAGGAGGACCACTATGGAGATCTATATGATATCAGGATG 960
Qy 961 TTGAGTTTGAATTAATTTGCTTTCATCTGCGCATCTCTGCGAGTGTCTGCAAGCTGAT 1020
Db 961 TTGAGTTTGAATTAATTTGCTTTCATCTGCGCATCTCTGCGAGTGTCTGCAAGCTGAT 1020
Qy 1021 ACAGAAACCCAGAGATAAGATTTGTTTAAAGATGAAGAACTTTCTGGATGATCAGAG 1080
Db 1021 ACAGAAACCCAGAGATAAGATTTGTTTAAAGATGAAGAACTTTCTGGATGATCAGAG 1080
Qy 1081 GATATGCTGTTTCCAGATTTATCCCAATCCATACATTAAGTTTTCAGGACCTG 1140
Db 1081 GATATGCTGTTTCCAGATTTATCCCAATCCATACATTAAGTTTTCAGGACCTG 1140
Qy 1141 TGAAGAAATAGATGCGCCCTGTTGATAGACCAAGAAACCACTTCTTCTTTGG 1200
Db 1141 TGAAGAAATAGATGCGCCCTGTTGATAGACCAAGAAACCACTTCTTCTTTGG 1200

QY 1201 GCATTTGGTGTGAGGTTTGATGAATGACCCAAACCATGGACAAAGGATTCGCCGAGA 1260
DB |||||||
QY 1201 GCATTTGGTGTGAGGTTTGATGAATGACCCAAACCATGGACAAAGGATTCGCCGAGA 1260
DB |||||||
QY 1261 GAGTGGTAAAAACATTTTCCCTGGAAATCAGTATCCGTTGTTGATGCTGCTTTCCAGTACAAAAG 1320
DB |||||||
QY 1261 GAGTGGTAAAAACATTTTCCCTGGAAATCAGTATCCGTTGTTGATGCTGCTTTCCAGTACAAAAG 1320
DB |||||||
QY 1321 GATTTCTTTTTCAGCCGTGGATCAAGCAATTTGAATACAACTAATAGACAAAGAAATA 1380
DB |||||||
QY 1321 GATTTCTTTTTCAGCCGTGGATCAAGCAATTTGAATACAACTAATAGACAAAGAAATA 1380
DB |||||||
QY 1381 TTACCCGAATCATGAGAACTAATACCTTTGTTTCAATGCAAGAAACCAAGAACTCCCTCAT 1440
DB |||||||
QY 1381 TTACCCGAATCATGAGAACTAATACCTTTGTTTCAATGCAAGAAACCAAGAACTCCCTCAT 1440
DB |||||||
QY 1441 TTGGTTTTGATATCAACAAAGGAAAAAGCAATTCAGAGGCATAAAGATATTGTATCATA 1500
DB |||||||
QY 1441 TTGGTTTTGATATCAACAAAGGAAAAAGCAATTCAGAGGCATAAAGATATTGTATCATA 1500
DB |||||||
QY 1501 AGAGTTTAAGCTTGTATTTTGGTATTTGTTCAATTTGCTGAAAAACACATTTCTATTTATC 1560
DB |||||||
QY 1501 AGAGTTTAAGCTTGTATTTTGGTATTTGTTCAATTTGCTGAAAAACACATTTCTATTTATC 1560
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QY 1561 AATAAATTCATAGACCTAAATAAACCCTCAACAGAGTCTTTTAAATATAAATTTCTGTTCAA 1620
DB |||||||
QY 1561 AATAAATTCATAGACCTAAATAAACCCTCAACAGAGTCTTTTAAATATAAATTTCTGTTCAA 1620
DB |||||||
QY 1621 AATAGAA 1627
DB |||||||
QY 1621 AATAGAA 1627
DB |||||||

RESULT 11

US-10-137-865-191
; Sequence 191, Application US/10137865
; Publication No. US20030032155A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Beresini, Maureen
; APPLICANT: DeForge, Laura
; APPLICANT: Desnoyers, Luc
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Sherwood, Steven
; APPLICANT: Smith, Victoria
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Watanabe, Colin K
; APPLICANT: Wood, William
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P3330R1C154
; CURRENT APPLICATION NUMBER: US/10/137,865
; PRIORITY FILING DATE: 2002-05-03
; Prior Application removed - See Palm or File Wrapper
; NUMBER OF SEQ ID NOS: 550
; SEQ ID NO 191
; LENGTH: 1647
; TYPE: DNA
; ORGANISM: Homo Sapien
US-10-137-865-191

Query Match 99.9%; Score 1625.4; DB 14; Length 1647;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 1626; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GCTTCAGCTGAAAGAGAGAGGAAATGAAGGCGCTTCTGCTTCTGCTTCTGCTTCTTATAA 60
DB |||||||
QY 1 GCTTCAGCTGAAAGAGAGAGGAAATGAAGGCGCTTCTGCTTCTGCTTCTTATAA 60
DB |||||||
QY 61 CATTTTCTTCTGCAATTTCCCTTAGTCCGGATGACGGAATGAAGAAATATCAACTGG 120
DB |||||||
QY 61 CATTTTCTTCTGCAATTTCCCTTAGTCCGGATGACGGAATGAAGAAATATCAACTGG 120
DB |||||||
QY 121 CTCAGCATATCTCAACCAAGTTCTACTCTCTTGAATAGAGGGAATCATCTTGTCAA 180
DB |||||||
QY 121 CTCAGCATATCTCAACCAAGTTCTACTCTCTTGAATAGAGGGAATCATCTTGTCAA 180
DB |||||||
QY 181 GCAAGATAGGAGTCTCATAGATGACAAATTCGGGAAATGCAAGCAATTTTGGATTGA 240
DB |||||||
QY 181 GCAAGATAGGAGTCTCATAGATGACAAATTCGGGAAATGCAAGCAATTTTGGATTGA 240
DB |||||||
QY 241 CAGTGACTGAAAACTGGAGTCAACACCCCTTGAGATCATGAAGACACCCAGTGTGGGG 300
DB |||||||
QY 241 CAGTGACTGAAAACTGGAGTCAACACCCCTTGAGATCATGAAGACACCCAGTGTGGGG 300
DB |||||||
QY 301 TGCCTGATGTGGGCGAGTATGCTACACCTCCCTGGGTGGAGAAATACAACTCACT 360
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QY 301 TGCCTGATGTGGGCGAGTATGCTACACCTCCCTGGGTGGAGAAATACAACTCACT 360
DB |||||||
QY 361 ACAGATATTAATTAATCTACTCCGGATATGGACGAGCTGCTGTGATGAGGCTATCCAA 420
DB |||||||
QY 361 ACAGATATTAATTAATCTACTCCGGATATGGACGAGCTGCTGTGATGAGGCTATCCAA 420
DB |||||||
QY 421 AAGGTTTGAAGTGTGGAGCAAGTCACTCCCACTAAATTCACCAAGATTTCAAAGGGGA 480
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QY 421 AAGGTTTGAAGTGTGGAGCAAGTCACTCCCACTAAATTCACCAAGATTTCAAAGGGGA 480
DB |||||||
QY 481 TTGCAGACATCATGATTTGCTTTAGGACTCGAGTCCATGCTCGGTCTCTGCTATTTTG 540
DB |||||||
QY 481 TTGCAGACATCATGATTTGCTTTAGGACTCGAGTCCATGCTCGGTCTCTGCTATTTTG 540
DB |||||||
QY 541 ATGCTCCCTTGGAGTGTGGGCAATGCTTTCCTCTGCTGCTGCTGCTGCTGCTGCTGCT 600
DB |||||||
QY 541 ATGCTCCCTTGGAGTGTGGGCAATGCTTTCCTCTGCTGCTGCTGCTGCTGCTGCTGCT 600
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QY 601 CTCATTTTGTGAGGATGAAATCTGGAACAAGATGGAGCAGGATTCAACTTTGTTTCTG 660
DB |||||||
QY 601 CTCATTTTGTGAGGATGAAATCTGGAACAAGATGGAGCAGGATTCAACTTTGTTTCTG 660
DB |||||||
QY 661 TGGCTGCTCATGAATTTGGTCAATGCACTGGGCTCTCTCACTCCAATGATCAACAGCT 720
DB |||||||
QY 661 TGGCTGCTCATGAATTTGGTCAATGCACTGGGCTCTCTCACTCCAATGATCAACAGCT 720
DB |||||||
QY 721 TGATGTTCCCAATTTATGTTCTCCCTGGATCCAGAAATACCCACTTTCTCAGGATGATA 780
DB |||||||
QY 721 TGATGTTCCCAATTTATGTTCTCCCTGGATCCAGAAATACCCACTTTCTCAGGATGATA 780
DB |||||||
QY 781 TCAATGGAATCCAGTCCCATCTATGAGGCTCTGCTTAAGTACCTGCTAAGCCAAAGGAAC 840
DB |||||||
QY 781 TCAATGGAATCCAGTCCCATCTATGAGGCTCTGCTTAAGTACCTGCTAAGCCAAAGGAAC 840
DB |||||||
QY 841 CCATATACCCCATGCTGTGACCTGACTTTTGACGCTATCACAACTTTCCGCA 900
DB |||||||
QY 841 CCATATACCCCATGCTGTGACCTGACTTTTGACGCTATCACAACTTTCCGCA 900
DB |||||||
QY 901 GAGAGTAAATGTTCTTTAAAGGCGAGGACCTATGAGGATCTATGATATCAGGATG 960
DB |||||||
QY 901 GAGAGTAAATGTTCTTTAAAGGCGAGGACCTATGAGGATCTATGATATCAGGATG 960
DB |||||||
QY 961 TTGAGTTTGAATTAATTTGCTTTCAATTCGGCCATCTCTGCCAGCTGATCTGCAAGTGCAT 1020
DB |||||||
QY 961 TTGAGTTTGAATTAATTTGCTTTCAATTCGGCCATCTCTGCCAGCTGATCTGCAAGTGCAT 1020
DB |||||||
QY 1021 ACAGAAACCCAGAGATAAGATTTCTGGTTTTTAAAGATGAAAACTTTCTGGATGATCAGAG 1080
DB |||||||
QY 1021 ACAGAAACCCAGAGATAAGATTTCTGGTTTTTAAAGATGAAAACTTTCTGGATGATCAGAG 1080
DB |||||||
QY 1081 GATATGCTGCTTGGCAGATTTATCCCAATCCATCATATAGGTTTTTCCAGACGCTG 1140
DB |||||||

1081 GATATCTGCTGCGAGATTATCCCAATCCATCATATAGTTTCCAGGACGTG 1140
1141 TGAAGAAATAGATGAGCGCTGCTGTAAGACCAAGAAAAACCTACTTTGTGG 1200
1141 TGAAGAAATAGATGAGCGCTGCTGTAAGACCAAGAAAAACCTACTTTGTGG 1200
1201 GCATTTGGTCTGGAGTTTGATGAATGACCAACCATGGACAAAGGATTCGGCAGA 1260
1201 GCATTTGGTCTGGAGTTTGATGAATGACCAACCATGGACAAAGGATTCGGCAGA 1260
1261 GAGTGTAAACACTTTCCTGGATCAGTATCCGTGTGATGCTTTCCAGTACAAAG 1320
1261 GAGTGTAAACACTTTCCTGGATCAGTATCCGTGTGATGCTTTCCAGTACAAAG 1320
1321 GATTTCTTTTTCAGCGGTGATCAAGCAATTTGAATACAAATTAAGACAAAGAA 1380
1321 GATTTCTTTTTCAGCGGTGATCAAGCAATTTGAATACAAATTAAGACAAAGAA 1380
1381 TTACCCGAATCATGAGAACTAATTAATTTGGTTTCAATGCAAGAACCAAGAACTCCTCAT 1440
1381 TTACCCGAATCATGAGAACTAATTAATTTGGTTTCAATGCAAGAACCAAGAACTCCTCAT 1440
1441 TTGGTTTGTATCAACAGGAAAGCAATTCAGGAGCATTAAGATTTGTATCAT 1500
1441 TTGGTTTGTATCAACAGGAAAGCAATTCAGGAGCATTAAGATTTGTATCAT 1500
1501 AGAGTTTAAAGCTTTTATTTTGGTATTTGTTCAATTTGCTGAAACCACTTCTATTC 1560
1501 AGAGTTTAAAGCTTTTATTTTGGTATTTGTTCAATTTGCTGAAACCACTTCTATTC 1560
1561 AATAATTCATAGACCTTAATAAATCAACCTCAAGCTTTTATATATAAATTCCTTCAA 1620
1561 AATAATTCATAGACCTTAATAAATCAACCTCAAGCTTTTATATATAAATTCCTTCAA 1620
1621 AATAGAA 1627
1621 AATAGAA 1627

RESULT 12

US-10-140-474-191
; Sequence 191, Application US/10140474
; Publication No. US2003032156A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Beresini, Maureen
; APPLICANT: DeForge, Laura
; APPLICANT: Desnoyers, Luc
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Sherwood, Steven
; APPLICANT: Smith, Victoria
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Watanabe, Colin K
; APPLICANT: Wood, William
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE OF INVENTION: ACIDS ENCODING THE SAME
; FILE REFERENCE: P3330R1C162
; CURRENT APPLICATION NUMBER: US/10/140,474
; CURRENT FILING DATE: 2002-05-06
; Prior Application removed - See Palm or File Wrapper
; NUMBER OF SEQ ID NOS: 550
; SEQ ID NO 191
; LENGTH: 1647
; TYPE: DNA
; ORGANISM: Homo Sapien

US-10-140-474-191

Query Match 99.9%; Score 1625.4; DB 14; Length 1647;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 1626; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1 GCTTTCAGCTGAAGAAAGAGAGGAATGAAGCGCCTTCTGCTTCTGTTGTTGTTCTTTATAA 60
Db 1 GCTTTCAGCTGAAGAAAGAGAGGAATGAAGCGCCTTCTGCTTCTGTTGTTGTTCTTTATAA 60
QY 61 CATTTTCTTCTGCAATTCCTTAGTCGGGATGCGGAAATGAAGAAATATGCAACTGG 120
Db 61 CATTTTCTTCTGCAATTCCTTAGTCGGGATGCGGAAATGAAGAAATATGCAACTGG 120
QY 121 CTGAGGCATATCTCAACCACTGCTCTCTCTTGAATAGAGGAATCACTTTGTTCAA 180
Db 121 CTGAGGCATATCTCAACCACTGCTCTCTCTTGAATAGAGGAATCACTTTGTTCAA 180
QY 181 GCAAGAAATAGAGCTCTCATAGATGACAAAATTCGGGAAATGCAAGCAATTTTGGATTGA 240
Db 181 GCAAGAAATAGAGCTCTCATAGATGACAAAATTCGGGAAATGCAAGCAATTTTGGATTGA 240
QY 241 CAGTGAATGAAATCTGAGCTCAACACCTTGAATCATGAAGACACCCAGGTGTGGG 300
Db 241 CAGTGAATGAAATCTGAGCTCAACACCTTGAATCATGAAGACACCCAGGTGTGGG 300
QY 301 TGGCTGATGCGGCCAGTATGGCTTACACCTTCCCTGGGTGAGAAAATCAACCTCACCT 360
Db 301 TGGCTGATGCGGCCAGTATGGCTTACACCTTCCCTGGGTGAGAAAATCAACCTCACCT 360
QY 361 ACAGAAATATAAATACTATACCTCCGGATATGCGAGCTGCTGTGATGAGGCTATCCAAG 420
Db 361 ACAGAAATATAAATACTATACCTCCGGATATGCGAGCTGCTGTGATGAGGCTATCCAAG 420
QY 421 AAGTTTGAAGTGTGGAGCAAAAGTCACTCCCTAAATTCACCAAGATTTCAAAGGGGA 480
Db 421 AAGTTTGAAGTGTGGAGCAAAAGTCACTCCCTAAATTCACCAAGATTTCAAAGGGGA 480
QY 481 TTGAGACATCATGATGCTTTAGGACTCGAGTCCATGCTGGGTGCTCGCTATTTTG 540
Db 481 TTGAGACATCATGATGCTTTAGGACTCGAGTCCATGCTGGGTGCTCGCTATTTTG 540
QY 541 ATGCTCCCTTGGGAGTGTGGCCATGCTTTCCTCTGCTGCTGGGTGCTGGGTGCTGACA 600
Db 541 ATGCTCCCTTGGGAGTGTGGCCATGCTTTCCTCTGCTGCTGGGTGCTGGGTGCTGACA 600
QY 601 CTCATTTTGAAGATGAAATCTGAGCAACAGGATGAGGAGGATGAGGAGGATTTCTTTG 660
Db 601 CTCATTTTGAAGATGAAATCTGAGCAACAGGATGAGGAGGATGAGGAGGATTTCTTTG 660
QY 661 TGGCTGCTCATGAATTTGGTCACTGCGGCTCTCTCACTCCAATGATCAAAACAGCT 720
Db 661 TGGCTGCTCATGAATTTGGTCACTGCGGCTCTCTCACTCCAATGATCAAAACAGCT 720
QY 721 TGATGTTCCCAAAATATGCTTCCCTGGATCCAGAAAATACCCACTTTCTCAGGATGATA 780
Db 721 TGATGTTCCCAAAATATGCTTCCCTGGATCCAGAAAATACCCACTTTCTCAGGATGATA 780
QY 781 TCAATGGAATCCAGTCCATCTATGAGGCTGCTGCTTGAAGTCTTGAAGCAAGGAAAC 840
Db 781 TCAATGGAATCCAGTCCATCTATGAGGCTGCTGCTTGAAGTCTTGAAGCAAGGAAAC 840
QY 841 CCATATACCCCATGCTGCTGACCTGCTGCTTGAAGTCTTGAAGTCTTGAAGTCTTGAAG 900
Db 841 CCATATACCCCATGCTGCTGACCTGCTGCTTGAAGTCTTGAAGTCTTGAAGTCTTGAAG 900
QY 901 GAGAAGTAAATGTTCTTTAAAGGAGGACCTTATGAGGATCTATGATATACCGATG 960
Db 901 GAGAAGTAAATGTTCTTTAAAGGAGGACCTTATGAGGATCTATGATATACCGATG 960
QY 961 TTGAGTTGAATTAATGCTTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1020
Db 961 TTGAGTTGAATTAATGCTTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1020

1021 ACAGAACCCAGAGATAAGATTCTGGTTTAAAGATGAAACTTCTCGATCATCAGAG 1080
1021 ACAGAACCCAGAGATAAGATTCTGGTTTAAAGATGAAACTTCTCGATCATCAGAG 1080
1081 GATATGCTGTCTTCCAGATTATCCAAATCCATCCATCCATCACTAGGTTTCCAGGACGTG 1140
1081 GATATGCTGTCTTCCAGATTATCCAAATCCATCCATCCATCACTAGGTTTCCAGGACGTG 1140
1141 TGAAGAAATAGATGACCGCTGTGTGATAAGACCAAGAAATCCAGGACGTG 1200
1141 TGAAGAAATAGATGACCGCTGTGTGATAAGACCAAGAAATCCAGGACGTG 1200
1201 GCATTTGGTGTGGAGTTTGAATGAAATGACCAACCAATGACCAAGGATTTCCCGCAGA 1260
1201 GCATTTGGTGTGGAGTTTGAATGAAATGACCAACCAATGACCAAGGATTTCCCGCAGA 1260
1261 GAGTGGTAAACACATTTCTCGAATCAGTATCCGTTGATGCTGCTTTCCAGTACAAAG 1320
1261 GAGTGGTAAACACATTTCTCGAATCAGTATCCGTTGATGCTGCTTTCCAGTACAAAG 1320
1321 GATTTCTTTTTCAGCGTGTGATCAAGCAATTTGAATACAAATTAAGACAAAGATA 1380
1321 GATTTCTTTTTCAGCGTGTGATCAAGCAATTTGAATACAAATTAAGACAAAGATA 1380
1381 TTACCGGAATCATGAGAACTAATACTTGGTTTCAATGCAAGAAACCAAGAAACTCTCAT 1440
1381 TTACCGGAATCATGAGAACTAATACTTGGTTTCAATGCAAGAAACCAAGAAACTCTCAT 1440
1441 TTGGTTTTCATATCAAGGAAAGCAATTCAGGAGGCATTAAGATATTGTATCAT 1500
1441 TTGGTTTTCATATCAAGGAAAGCAATTCAGGAGGCATTAAGATATTGTATCAT 1500
1501 AGAGTTTAAAGCTGTTTATTTTGGTATTTGTTTCAATTTGCTGAAACACTTCTATTC 1560
1501 AGAGTTTAAAGCTGTTTATTTTGGTATTTGTTTCAATTTGCTGAAACACTTCTATTC 1560
1561 AATAAATTCATAGACCTAAATATAACCTCAACAGGTCTTTTAAATATAAATTCGCTTCAA 1620
1561 AATAAATTCATAGACCTAAATATAACCTCAACAGGTCTTTTAAATATAAATTCGCTTCAA 1620
1621 AATAGAA 1627
1621 AATAGAA 1627

RESULT 13

US-10-142-431-191
; Sequence 191, Application US/10142431
; Publication No. US20030036179A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Beresini, Maureen
; APPLICANT: DeForge, Laura
; APPLICANT: Desnoyers, Luc
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Sherwood, Steven
; APPLICANT: Smith, Victoria
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Watanabe, Colin K
; APPLICANT: Wood, William
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE OF INVENTION: ACIDS ENCODING THE SAME
; FILE REFERENCE: P3330R1C251
; CURRENT APPLICATION NUMBER: US/10/142,431
; CURRENT FILING DATE: 2002-05-10

; Prior Application removed - See File Wrapper or Palm

; NUMBER OF SEQ ID NOS: 550

; SEQ ID NO 191

; LENGTH: 1647

; TYPE: DNA

; ORGANISM: Homo Sapien

US-10-142-431-191

Query Match 99.9%; Score 1625.4; DB 14; Length 1647;

Best Local Similarity 99.9%; Pred. No. 0;

Matches 1626; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GCTTCAGCTGGAAGAAGAGAGAAATCAAGCGCTTCTGCTTCTGCTTCTGCTTCTTATAA 60

Db 1 GCTTCAGCTGGAAGAAGAGAGAAATCAAGCGCTTCTGCTTCTGCTTCTGCTTCTTATAA 60

QY 61 CATTTTCTTCTCATTTTCCCTTAGTCCGGATGACGAAATGAAGAAATATGCAACTGG 120

Db 61 CATTTTCTTCTCATTTTCCCTTAGTCCGGATGACGAAATGAAGAAATATGCAACTGG 120

QY 121 CTCAGCATATCTCAACAGATTCTACTCTCTTGAATAGAGGGAATCATCTTGTTCATA 180

Db 121 CTCAGCATATCTCAACAGATTCTACTCTCTTGAATAGAGGGAATCATCTTGTTCATA 180

QY 181 GCAAGAAATAGGAGTCTCATAGATGACAAATTCGGGAAATCAAGCATTTTGTGATGA 240

Db 181 GCAAGAAATAGGAGTCTCATAGATGACAAATTCGGGAAATCAAGCATTTTGTGATGA 240

QY 241 CAGTGACTGGAAAACTGGACTCAAAACACCTTGAGATCATGAAGACACCCAGGTGTGGG 300

Db 241 CAGTGACTGGAAAACTGGACTCAAAACACCTTGAGATCATGAAGACACCCAGGTGTGGG 300

QY 301 TGCCTGATGTGGCCAGTATGGCTACACCTCCCTGGGTGGAGAAATAACAACCTCACT 360

Db 301 TGCCTGATGTGGCCAGTATGGCTACACCTCCCTGGGTGGAGAAATAACAACCTCACT 360

QY 361 ACAGAAATATAACTATCTCCGATATGGCAGCTGCTGTGATGAGGCTATCCAG 420

Db 361 ACAGAAATATAACTATCTCCGATATGGCAGCTGCTGTGATGAGGCTATCCAG 420

QY 421 AAGGTTTGAAGTGTGGAGCAAAAGTCACTCCACTAAAAATTCACCAAGATTTCAAAGGGA 480

Db 421 AAGGTTTGAAGTGTGGAGCAAAAGTCACTCCACTAAAAATTCACCAAGATTTCAAAGGGA 480

QY 481 TTGAGACATCATGATTCCTTTAGGACTCCAGTCCATGGTCTCGTCTATTTTG 540

Db 481 TTGAGACATCATGATTCCTTTAGGACTCCAGTCCATGGTCTCGTCTATTTTG 540

QY 541 ATGCTCCCTGGGAGTCTTGGCCATGCTTTCCTCTGCTCGGCTCGGCTGAGCA 600

Db 541 ATGCTCCCTGGGAGTCTTGGCCATGCTTTCCTCTGCTCGGCTCGGCTGAGCA 600

QY 601 CTCATTTTGAATGAGATGAAACTGGACCAAGGATGGAGCAGGATTCAACTTGTTCCTTG 660

Db 601 CTCATTTTGAATGAGATGAAACTGGACCAAGGATGGAGCAGGATTCAACTTGTTCCTTG 660

QY 661 TGGCTGCTCATGAATTTGGTCAATGCACTGGGGCTCTCTCACTCCAATGATCAACAGCT 720

Db 661 TGGCTGCTCATGAATTTGGTCAATGCACTGGGGCTCTCTCACTCCAATGATCAACAGCT 720

QY 721 TGATGTTCCCAAAATATGCTCCCTGGATCCAGAAATACCCACTTTCTCAGGATGATA 780

Db 721 TGATGTTCCCAAAATATGCTCCCTGGATCCAGAAATACCCACTTTCTCAGGATGATA 780

QY 781 TCAATGGAATCCAGTCCATCTATGAGGCTCTGCTTAAGTACCTGCTAAGCAAGGAAC 840

Db 781 TCAATGGAATCCAGTCCATCTATGAGGCTCTGCTTAAGTACCTGCTAAGCAAGGAAC 840

QY 841 CCATATACCCCATGCTGTGACCTGACTTGAATTTTGACGCTATCAAACTTTCCGCA 900

Db 841 CCATATACCCCATGCTGTGACCTGACTTGAATTTTGACGCTATCAAACTTTCCGCA 900

QY 901 GAGAAATATGCTTTTAAAGGACGACCTATGAGGATCTATATGATATCAGGATG 960

901	Db	GAGAAGTAATGTTCTTTAAAGGAGGAGCACCCTATGGAGGATCTATTAATGATATCACGGATG	960
961	Qy	TTGAGTTTGAATTAATGCTTCAFTCTGGCCATCTCTGCCAGCTGATCTGCAAGCTGCAT	1020
961	Db	TTGAGTTTGAATTAATGCTTCAFTCTGGCCATCTCTGCCAGCTGATCTGCAAGCTGCAT	1020
1021	Qy	ACGAGAACCCGACAGATAGATTTCTGGTTTTTAAAGATGAATAAATCTTCTGGATGATCAGAG	1080
1021	Db	ACGAGAACCCGACAGATAGATTTCTGGTTTTTAAAGATGAATAAATCTTCTGGATGATCAGAG	1080
1081	Qy	GATATGCTGCTTGGCCAGATTTATCCCAATCCATCCATACATTAGTGTCTTCCAGGACGTG	1140
1081	Db	GATATGCTGCTTGGCCAGATTTATCCCAATCCATCCATACATTAGTGTCTTCCAGGACGTG	1140
1141	Qy	TGAAGAAAATAGATGACGCGTCTGTGATGAAGACCAAGAATAAACTACTTCTTTGTGG	1200
1141	Db	TGAAGAAAATAGATGACGCGTCTGTGATGAAGACCAAGAATAAACTACTTCTTTGTGG	1200
1201	Qy	GCATTTGGTCTGGAGGTTTGATGAAATGACCCAAACCATGGACAAGGATTCCTCCGACA	1260
1201	Db	GCATTTGGTCTGGAGGTTTGATGAAATGACCCAAACCATGGACAAGGATTCCTCCGACA	1260
1261	Qy	GAGTGTAAACACTTTTCTGGAAATCAGTATCGGTGTGATGTGCTTTCCAGTACAAAG	1320
1261	Db	GAGTGTAAACACTTTTCTGGAAATCAGTATCGGTGTGATGTGCTTTCCAGTACAAAG	1320
1321	Qy	GATTCCTTTTTCAGCGGTGGATCAAGCAATTTGAAATCAACATTAAGACAAGAATA	1380
1321	Db	GATTCCTTTTTCAGCGGTGGATCAAGCAATTTGAAATCAACATTAAGACAAGAATA	1380
1381	Qy	TTACCCGAATCATGAGAACTAATACTTTGTTTCAATGCAAGAACCAAGAACTCTCTCAT	1440
1381	Db	TTACCCGAATCATGAGAACTAATACTTTGTTTCAATGCAAGAACCAAGAACTCTCTCAT	1440
1441	Qy	TTGTTTTTGATATCAACAGGAAAGACACATTGAGGAGGATTAAGATATTTGATCATATA	1500
1441	Db	TTGTTTTTGATATCAACAGGAAAGACACATTGAGGAGGATTAAGATATTTGATCATATA	1500
1501	Qy	AGATTTAAGTTGTTTATTTTTGGTATTTGTTCAATTTGCTGAAAGACACTTCTATTATC	1560
1501	Db	AGATTTAAGTTGTTTATTTTTGGTATTTGTTCAATTTGCTGAAAGACACTTCTATTATC	1560
1561	Qy	AATAAAATTCATAGACCTAAAATAAATCAACAGGTCTTTTAAATATAAAATTCGTCTCAA	1620
1561	Db	AATAAAATTCATAGACCTAAAATAAATCAACAGGTCTTTTAAATATAAAATTCGTCTCAA	1620
1621	Qy	AATAGAA	1627
1621	Db	AATAGAA	1627

481	TTGCAGACATCATGATTGCCCTTTTAGGACTCGAGTCCATGTCGGTCTCGCTGCTATTATTG	541
QY	ATGTCCTCTGGGAGTCTGGCCATACGCTTTCTCTCTGTCGCGGTCTGGTCTGGTGCACA	600
481	ATGTCCTCTGGGAGTCTGGCCATACGCTTTCTCTCTGTCGCGGTCTGGTCTGGTGCACA	600
QY	CTCATTTTGTAGAGGATGAAACATGGACCAAGGATGGAGCAGGATTCAACTGTCTTTCTTG	660
481	CTCATTTTGTAGAGGATGAAACATGGACCAAGGATGGAGCAGGATTCAACTGTCTTTCTTG	660
QY	TGGCTGCTCATGAATTGGTTCATGCACCTGGGCGTCTCTCACTCCAAATGATCAAAACAGCT	720
481	TGGCTGCTCATGAATTGGTTCATGCACCTGGGCGTCTCTCACTCCAAATGATCAAAACAGCT	720
QY	TGATGTTCCCAAAATTATGTCTCCCTGGATCCAGAAATACCCACTTTCTCAGAGTATA	780
481	TGATGTTCCCAAAATTATGTCTCCCTGGATCCAGAAATACCCACTTTCTCAGAGTATA	780
QY	TCAATGGAAATCCAGTCCATCTATGGAGTCTGCCTTAAGTACCTGCTAAGCCAAAGGAAC	840
481	TCAATGGAAATCCAGTCCATCTATGGAGTCTGCCTTAAGTACCTGCTAAGCCAAAGGAAC	840
QY		

QY 841 CCACTATACCCCATGCTGTGACCCCTGACTTTTGGACGCTATCAAACTTCCGCA 900
DB 841 CCACTATACCCCATGCTGTGACCCCTGACTTTTGGACGCTATCAAACTTCCGCA 900
QY 901 GAGAAGTAAATGTTCTTTAAAGCAGCAGCCTATGAGGATCTATTATGATATCAAGGATG 960
DB 901 GAGAAGTAAATGTTCTTTAAAGCAGCAGCCTATGAGGATCTATTATGATATCAAGGATG 960
QY 961 TTGAGTTGAATTAATGTTCTTCAATCTGSCCATCTCTGCGAGCTGATCTGCAAGCTGCAT 1020
DB 961 TTGAGTTGAATTAATGTTCTTCAATCTGSCCATCTCTGCGAGCTGATCTGCAAGCTGCAT 1020
QY 1021 ACGAGAACCCAGAGATAGATTCTGTGTTTAAAGATGAAAACCTCTGGATGATCAGAG 1080
DB 1021 ACGAGAACCCAGAGATAGATTCTGTGTTTAAAGATGAAAACCTCTGGATGATCAGAG 1080
QY 1081 GATATGCTGTCTTGGCAGATTATCCAAATCCATCAATAGTATTTCCAGGACGTG 1140
DB 1081 GATATGCTGTCTTGGCAGATTATCCAAATCCATCAATAGTATTTCCAGGACGTG 1140
QY 1141 TGAAGAAATAGATGAGCGCTGTGTGATAAGACCAAGAAAACCTACTTCTTTTGG 1200
DB 1141 TGAAGAAATAGATGAGCGCTGTGTGATAAGACCAAGAAAACCTACTTCTTTTGG 1200
QY 1201 GCATTTGGTCTGGAGGTTTGTGATGAATGACCCCAACCATGACAAAGGATTCGCCGAGA 1260
DB 1201 GCATTTGGTCTGGAGGTTTGTGATGAATGACCCCAACCATGACAAAGGATTCGCCGAGA 1260
QY 1261 GAGTGGTAAAAACACTTTCTCGGAATCAGTATCCGTTGTTGATGCTGCTTTCCAGTACAAG 1320
DB 1261 GAGTGGTAAAAACACTTTCTCGGAATCAGTATCCGTTGTTGATGCTGCTTTCCAGTACAAG 1320
QY 1321 GATTCCTCTTTTACGCGCTGGATCAAGCAATTTGAATACAACTTAAGA CAAGAATA 1380
DB 1321 GATTCCTCTTTTACGCGCTGGATCAAGCAATTTGAATACAACTTAAGA CAAGAATA 1380
QY 1381 TTACCCGATCATGAGACTTACTTGGTTTCAATGCAAGAACCAAGAACTCTCAT 1440
DB 1381 TTACCCGATCATGAGACTTACTTGGTTTCAATGCAAGAACCAAGAACTCTCAT 1440
QY 1441 TTGGTTTGTATATCAAGGAAAAAGCACATTCAGAGGCAATAAGATATTGTATCAT 1500
DB 1441 TTGGTTTGTATATCAAGGAAAAAGCACATTCAGAGGCAATAAGATATTGTATCAT 1500
QY 1501 AGAGTTAAGCTGTTTATTTTGGTATTTGTTCAATTTGCTGAAAAACACTTCTATTATC 1560
DB 1501 AGAGTTAAGCTGTTTATTTTGGTATTTGTTCAATTTGCTGAAAAACACTTCTATTATC 1560
QY 1561 AATAAATTCATAGACCTAAATAAACCCTCAACAGGTCCTTTAATAAATTCGCTTCAA 1620
DB 1561 AATAAATTCATAGACCTAAATAAACCCTCAACAGGTCCTTTAATAAATTCGCTTCAA 1620
QY 1621 AATAGAA 1627
DB 1621 AATAGAA 1627

RESULT 15

US-10-140-002-191
; Sequence 191, Application US/10140002
; Publication No. US20030037623A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Beresini, Maureen
; APPLICANT: DeForge, Laura
; APPLICANT: Desnoyers, Luc
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Gurney, Austin L.

; APPLICANT: Sherwood, Steven
; APPLICANT: Smith, Victoria
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Watanabe, Colin K
; APPLICANT: Wood, William
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE OF INVENTION: ACIDS ENCODING THE SAME
; FILE REFERENCE: P3330R1C59
; CURRENT APPLICATION NUMBER: US/10/140,002
; PRIOR FILING DATE: 2002-05-06
; Prior Application removed - See Palm or File Wrapper
; NUMBER OF SEQ ID NOS: 550
; SEQ ID NO 191
; LENGTH: 1647
; TYPE: DNA
; ORGANISM: Homo Sapien
US-10-140-002-191

Query Match 99.9%; Score 1625.4; DB 14; Length 1647;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 1626; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1 GCTTCAGCTGAAGAAAGAGAGGAATGAAGCGCTTCTGCTTCTGTGTTTGTCTTTATAA 60
DB 1 GCTTCAGCTGAAGAAAGAGAGGAATGAAGCGCTTCTGCTTCTGTGTTTGTCTTTATAA 60
QY 61 CATTTTCTTCTGCAATTTCCCTTAGTCCGGATGACGGAAAAATGAAGAAAATATGCAACTGG 120
DB 61 CATTTTCTTCTGCAATTTCCCTTAGTCCGGATGACGGAAAAATGAAGAAAATATGCAACTGG 120
QY 121 CTCAGGCATATCTCAACAGTCTTACTCTCTTGAATAGAGGGAATCATCTGTGTTCAA 180
DB 121 CTCAGGCATATCTCAACAGTCTTACTCTCTTGAATAGAGGGAATCATCTGTGTTCAA 180
QY 181 GCAAGAAATAGGAGTCTCATAGATGACAAAATTCGGGAAATGCAAGCATTTTGTGATTGA 240
DB 181 GCAAGAAATAGGAGTCTCATAGATGACAAAATTCGGGAAATGCAAGCATTTTGTGATTGA 240
QY 241 CAGTCACTGGAAAACTGGACTCAAAACCCCTTGAGATCATGAAGACACCCAGGTGTGGGG 300
DB 241 CAGTCACTGGAAAACTGGACTCAAAACCCCTTGAGATCATGAAGACACCCAGGTGTGGGG 300
QY 301 TGCCGTGATGTGGCCAGTATGCTTACACCCCTCCCTGGGTGGAGAAAATACACCTCACCT 360
DB 301 TGCCGTGATGTGGCCAGTATGCTTACACCCCTCCCTGGGTGGAGAAAATACACCTCACCT 360
QY 361 ACAGAAATATAACTATATCTCCGGATATGGACAGCTGCTGTGATGAGGCTATCCAG 420
DB 361 ACAGAAATATAACTATATCTCCGGATATGGACAGCTGCTGTGATGAGGCTATCCAG 420
QY 421 AAGGTTTGAAGTGTGGAGCAAAAGTCACTCCACTAAAAATTCACCAAGATTTCAAGGGGA 480
DB 421 AAGGTTTGAAGTGTGGAGCAAAAGTCACTCCACTAAAAATTCACCAAGATTTCAAGGGGA 480
QY 481 TTGCAGACATCATGATTTGCTTTAGGACTCCAGTCCATGCTCGGTCTCTCGCTATTG 540
DB 481 TTGCAGACATCATGATTTGCTTTAGGACTCCAGTCCATGCTCGGTCTCTCGCTATTG 540
QY 541 ATGGTCCCTTTGGAGTGTCTTGGCCATGCTTTCCTCCCTGGTCCGGTCTGGGTGTGACA 600
DB 541 ATGGTCCCTTTGGAGTGTCTTGGCCATGCTTTCCTCCCTGGTCCGGTCTGGGTGTGACA 600
QY 601 CTCATTTTGTAGGATGAAAACTGGACCAAGGATGGAGGATTCAACTTGTTCCTT 660
DB 601 CTCATTTTGTAGGATGAAAACTGGACCAAGGATGGAGGATTCAACTTGTTCCTT 660
QY 661 TGGCTGCTCATGAATTTGGTCTATGCACTGGGCTCTCTCACTCCAATGATCAACAGCT 720
DB 661 TGGCTGCTCATGAATTTGGTCTATGCACTGGGCTCTCTCACTCCAATGATCAACAGCT 720
QY 721 TGATGTTCCAAATTTATGTCTCCCTGGATCCCAAGAAAATACCCACTTTTCTCAGGATGATA 780

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OM protein - protein search, using sw model

Run on: November 15, 2004, 20:58:11 ; Search time 94 seconds
(without alignments)
1930.949 Million cell updates/sec

Title: US-10-729-807-10

Perfect score: 2763

Sequence: 1 MKRLLLCLEFFITFSSAFPL.....SLSLFIIGIVHLLKNTSIYQ 513

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1568699 seqs, 353819137 residues

Total number of hits satisfying chosen parameters: 1568699

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications AA.*
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2: /cgn2_6/ptodata/1/pubpaa/FCT_NEW_PUB.pep.*
3: /cgn2_6/ptodata/1/pubpaa/US06_NEW_PUB.pep.*
4: /cgn2_6/ptodata/1/pubpaa/US06_PUBCOMB.pep.*
5: /cgn2_6/ptodata/1/pubpaa/US07_NEW_PUB.pep.*
6: /cgn2_6/ptodata/1/pubpaa/FCTUS_PUBCOMB.pep.*
7: /cgn2_6/ptodata/1/pubpaa/US08_NEW_PUB.pep.*
8: /cgn2_6/ptodata/1/pubpaa/US08_PUBCOMB.pep.*
9: /cgn2_6/ptodata/1/pubpaa/US09A_PUBCOMB.pep.*
10: /cgn2_6/ptodata/1/pubpaa/US09B_PUBCOMB.pep.*
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12: /cgn2_6/ptodata/1/pubpaa/US09_NEW_PUB.pep.*
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16: /cgn2_6/ptodata/1/pubpaa/US10D_PUBCOMB.pep.*
17: /cgn2_6/ptodata/1/pubpaa/US10_NEW_PUB.pep.*
18: /cgn2_6/ptodata/1/pubpaa/US10_NEW_PUB.pep.*
19: /cgn2_6/ptodata/1/pubpaa/US60_NEW_PUB.pep.*
20: /cgn2_6/ptodata/1/pubpaa/US60_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Match	Length	DB ID	Description
1	2763	100.0	513	10	US-09-862-631-4
2	2763	100.0	513	16	US-10-729-807-10
3	2752	99.6	513	10	US-09-759-1308-173
4	2752	99.6	513	14	US-10-028-072-192
5	2752	99.6	513	14	US-10-140-808-192
6	2752	99.6	513	14	US-10-421-049-192
7	2752	99.6	513	14	US-10-123-904-192
8	2752	99.6	513	14	US-10-140-470-192
9	2752	99.6	513	14	US-10-175-746-192
10	2752	99.6	513	14	US-10-176-918-192
11	2752	99.6	513	14	US-10-176-921-192
12	2752	99.6	513	14	US-10-137-865-192
13	2752	99.6	513	14	US-10-140-474-192

14	2752	99.6	513	14	US-10-142-431-192	Sequence 192, App
15	2752	99.6	513	14	US-10-143-114-192	Sequence 192, App
16	2752	99.6	513	14	US-10-140-002-192	Sequence 192, App
17	2752	99.6	513	14	US-10-142-419-192	Sequence 192, App
18	2752	99.6	513	14	US-10-123-262-192	Sequence 192, App
19	2752	99.6	513	14	US-10-142-423-192	Sequence 192, App
20	2752	99.6	513	14	US-10-121-050-192	Sequence 192, App
21	2752	99.6	513	14	US-10-141-755-192	Sequence 192, App
22	2752	99.6	513	14	US-10-143-032-192	Sequence 192, App
23	2752	99.6	513	14	US-10-123-108-192	Sequence 192, App
24	2752	99.6	513	14	US-10-123-236-192	Sequence 192, App
25	2752	99.6	513	14	US-10-123-261-192	Sequence 192, App
26	2752	99.6	513	14	US-10-140-921-192	Sequence 192, App
27	2752	99.6	513	14	US-10-140-928-192	Sequence 192, App
28	2752	99.6	513	14	US-10-121-045-192	Sequence 192, App
29	2752	99.6	513	14	US-10-123-292-192	Sequence 192, App
30	2752	99.6	513	14	US-10-123-903-192	Sequence 192, App
31	2752	99.6	513	14	US-10-124-819-192	Sequence 192, App
32	2752	99.6	513	14	US-10-124-822-192	Sequence 192, App
33	2752	99.6	513	14	US-10-140-925-192	Sequence 192, App
34	2752	99.6	513	14	US-10-160-498-192	Sequence 192, App
35	2752	99.6	513	14	US-10-124-824-192	Sequence 192, App
36	2752	99.6	513	14	US-10-127-825A-192	Sequence 192, App
37	2752	99.6	513	14	US-10-127-828A-192	Sequence 192, App
38	2752	99.6	513	14	US-10-127-835A-192	Sequence 192, App
39	2752	99.6	513	14	US-10-127-839A-192	Sequence 192, App
40	2752	99.6	513	14	US-10-127-901A-192	Sequence 192, App
41	2752	99.6	513	14	US-10-128-693A-192	Sequence 192, App
42	2752	99.6	513	14	US-10-131-813A-192	Sequence 192, App
43	2752	99.6	513	14	US-10-131-818A-192	Sequence 192, App
44	2752	99.6	513	14	US-10-131-823A-192	Sequence 192, App
45	2752	99.6	513	14	US-10-131-824A-192	Sequence 192, App

ALIGNMENTS

RESULT 1
US-09-862-631-4
; Sequence 4, Application US/09862631
; Publication No. US20030032164M1
; GENERAL INFORMATION:
; APPLICANT: Holmgren, Erik
; APPLICANT: Kihlen, Mats
; APPLICANT: Wood, Tim
; APPLICANT: Ekblom, Jonas
; TITLE OF INVENTION: Novel Matrix Metalloproteinases
; FILE REFERENCE: 00014regUS
; CURRENT APPLICATION NUMBER: US/09/862,631
; CURRENT FILING DATE: 2000-05-22
; PRIOR APPLICATION NUMBER: 206119
; PRIOR FILING DATE: 2000-05-22
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 4
; LENGTH: 513
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-862-631-4

Query Match 100.0%; Score 2763; DB 10; Length 513;
Best Local Similarity 100.0%; Pred. No. 1,2e-257;
Matches 513; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy	1	MKRLLLLCLEFFITFSSAFPLVRMTENENMQLAQAYLNQFYSLEIEGNHLVQSKNRSLID 60
Db	1	MKRLLLLCLEFFITFSSAFPLVRMTENENMQLAQAYLNQFYSLEIEGNHLVQSKNRSLID 60
Qy	61	DKIREMQAFGLTVTGKLDNTLEIMKTPRCGVDPVGVQGYVTLPGWRKYNLTVRIINVT 120
Db	61	DKIREMQAFGLTVTGKLDNTLEIMKTPRCGVDPVGVQGYVTLPGWRKYNLTVRIINVT 120
Qy	121	DMARAAVDEIAIQGLEVWVKVTPLEKFTKISKGIADIMAFRTVRVHGRCPRYFDGVLG 180

Tue Nov 16 16:10:21 2004

Db 121 DMARAAVDEAIOEGLEWNSKVTPKFTKISKGIADIMIAFRTRVHGRCPRYFDGPGVLG 180
Qy 181 HAPFPGLGGTHFDEENWTKGAGFNLFLVAAHEFGHALGLSHNDOTALMFPNYS 240
Db 181 HAPFPGLGGTHFDEENWTKGAGFNLFLVAAHEFGHALGLSHNDOTALMFPNYS 240
Qy 241 LDPKPYPLSODDINGIQSYGGLPKVPAPKPKPTTIPHACDPLTTPDAITTFREVMFFKG 300
Db 241 LDPKPYPLSODDINGIQSYGGLPKVPAPKPKPTTIPHACDPLTTPDAITTFREVMFFKG 300
Qy 301 RHLWRIYDITVEFELIASFWPSLPADLOAAAYENPRDKLVKDFENFWMIRGYAVLPDY 360
Db 301 RHLWRIYDITVEFELIASFWPSLPADLOAAAYENPRDKLVKDFENFWMIRGYAVLPDY 360
Qy 361 PKSHTLGPGRVKKIDAAVCDKTRTKTYFFVGIWCRFDEMTQTMKGFPQVRVXHPFG 420
Db 361 PKSHTLGPGRVKKIDAAVCDKTRTKTYFFVGIWCRFDEMTQTMKGFPQVRVXHPFG 420
Qy 421 ISIRVDAAFQYKGFPPFRSGSKOFEYNIKTKNITRIMRTNFWQCKEPKNSFGFDINKE 480
Db 421 ISIRVDAAFQYKGFPPFRSGSKOFEYNIKTKNITRIMRTNFWQCKEPKNSFGFDINKE 480
Qy 481 KAHSGGKILYHKSLSLFIFGIHVHLKNTSIYQ 513
Db 481 KAHSGGKILYHKSLSLFIFGIHVHLKNTSIYQ 513

RESULT 2

US-10-729-807-10
; Sequence 10, Application US/10729807
; Publication No. US20040132158A1
; GENERAL INFORMATION:
; APPLICANT: BANDMAN, Olga; HILLMAN, Jennifer L.
; APPLICANT: TANG, Y. Tom; LAL, Preeti G.
; APPLICANT: YUE, Henry; AZIMZAI, Yalda
; APPLICANT: BAUGHN, Marian R.; LU, Dyoung Aina M.
; TITLE OF INVENTION: HUMAN PEPTIDASES
; FILE REFERENCE: PF-0651-1 DIV
; CURRENT APPLICATION NUMBER: US/10729,807
; CURRENT FILING DATE: 2003-12-05
; PRIOR APPLICATION NUMBER: US 09/889,238
; PRIOR FILING DATE: 2002-01-24
; PRIOR APPLICATION NUMBER: PCT/US00/00641
; PRIOR FILING DATE: 2000-01-11
; PRIOR APPLICATION NUMBER: US 60/172,247
; PRIOR FILING DATE: 1999-01-11
; PRIOR APPLICATION NUMBER: US 60/132,253
; PRIOR FILING DATE: 1999-05-03
; PRIOR APPLICATION NUMBER: US 60/136,653
; PRIOR FILING DATE: 1999-05-27
; NUMBER OF SEQ ID NOS: 39
; SOFTWARE: PERL Program
; SEQ ID NO 10
; LENGTH: 513
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc feature
; OTHER INFORMATION: Incyte ID No: 3772696CD1
US-10-729-807-10
Query Match 100.0%; Score 2763; DB 16; Length 513;
Best Local Similarity 100.0%; Pred. No. 1.2e-257;
Matches 513; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 1 MKRLLLCLFFTFSSAPFLVMTNEENWQAAQVNLQFYSLTEGHNHVSQKNSLID 60
Qy 61 DKIREMQAFGLTVTKGLDSNTLEIMKTPRCGVPDVGQGYTLPGWRKYNLTIRIINTP 120
Db 61 DKIREMQAFGLTVTKGLDSNTLEIMKTPRCGVPDVGQGYTLPGWRKYNLTIRIINTP 120

Qy 121 DMARAAVDEAIOEGLEWNSKVTPKFTKISKGIADIMIAFRTRVHGRCPRYFDGPGVLG 180
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Qy 181 HAPFPGLGGTHFDEENWTKGAGFNLFLVAAHEFGHALGLSHNDOTALMFPNYS 240
Db 181 HAPFPGLGGTHFDEENWTKGAGFNLFLVAAHEFGHALGLSHNDOTALMFPNYS 240
Qy 241 LDPKPYPLSODDINGIQSYGGLPKVPAPKPKPTTIPHACDPLTTPDAITTFREVMFFKG 300
Db 241 LDPKPYPLSODDINGIQSYGGLPKVPAPKPKPTTIPHACDPLTTPDAITTFREVMFFKG 300
Qy 301 RHLWRIYDITVEFELIASFWPSLPADLOAAAYENPRDKLVKDFENFWMIRGYAVLPDY 360
Db 301 RHLWRIYDITVEFELIASFWPSLPADLOAAAYENPRDKLVKDFENFWMIRGYAVLPDY 360
Qy 361 PKSHTLGPGRVKKIDAAVCDKTRTKTYFFVGIWCRFDEMTQTMKGFPQVRVXHPFG 420
Db 361 PKSHTLGPGRVKKIDAAVCDKTRTKTYFFVGIWCRFDEMTQTMKGFPQVRVXHPFG 420
Qy 421 ISIRVDAAFQYKGFPPFRSGSKOFEYNIKTKNITRIMRTNFWQCKEPKNSFGFDINKE 480
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Qy 481 KAHSGGKILYHKSLSLFIFGIHVHLKNTSIYQ 513
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RESULT 3

US-09-759-130B-173
; Sequence 173, Application US/09759130B
; Publication No. US20030022279A1
; GENERAL INFORMATION:
; APPLICANT: Millennium Pharmaceuticals, Inc.
; APPLICANT: McCarthy, Sean A
; APPLICANT: Fraser, Christopher C
; APPLICANT: Sharp, John D
; APPLICANT: Barnes, Thomas S
; APPLICANT: Kirst, Susan J
; APPLICANT: Mackay, Charles R
; APPLICANT: Myers, Paul S
; APPLICANT: Leiby, Kevin R
; APPLICANT: Wrighton, Nicolas
; APPLICANT: Goodearl, Andrew
; APPLICANT: Holtzman, Douglas A
; TITLE OF INVENTION: NOVEL GENES ENCODING PROTEINS HAVING
; TITLE OF INVENTION: PROGNOSTIC, DIAGNOSTIC, PREVENTIVE, THERAPEUTIC, AND OTHER
; FILE REFERENCE: MPI00-5350MMIM
; CURRENT APPLICATION NUMBER: US/09759,130B
; CURRENT FILING DATE: 2002-09-16
; PRIOR APPLICATION NUMBER: US 09/479,249
; PRIOR FILING DATE: 2000-01-07
; PRIOR APPLICATION NUMBER: US 09/559,497
; PRIOR FILING DATE: 2000-04-27
; PRIOR APPLICATION NUMBER: US 09/578,063
; PRIOR FILING DATE: 2000-05-24
; PRIOR APPLICATION NUMBER: US 09/333,159
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; PRIOR APPLICATION NUMBER: US 09/596,194
; PRIOR FILING DATE: 2000-07-14
; PRIOR APPLICATION NUMBER: US 09/342,364
; PRIOR FILING DATE: 1999-06-29
; PRIOR APPLICATION NUMBER: US 09/608,452
; PRIOR FILING DATE: 2000-06-30
; PRIOR APPLICATION NUMBER: US 09/393,996
; PRIOR FILING DATE: 1999-09-10
; PRIOR APPLICATION NUMBER: US 09/602,871
; PRIOR FILING DATE: 2000-06-23
; PRIOR APPLICATION NUMBER: US 09/420,707
; PRIOR FILING DATE: 1999-10-19

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; NUMBER OF SEQ ID NOS: 460
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 173
; LENGTH: 513
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-759-130B-173

Query Match      99.6%; Score 2752; DB 10; Length 513;
Best Local Similarity 99.8%; Pred. No. 1.4e-256;
Matches 512; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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QY 61 DKIREMAFFGLTVTKLSDNTLEIMTKPCGVPDVGQYGTLPGRKYNLTTRIINYTP 120
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QY 181 HAPPGPGGLGDTHFDEDENTWKDAGFNLFLVAAHEFGHALGSHSNDQTALMFPNYS 240
Db 181 HAPPGPGGLGDTHFDEDENTWKDAGFNLFLVAAHEFGHALGSHSNDQTALMFPNYS 240
QY 241 LDPKPYLSQDDINGLSYGGLPKVPKPKPTIPHACDPLTFDAITTFREVMFFKG 300
Db 241 LDPKPYLSQDDINGLSYGGLPKVPKPKPTIPHACDPLTFDAITTFREVMFFKG 300
QY 301 RHLWRIYDITDVEFELIASFWPSLPADLQAAVENPRDKILVFKDENFWMIIRGYAVLPDY 360
Db 301 RHLWRIYDITDVEFELIASFWPSLPADLQAAVENPRDKILVFKDENFWMIIRGYAVLPDY 360
QY 361 PKSIHTLGPGRVKKIDAAVCCKTRTKTYFFVGICWCRFDEMTQTMKGFQQRVVKHFFG 420
Db 361 PKSIHTLGPGRVKKIDAAVCCKTRTKTYFFVGICWCRFDEMTQTMKGFQQRVVKHFFG 420
QY 421 ISIRVDAAFQYKGFFFSFGSKQFENYIKNTKITRIMRTNTWFOCKEPKNSFGFDINKE 480
Db 421 ISIRVDAAFQYKGFFFSFGSKQFENYIKNTKITRIMRTNTWFOCKEPKNSFGFDINKE 480
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Db 481 KAHSGGKILYHKLSLFTFGIVHLLKNTSIYQ 513

RESULT 4
US-10-028-072-192
; Sequence 192, Application US/10028072
; Publication No. US20030004311A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Beresini, Maureen
; APPLICANT: DeForge, Laura
; APPLICANT: Desnoyers, Luc
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Sherwood, Steven
; APPLICANT: Smith, Victoria
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Watanabe, Colin K
; APPLICANT: Wood, William
; APPLICANT: Zhang
; TITLE OF INVENTION:
; FILE REFERENCE:
; CURRENT APPLICATION NUMBER: US/10/028,072
; CURRENT FILING DATE: 2001-12-19
; PRIOR APPLICATION NUMBER: 60/049911
; PRIOR FILING DATE: 1997-06-18
; PRIOR APPLICATION NUMBER: 60/056974
; PRIOR FILING DATE: 1997-08-26
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; PRIOR FILING DATE: 1997-09-17
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; PRIOR APPLICATION NUMBER: 60/059836
; PRIOR FILING DATE: 1997-09-24
; PRIOR APPLICATION NUMBER: 60/062250
; PRIOR FILING DATE: 1997-10-17
; PRIOR APPLICATION NUMBER: 60/062285
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;; PRIOR FILING DATE: 1998-06-10
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;; PRIOR FILING DATE: 1998-06-24
;; PRIOR APPLICATION NUMBER: 60/090445
;; PRIOR FILING DATE: 1998-06-24
;; PRIOR APPLICATION NUMBER: 60/090538
;; PRIOR FILING DATE: 1998-06-24
;; PRIOR APPLICATION NUMBER: 60/090863
;; PRIOR FILING DATE: 1998-06-26
;; PRIOR APPLICATION NUMBER: 60/091360
;; PRIOR FILING DATE: 1998-07-01
;; PRIOR APPLICATION NUMBER: 60/091519
;; PRIOR FILING DATE: 1998-07-02
;; PRIOR APPLICATION NUMBER: 60/091982
;; PRIOR FILING DATE: 1998-07-07

Query Match 99.6%; Score 2752; DB 14; Length 513;
Best Local Similarity 99.8%; Pred. No. 1.4e-256;
Matches 512; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 MKRLLLLCLFFITFSSAPPLVRMTENENMOLAQAYLNQFYSLEIEGHLVQSKNRSLLD 60
Db 1 MKRLLLLFLFFITFSSAPPLVRMTENENMOLAQAYLNQFYSLEIEGHLVQSKNRSLLD 60

Qy 61 DKIREMQAFFGLTVTGKLDNSTLEIMTKPRCGVDVGQGYTLPCWRKYNLTIRIINTP 120
Db 61 DKIREMQAFFGLTVTGKLDNSTLEIMTKPRCGVDVGQGYTLPCWRKYNLTIRIINTP 120

Qy 121 DMARAANDVDEATQEGLEVWSKVTPKFTKISKGIAIDIMIAFTRVHGRCPRYDFDGLGVLG 180
Db 121 DMARAANDVDEATQEGLEVWSKVTPKFTKISKGIAIDIMIAFTRVHGRCPRYDFDGLGVLG 180

Qy 181 HAPPPGPGIGDTHFEDENNTKOGAGFNLFLVAAHEFGHALGLSHSNDQTALMPNYS 240
Db 181 HAPPPGPGIGDTHFEDENNTKOGAGFNLFLVAAHEFGHALGLSHSNDQTALMPNYS 240

Qy 241 LDPRKYPISQDDINGIQSIYGLPKVPAPKPEPTIPHACDPLTDAITTFRRVWFFKG 300
Db 241 LDPRKYPISQDDINGIQSIYGLPKVPAPKPEPTIPHACDPLTDAITTFRRVWFFKG 300

Qy 301 RHLWRIYDITDVEFELIASFWPSLPADLQAAAYENPRDKILYFKDENFWMIRGYAVLPDY 360
Db 301 RHLWRIYDITDVEFELIASFWPSLPADLQAAAYENPRDKILYFKDENFWMIRGYAVLPDY 360

Qy 361 PKSIHTLGPFGPVKXKIDAAVCDKTKTYFFVGICWRFEDMTQNDKGFQORVVKHFG 420
Db 361 PKSIHTLGPFGPVKXKIDAAVCDKTKTYFFVGICWRFEDMTQNDKGFQORVVKHFG 420

Qy 421 ISIRVDAAFQYKGFPPFFSFGSKOFEYNIKTKNITRIMRTNTWFOCKEPKNSSGFDINKE 480
Db 421 ISIRVDAAFQYKGFPPFFSFGSKOFEYNIKTKNITRIMRTNTWFOCKEPKNSSGFDINKE 480

Qy 481 KAHSGGKILYHKSLSLFIFGIVHLLKNTSIYQ 513
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;; PRIOR FILING DATE: 1998-02-09
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;; PRIOR FILING DATE: 1998-03-12
;; PRIOR APPLICATION NUMBER: 60/078910
;; PRIOR FILING DATE: 1998-03-20
;; PRIOR APPLICATION NUMBER: 60/079294
;; PRIOR FILING DATE: 1998-03-25
;; PRIOR APPLICATION NUMBER: 60/079663
;; PRIOR FILING DATE: 1998-02-27
;; PRIOR APPLICATION NUMBER: 60/079728
;; PRIOR FILING DATE: 1998-03-27
;; PRIOR APPLICATION NUMBER: 60/080165
;; PRIOR FILING DATE: 1998-03-31
;; PRIOR APPLICATION NUMBER: 60/081203
;; PRIOR FILING DATE: 1998-04-09
;; PRIOR APPLICATION NUMBER: 60/081229
;; PRIOR FILING DATE: 1998-04-09
;; PRIOR APPLICATION NUMBER: 60/081695
;; PRIOR FILING DATE: 1998-04-14
;; PRIOR APPLICATION NUMBER: 60/081817
;; PRIOR FILING DATE: 1998-04-15
;; PRIOR APPLICATION NUMBER: 60/081818
;; PRIOR FILING DATE: 1998-04-15
;; PRIOR APPLICATION NUMBER: 60/082999
;; PRIOR FILING DATE: 1998-04-24
;; PRIOR APPLICATION NUMBER: 60/083322
;; PRIOR FILING DATE: 1998-04-28
;; PRIOR APPLICATION NUMBER: 60/083545
;; PRIOR FILING DATE: 1998-04-29
;; PRIOR APPLICATION NUMBER: 60/084600
;; PRIOR FILING DATE: 1998-05-07
;; PRIOR APPLICATION NUMBER: 60/084627
;; PRIOR FILING DATE: 1998-05-07
;; PRIOR APPLICATION NUMBER: 60/084637
;; PRIOR FILING DATE: 1998-05-07
;; PRIOR APPLICATION NUMBER: 60/085149
;; PRIOR FILING DATE: 1998-05-12
;; PRIOR APPLICATION NUMBER: 60/085323
;; PRIOR FILING DATE: 1998-05-13
;; PRIOR APPLICATION NUMBER: 60/085338
;; PRIOR FILING DATE: 1998-05-13
;; PRIOR APPLICATION NUMBER: 60/085339
;; PRIOR FILING DATE: 1998-05-13
;; PRIOR APPLICATION NUMBER: 60/085579
;; PRIOR FILING DATE: 1998-05-15
;; PRIOR APPLICATION NUMBER: 60/085697
;; PRIOR FILING DATE: 1998-05-15
;; PRIOR APPLICATION NUMBER: 60/085704
;; PRIOR FILING DATE: 1998-05-15
;; PRIOR APPLICATION NUMBER: 60/086414
;; PRIOR FILING DATE: 1998-05-22
;; PRIOR APPLICATION NUMBER: 60/086430
;; PRIOR FILING DATE: 1998-05-22
;; PRIOR APPLICATION NUMBER: 60/087106
;; PRIOR FILING DATE: 1998-05-28
;; PRIOR APPLICATION NUMBER: 60/088026
;; PRIOR FILING DATE: 1998-06-04

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RESULT 5
US-10-140-808-192
; Sequence 192, Application US/10140808
; Publication No. US20030017563A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Beresini, Maureen
; APPLICANT: DeForge, Laura
; APPLICANT: Desnoyers, Luc
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Smith, Victoria
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Watanabe, Colin K
; APPLICANT: Wood, William
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P3330R1C182
; CURRENT APPLICATION NUMBER: US/10/140, 808
; Prior Application removed - See File Wrapper or Palm
; NUMBER OF SEQ ID NOS: 550
; SEQ ID NO 192
; LENGTH: 513
; TYPE: PRT
; ORGANISM: Homo Sapien
US-10-140-808-192

Query Match
Best Local Similarity 99.6%; Score 2752; DB 14; Length 513;
Matches 512; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 MKRLLLCLFFITFSAPFLVMTENEENMQLAQAYLNOFYSLIEGHNHLVQSKNRLSD 60
DB 1 MKRLLLCLFFITFSAPFLVMTENEENMQLAQAYLNOFYSLIEGHNHLVQSKNRLSD 60
QY 61 DKIREMAFFGLTVTGKLDNLTLEIMKTPRCGVPDVGQGYTLPGWRKYNLTIRIINYP 120
DB 61 DKIREMAFFGLTVTGKLDNLTLEIMKTPRCGVPDVGQGYTLPGWRKYNLTIRIINYP 120
QY 121 DMARAANDVAIOEGLEVMSKVTPKFTKISKGIADIMIAFRTRVHGRCPRYFDGPGVLG 180
DB 121 DMARAANDVAIOEGLEVMSKVTPKFTKISKGIADIMIAFRTRVHGRCPRYFDGPGVLG 180
QY 181 HAPPPGGLGGDTHDEDENTKDGAGNLFVAHAHEFGHALGLSHSDQALMFPNYS 240
DB 181 HAPPPGGLGGDTHDEDENTKDGAGNLFVAHAHEFGHALGLSHSDQALMFPNYS 240
QY 241 LDPRKYPISQDDINGIOSIYGLPKVPKPKPTIIPACDPDLTDAITTTFRVWPFKG 300
DB 241 LDPRKYPISQDDINGIOSIYGLPKVPKPKPTIIPACDPDLTDAITTTFRVWPFKG 300
QY 301 RHLWRIYDITDVEFELIASFWPSLPADLQAAAYENPRDKILVFDENFWMIRGYAVLPDY 360
DB 301 RHLWRIYDITDVEFELIASFWPSLPADLQAAAYENPRDKILVFDENFWMIRGYAVLPDY 360
QY 361 PKSIHTLGFGRVKKIDAAVCDKTRKTYFFVGIWCFRDEMOTQMDKGFQVRVVKHPPG 420
DB 361 PKSIHTLGFGRVKKIDAAVCDKTRKTYFFVGIWCFRDEMOTQMDKGFQVRVVKHPPG 420
QY 421 ISIRVDAAFQYKGFPPFSRGSQFPEYNIKTNIITRIMTNTWFOCKEPKNSFGFDINKE 480
DB 421 ISIRVDAAFQYKGFPPFSRGSQFPEYNIKTNIITRIMTNTWFOCKEPKNSFGFDINKE 480
QY 481 KAHSGGKILYHKLSLFIIGIVHLLKNTSIYQ 513
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DB 481 KAHSGGKILYHKLSLFIIGIVHLLKNTSIYQ 513

RESULT 6
US-10-121-049-192
; Sequence 192, Application US/10121049
; Publication No. US20030022239A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Beresini, Maureen
; APPLICANT: DeForge, Laura
; APPLICANT: Desnoyers, Luc
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Sherwood, Steven
; APPLICANT: Smith, Victoria
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Watanabe, Colin K
; APPLICANT: Wood, William
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P3330R1C17
; CURRENT APPLICATION NUMBER: US/10/121, 049
; CURRENT FILING DATE: 2002-04-12
; Prior Application removed - See File Wrapper or Palm
; NUMBER OF SEQ ID NOS: 550
; SEQ ID NO 192
; LENGTH: 513
; TYPE: PRT
; ORGANISM: Homo Sapien
US-10-121-049-192
```

```
Query Match
Best Local Similarity 99.6%; Score 2752; DB 14; Length 513;
Matches 512; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 MKRLLLCLFFITFSAPFLVMTENEENMQLAQAYLNOFYSLIEGHNHLVQSKNRLSD 60
DB 1 MKRLLLCLFFITFSAPFLVMTENEENMQLAQAYLNOFYSLIEGHNHLVQSKNRLSD 60
QY 61 DKIREMAFFGLTVTGKLDNLTLEIMKTPRCGVPDVGQGYTLPGWRKYNLTIRIINYP 120
DB 61 DKIREMAFFGLTVTGKLDNLTLEIMKTPRCGVPDVGQGYTLPGWRKYNLTIRIINYP 120
QY 121 DMARAANDVAIOEGLEVMSKVTPKFTKISKGIADIMIAFRTRVHGRCPRYFDGPGVLG 180
DB 121 DMARAANDVAIOEGLEVMSKVTPKFTKISKGIADIMIAFRTRVHGRCPRYFDGPGVLG 180
QY 181 HAPPPGGLGGDTHDEDENTKDGAGNLFVAHAHEFGHALGLSHSDQALMFPNYS 240
DB 181 HAPPPGGLGGDTHDEDENTKDGAGNLFVAHAHEFGHALGLSHSDQALMFPNYS 240
QY 241 LDPRKYPISQDDINGIOSIYGLPKVPKPKPTIIPACDPDLTDAITTTFRVWPFKG 300
DB 241 LDPRKYPISQDDINGIOSIYGLPKVPKPKPTIIPACDPDLTDAITTTFRVWPFKG 300
QY 301 RHLWRIYDITDVEFELIASFWPSLPADLQAAAYENPRDKILVFDENFWMIRGYAVLPDY 360
DB 301 RHLWRIYDITDVEFELIASFWPSLPADLQAAAYENPRDKILVFDENFWMIRGYAVLPDY 360
QY 361 PKSIHTLGFGRVKKIDAAVCDKTRKTYFFVGIWCFRDEMOTQMDKGFQVRVVKHPPG 420
DB 361 PKSIHTLGFGRVKKIDAAVCDKTRKTYFFVGIWCFRDEMOTQMDKGFQVRVVKHPPG 420
QY 421 ISIRVDAAFQYKGFPPFSRGSQFPEYNIKTNIITRIMTNTWFOCKEPKNSFGFDINKE 480
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Db 421 ISIRVDAAFQYKGFPPFSRSGSKQFEYNIKNTIRMTNTWTFQCKEPKNSFGPDINKE 480
QY 481 KAHSGGKILYHKLSLSLFIPIGVHLLKNTSIYQ 513
Db 481 KAHSGGKILYHKLSLSLFIPIGVHLLKNTSIYQ 513

RESULT 7

US-10-123-904-192
; Sequence 192, Application US/10123904
; Publication No. US2003002328A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Beresini, Maureen
; APPLICANT: Deforge, Laura
; APPLICANT: Desnoyers, Luc
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Goddard, Paul J.
; APPLICANT: Godowski, Paul J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Sherwood, Steven
; APPLICANT: Smith, Victoria
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Watanabe, Colin K
; APPLICANT: Wood, William
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P3330R1C54
; CURRENT APPLICATION NUMBER: US/10/123.904
; CURRENT FILING DATE: 2002-04-16
; Prior Application removed - See File Wrapper or Palm
; NUMBER OF SEQ ID NOS: 550
; SEQ ID NO 192
; LENGTH: 513
; TYPE: PRT
; ORGANISM: Homo Sapien
US-10-123-904-192

Query Match 99.6%; Score 2752; DB 14; Length 513;
Best Local Similarity 99.8%; Pred. No. 1.4e-256;
Matches 512; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 MKRLLLCLFFITFSAPPLVRMTENEENMQLAQAYLNQFYSLEIEGHNHLSVQSKNRSLLID 60
Db 1 MKRLLLCLFFITFSAPPLVRMTENEENMQLAQAYLNQFYSLEIEGHNHLSVQSKNRSLLID 60
QY 61 DKIREMQAFGLTVTGKLSNTLEIMKTPRCGPDVGVGYTLPGWRKYNLYRIINYP 120
Db 61 DKIREMQAFGLTVTGKLSNTLEIMKTPRCGPDVGVGYTLPGWRKYNLYRIINYP 120
QY 121 DMARAADVAIIOEGLEVMSKVTPKFTKISKGIADIMIAFRTRVHRCRCRYFDGPGVLG 180
Db 121 DMARAADVAIIOEGLEVMSKVTPKFTKISKGIADIMIAFRTRVHRCRCRYFDGPGVLG 180
QY 181 HAPPPGPGGGDTHFDEENWTKDAGFNLFLVAAHEFGHALGSHNSDQTALMFPNYS 240
Db 181 HAPPPGPGGGDTHFDEENWTKDAGFNLFLVAAHEFGHALGSHNSDQTALMFPNYS 240
QY 241 LDPKYPKLSQDDINGIQSIYGGIPLKVPKPKPTIIPACDPLTFDAITTFREVMFPFG 300
Db 241 LDPKYPKLSQDDINGIQSIYGGIPLKVPKPKPTIIPACDPLTFDAITTFREVMFPFG 300
QY 301 RHLWRIYDITDVEFELIASFWPSLPADLQAAAYENPRDKILVFKDENFWMIRGYAVLPDY 360
Db 301 RHLWRIYDITDVEFELIASFWPSLPADLQAAAYENPRDKILVFKDENFWMIRGYAVLPDY 360
QY 361 PKSIHTLGFGRVKKIDAAVCDDKTRTKTYFVGIWCRFDEMTQTDKGFPPQVRVHFPG 420
Db 361 PKSIHTLGFGRVKKIDAAVCDDKTRTKTYFVGIWCRFDEMTQTDKGFPPQVRVHFPG 420

QY 421 ISIRVDAAFQYKGFPPFSRSGSKQFEYNIKNTIRMTNTWTFQCKEPKNSFGPDINKE 480
Db 421 ISIRVDAAFQYKGFPPFSRSGSKQFEYNIKNTIRMTNTWTFQCKEPKNSFGPDINKE 480
QY 481 KAHSGGKILYHKLSLSLFIPIGVHLLKNTSIYQ 513
Db 481 KAHSGGKILYHKLSLSLFIPIGVHLLKNTSIYQ 513

RESULT 8

US-10-140-470-192
; Sequence 192, Application US/10140470
; Publication No. US20030022331A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Beresini, Maureen
; APPLICANT: Deforge, Laura
; APPLICANT: Desnoyers, Luc
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Sherwood, Steven
; APPLICANT: Smith, Victoria
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Watanabe, Colin K
; APPLICANT: Wood, William
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P3330R1C160
; CURRENT APPLICATION NUMBER: US/10/140.470
; CURRENT FILING DATE: 2002-05-06
; Prior Application removed - See Palm or File Wrapper
; NUMBER OF SEQ ID NOS: 550
; SEQ ID NO 192
; LENGTH: 513
; TYPE: PRT
; ORGANISM: Homo Sapien
US-10-140-470-192

Query Match 99.6%; Score 2752; DB 14; Length 513;
Best Local Similarity 99.8%; Pred. No. 1.4e-256;
Matches 512; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 MKRLLLCLFFITFSAPPLVRMTENEENMQLAQAYLNQFYSLEIEGHNHLSVQSKNRSLLID 60
Db 1 MKRLLLCLFFITFSAPPLVRMTENEENMQLAQAYLNQFYSLEIEGHNHLSVQSKNRSLLID 60
QY 61 DKIREMQAFGLTVTGKLSNTLEIMKTPRCGPDVGVGYTLPGWRKYNLYRIINYP 120
Db 61 DKIREMQAFGLTVTGKLSNTLEIMKTPRCGPDVGVGYTLPGWRKYNLYRIINYP 120
QY 121 DMARAADVAIIOEGLEVMSKVTPKFTKISKGIADIMIAFRTRVHRCRCRYFDGPGVLG 180
Db 121 DMARAADVAIIOEGLEVMSKVTPKFTKISKGIADIMIAFRTRVHRCRCRYFDGPGVLG 180
QY 181 HAPPPGPGGGDTHFDEENWTKDAGFNLFLVAAHEFGHALGSHNSDQTALMFPNYS 240
Db 181 HAPPPGPGGGDTHFDEENWTKDAGFNLFLVAAHEFGHALGSHNSDQTALMFPNYS 240
QY 241 LDPKYPKLSQDDINGIQSIYGGIPLKVPKPKPTIIPACDPLTFDAITTFREVMFPFG 300
Db 241 LDPKYPKLSQDDINGIQSIYGGIPLKVPKPKPTIIPACDPLTFDAITTFREVMFPFG 300
QY 301 RHLWRIYDITDVEFELIASFWPSLPADLQAAAYENPRDKILVFKDENFWMIRGYAVLPDY 360
Db 301 RHLWRIYDITDVEFELIASFWPSLPADLQAAAYENPRDKILVFKDENFWMIRGYAVLPDY 360


```

QY 361 PKSHTLGFGRVKKIDAAVCDKTRKTYFFVGIWCRFDEMTQTMKGFPQRRVVKHFP 420
Db 361 PKSHTLGFGRVKKIDAAVCDKTRKTYFFVGIWCRFDEMTQTMKGFPQRRVVKHFP 420
QY 421 ISIRVDAAFQYKGFPPFSRSGSKQFEYNIKNTIRIMRTNTWFOCKBPKNSSFGFDINKE 480
Db 421 ISIRVDAAFQYKGFPPFSRSGSKQFEYNIKNTIRIMRTNTWFOCKBPKNSSFGFDINKE 480
QY 481 KAHSGGKILYHKSLSLFIFGIVHLLKNTSIYQ 513
Db 481 KAHSGGKILYHKSLSLFIFGIVHLLKNTSIYQ 513

RESULT 9
US-10-175-746-192
; Sequence 192, Application US/10175746
; Publication No. US20030027270A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Beresini, Maureen
; APPLICANT: DeForge, Laura
; APPLICANT: Desnoyers, Luc
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Sherwood, Steven
; APPLICANT: Smith, Victoria
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Watanabe, Colin K
; APPLICANT: Wood, William
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P3330RIC353
; CURRENT APPLICATION NUMBER: US/10/175,746
; Prior Filing Date: 2002-06-19
; NUMBER OF SEQ ID NOS: 550
; SEQ ID NO 192
; LENGTH: 513
; TYPE: PRT
; ORGANISM: Homo Sapien
US-10-175-746-192

Query Match 99.6%; Score 2752; DB 14; Length 513;
Best Local Similarity 99.8%; Pred. No. 1.4e-256;
Matches 512; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 MKRLLLCLFFITFSSAPPLVMTENEENMQLAQAYLNQFYSLEIEGHNHLSVSKNSRLID 60
Db 1 MKRLLLCLFFITFSSAPPLVMTENEENMQLAQAYLNQFYSLEIEGHNHLSVSKNSRLID 60
QY 61 DKIREMQAFFGLTVTGKLDNTLEIMKTPRCGVPDVGQGYTLPGWRKYNLTIRIINTP 120
Db 61 DKIREMQAFFGLTVTGKLDNTLEIMKTPRCGVPDVGQGYTLPGWRKYNLTIRIINTP 120
QY 121 DMARAANDBAIQEGLEWVSKVTPKFTKISKGIADIMIAFRTRVHRCPCRYFDGPGVLG 180
Db 121 DMARAANDBAIQEGLEWVSKVTPKFTKISKGIADIMIAFRTRVHRCPCRYFDGPGVLG 180
QY 181 HAPPPGPGGGTHFDEDEENWKDGAGFNLFLVAHFHGHALGSHSNDQTALMPFNYS 240
Db 181 HAPPPGPGGGTHFDEDEENWKDGAGFNLFLVAHFHGHALGSHSNDQTALMPFNYS 240
QY 241 LDPRKYPISQDDINGIQSIYGLGPKVPKPKPTPIPHACDPLTDAITTFREVMFPKG 300
Db 241 LDPRKYPISQDDINGIQSIYGLGPKVPKPKPTPIPHACDPLTDAITTFREVMFPKG 300
QY 301 RHLWRIYYDITDVEFELIASFWFSLPADLQAAYENPRDKILVFDENFWMIRGYAVLPDY 360

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Db 301 RHLWRIYYDITDVEFELIASFWFSLPADLQAAYENPRDKILVFDENFWMIRGYAVLPDY 360
QY 361 PKSHTLGFGRVKKIDAAVCDKTRKTYFFVGIWCRFDEMTQTMKGFPQRRVVKHFP 420
Db 361 PKSHTLGFGRVKKIDAAVCDKTRKTYFFVGIWCRFDEMTQTMKGFPQRRVVKHFP 420
QY 421 ISIRVDAAFQYKGFPPFSRSGSKQFEYNIKNTIRIMRTNTWFOCKBPKNSSFGFDINKE 480
Db 421 ISIRVDAAFQYKGFPPFSRSGSKQFEYNIKNTIRIMRTNTWFOCKBPKNSSFGFDINKE 480
QY 481 KAHSGGKILYHKSLSLFIFGIVHLLKNTSIYQ 513
Db 481 KAHSGGKILYHKSLSLFIFGIVHLLKNTSIYQ 513

RESULT 10
US-10-176-918-192
; Sequence 192, Application US/10176918
; Publication No. US20030027275A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Beresini, Maureen
; APPLICANT: DeForge, Laura
; APPLICANT: Desnoyers, Luc
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Sherwood, Steven
; APPLICANT: Smith, Victoria
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Watanabe, Colin K
; APPLICANT: Wood, William
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P3330RIC382
; CURRENT APPLICATION NUMBER: US/10/176,918
; Prior Filing Date: 2002-06-20
; NUMBER OF SEQ ID NOS: 550
; SEQ ID NO 192
; LENGTH: 513
; TYPE: PRT
; ORGANISM: Homo Sapien
US-10-176-918-192

Query Match 99.6%; Score 2752; DB 14; Length 513;
Best Local Similarity 99.8%; Pred. No. 1.4e-256;
Matches 512; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 MKRLLLCLFFITFSSAPPLVMTENEENMQLAQAYLNQFYSLEIEGHNHLSVSKNSRLID 60
Db 1 MKRLLLCLFFITFSSAPPLVMTENEENMQLAQAYLNQFYSLEIEGHNHLSVSKNSRLID 60
QY 61 DKIREMQAFFGLTVTGKLDNTLEIMKTPRCGVPDVGQGYTLPGWRKYNLTIRIINTP 120
Db 61 DKIREMQAFFGLTVTGKLDNTLEIMKTPRCGVPDVGQGYTLPGWRKYNLTIRIINTP 120
QY 121 DMARAANDBAIQEGLEWVSKVTPKFTKISKGIADIMIAFRTRVHRCPCRYFDGPGVLG 180
Db 121 DMARAANDBAIQEGLEWVSKVTPKFTKISKGIADIMIAFRTRVHRCPCRYFDGPGVLG 180
QY 181 HAPPPGPGGGTHFDEDEENWKDGAGFNLFLVAHFHGHALGSHSNDQTALMPFNYS 240
Db 181 HAPPPGPGGGTHFDEDEENWKDGAGFNLFLVAHFHGHALGSHSNDQTALMPFNYS 240
QY 241 LDPRKYPISQDDINGIQSIYGLGPKVPKPKPTPIPHACDPLTDAITTFREVMFPKG 300

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Db 241 LDRPKYPLSODDINGIQSIYGGIPKVPAPKEPTIPHACDPDLTDFDAITTRREVMPFKG 300
QY 301 RHLWRIYDITDVEFELIASFWPSLPADLQAAAYENPRDKILVFKDENFWMIRGYAVLPDY 360
Db 301 RHLWRIYDITDVEFELIASFWPSLPADLQAAAYENPRDKILVFKDENFWMIRGYAVLPDY 360
QY 361 PKSHTLGFGRVKKIDAAVCDKTRKTYFFVGIWCRWRFDEMOTMDKGGPQVRVVKHFFG 420
Db 361 PKSHTLGFGRVKKIDAAVCDKTRKTYFFVGIWCRWRFDEMOTMDKGGPQVRVVKHFFG 420
QY 421 ISIRVDAAFQYKGGFFFSRSGSKOPEYNIKTNITRIMRTNTWFOCKEPKNSSGFDINKE 480
Db 421 ISIRVDAAFQYKGGFFFSRSGSKOPEYNIKTNITRIMRTNTWFOCKEPKNSSGFDINKE 480
QY 481 KAHSGGKILYHKSLSLFIPIGVHLLKNTSIYQ 513
Db 481 KAHSGGKILYHKSLSLFIPIGVHLLKNTSIYQ 513

RESULT 11
US-10-176-921-192
; Sequence 192, Application US/10176921
; Publication No. US20030027276A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Beresini, Maureen
; APPLICANT: DeForge, Laura
; APPLICANT: Desnoyers, Luc
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Geritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Smith, Victoria
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Watanabe, Colin K
; APPLICANT: Wood, William
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; TITLE OF INVENTION: ACIDS ENCODING THE SAME
; FILE REFERENCE: P3330RLC288
; CURRENT APPLICATION NUMBER: US/10/176,921
; CURRENT FILING DATE: 2002-06-20
; Prior Application removed - See File Wrapper or Palm
; NUMBER OF SEQ ID NOS: 550
; SEQ ID NO 192
; LENGTH: 513
; TYPE: PRT
; ORGANISM: Homo Sapien
US-10-176-921-192

Query Match 99.6%; Score 2752; DB 14; Length 513;
Best Local Similarity 99.8%; Pred. No. 1.4e-256;
Matches 512; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1 MKRLLLCIFFITFSSAPFLVMTENEENMQLAQAYLNQFYSLEIEGHNHLSVQSKRSLID 60
Db 1 MKRLLLCIFFITFSSAPFLVMTENEENMQLAQAYLNQFYSLEIEGHNHLSVQSKRSLID 60
QY 61 DKIREMQAFGLTVTKLDSNTLEIMTKPRCGVPDVQGYGTYLPGWRKKNLYRIINYP 120
Db 61 DKIREMQAFGLTVTKLDSNTLEIMTKPRCGVPDVQGYGTYLPGWRKKNLYRIINYP 120
QY 121 DMARAADVAIOEGLEWWSKVTPKFTKISKGLADIIMIAFRTRVHGRCPRYFDGPGVLG 180
Db 121 DMARAADVAIOEGLEWWSKVTPKFTKISKGLADIIMIAFRTRVHGRCPRYFDGPGVLG 180
QY 181 HAFPPGPGGGDTHFDEDENTWKDAGFNLFLVAAHEFGHALGSHSNDQTALMFPNYS 240
Db 181 HAFPPGPGGGDTHFDEDENTWKDAGFNLFLVAAHEFGHALGSHSNDQTALMFPNYS 240

QY 241 LDRPKYPLSODDINGIQSIYGGIPKVPAPKEPTIPHACDPDLTDFDAITTRREVMPFKG 300
Db 241 LDRPKYPLSODDINGIQSIYGGIPKVPAPKEPTIPHACDPDLTDFDAITTRREVMPFKG 300
QY 301 RHLWRIYDITDVEFELIASFWPSLPADLQAAAYENPRDKILVFKDENFWMIRGYAVLPDY 360
Db 301 RHLWRIYDITDVEFELIASFWPSLPADLQAAAYENPRDKILVFKDENFWMIRGYAVLPDY 360
QY 361 PKSHTLGFGRVKKIDAAVCDKTRKTYFFVGIWCRWRFDEMOTMDKGGPQVRVVKHFFG 420
Db 361 PKSHTLGFGRVKKIDAAVCDKTRKTYFFVGIWCRWRFDEMOTMDKGGPQVRVVKHFFG 420
QY 421 ISIRVDAAFQYKGGFFFSRSGSKOPEYNIKTNITRIMRTNTWFOCKEPKNSSGFDINKE 480
Db 421 ISIRVDAAFQYKGGFFFSRSGSKOPEYNIKTNITRIMRTNTWFOCKEPKNSSGFDINKE 480
QY 481 KAHSGGKILYHKSLSLFIPIGVHLLKNTSIYQ 513
Db 481 KAHSGGKILYHKSLSLFIPIGVHLLKNTSIYQ 513

RESULT 12
US-10-137-865-192
; Sequence 192, Application US/10137865
; Publication No. US20030032155A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Beresini, Maureen
; APPLICANT: DeForge, Laura
; APPLICANT: Desnoyers, Luc
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Geritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Sherwood, Steven
; APPLICANT: Smith, Victoria
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Watanabe, Colin K
; APPLICANT: Wood, William
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; TITLE OF INVENTION: ACIDS ENCODING THE SAME
; FILE REFERENCE: P3330RLC154
; CURRENT APPLICATION NUMBER: US/10/137,865
; CURRENT FILING DATE: 2002-05-03
; Prior Application removed - See Palm or File Wrapper
; NUMBER OF SEQ ID NOS: 550
; SEQ ID NO 192
; LENGTH: 513
; TYPE: PRT
; ORGANISM: Homo Sapien
US-10-137-865-192

Query Match 99.6%; Score 2752; DB 14; Length 513;
Best Local Similarity 99.8%; Pred. No. 1.4e-256;
Matches 512; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1 MKRLLLCIFFITFSSAPFLVMTENEENMQLAQAYLNQFYSLEIEGHNHLSVQSKRSLID 60
Db 1 MKRLLLCIFFITFSSAPFLVMTENEENMQLAQAYLNQFYSLEIEGHNHLSVQSKRSLID 60
QY 61 DKIREMQAFGLTVTKLDSNTLEIMTKPRCGVPDVQGYGTYLPGWRKKNLYRIINYP 120
Db 61 DKIREMQAFGLTVTKLDSNTLEIMTKPRCGVPDVQGYGTYLPGWRKKNLYRIINYP 120
QY 121 DMARAADVAIOEGLEWWSKVTPKFTKISKGLADIIMIAFRTRVHGRCPRYFDGPGVLG 180
Db 121 DMARAADVAIOEGLEWWSKVTPKFTKISKGLADIIMIAFRTRVHGRCPRYFDGPGVLG 180

Db 61 DKIREMAQFGLTWTGKLDNTLEIMKTPRCGVDVGQYGYTLPGWRKYNLTIRIINVT 120
QY 121 DMARAAVDEAIQEGLEWVSKVTPKFTKISKGIADIMIAFRTRVHGRCPRYFDGPLVIG 180
Db 121 DMARAAVDEAIQEGLEWVSKVTPKFTKISKGIADIMIAFRTRVHGRCPRYFDGPLVIG 180
QY 181 HAFPPGGLGDDTHFDEENWTKDAGFNLFLVAHEFGHALGSHSNDOTALMFPNYS 240
Db 181 HAFPPGGLGDDTHFDEENWTKDAGFNLFLVAHEFGHALGSHSNDOTALMFPNYS 240
QY 241 LDPKPYLSODDINGIQSIYGGIPKVPKAPKEPTIPHACDPDLTDFDAITTFREVMFPKG 300
Db 241 LDPKPYLSODDINGIQSIYGGIPKVPKAPKEPTIPHACDPDLTDFDAITTFREVMFPKG 300
QY 301 RHLWRIYDITDVEFELIASFWPSLPADLQAAAYENPRDKILVFKDENFWMIRGYAVLPDY 360
Db 301 RHLWRIYDITDVEFELIASFWPSLPADLQAAAYENPRDKILVFKDENFWMIRGYAVLPDY 360
QY 361 PKSIIHTLGFPPGRVKKIDAAVCDKTRTKTYFFVGIWCMRDEMTQTMKGPPQVVKHFP 420
Db 361 PKSIIHTLGFPPGRVKKIDAAVCDKTRTKTYFFVGIWCMRDEMTQTMKGPPQVVKHFP 420
QY 421 ISIRVDAAFQYKGFPPFSRGSQKOFENIKTKNITRIMRTNTWFOCKEPKNSSGFDINKE 480
Db 421 ISIRVDAAFQYKGFPPFSRGSQKOFENIKTKNITRIMRTNTWFOCKEPKNSSGFDINKE 480
QY 481 KAHSGGKILYHKSLSLFIFGIVHLLKNTSIYQ 513
Db 481 KAHSGGKILYHKSLSLFIFGIVHLLKNTSIYQ 513

RESULT 15

US-10-143-114-192
; Sequence 192, Application US/10143114
; Publication No. US20030036180A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Beresini, Maureen
; APPLICANT: DeForge, Laura
; APPLICANT: Desnoyers, Luc
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Sherwood, Steven
; APPLICANT: Smith, Victoria
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Watanabe, Colin K
; APPLICANT: Wood, William
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P3330RIC211
; CURRENT APPLICATION NUMBER: US/10/143,114
; CURRENT FILING DATE: 2002-05-09
; Prior Application removed - See Palm or File Wrapper
; NUMBER OF SEQ ID NOS: 550
; SEQ ID NO 192
; LENGTH: 513
; TYPE: PRT
; ORGANISM: Homo Sapien
US-10-143-114-192

Query Match 99.6%; Score 2752; DB 14; Length 513;
Best Local Similarity 99.8%; Fred. No. 1.4e-256;
Matches 512; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1 MKRLLLCLEFFITSSAPPLVRMTENENMQLAQAYLNQFYSLIEGHNHVSQKNSRLID 60
Db 1 MKRLLLCLEFFITSSAPPLVRMTENENMQLAQAYLNQFYSLIEGHNHVSQKNSRLID 60

QY 61 DKIREMAQFGLTWTGKLDNTLEIMKTPRCGVDVGQYGYTLPGWRKYNLTIRIINVT 120
Db 61 DKIREMAQFGLTWTGKLDNTLEIMKTPRCGVDVGQYGYTLPGWRKYNLTIRIINVT 120
QY 121 DMARAAVDEAIQEGLEWVSKVTPKFTKISKGIADIMIAFRTRVHGRCPRYFDGPLVIG 180
Db 121 DMARAAVDEAIQEGLEWVSKVTPKFTKISKGIADIMIAFRTRVHGRCPRYFDGPLVIG 180
QY 181 HAFPPGGLGDDTHFDEENWTKDAGFNLFLVAHEFGHALGSHSNDOTALMFPNYS 240
Db 181 HAFPPGGLGDDTHFDEENWTKDAGFNLFLVAHEFGHALGSHSNDOTALMFPNYS 240
QY 241 LDPKPYLSODDINGIQSIYGGIPKVPKAPKEPTIPHACDPDLTDFDAITTFREVMFPKG 300
Db 241 LDPKPYLSODDINGIQSIYGGIPKVPKAPKEPTIPHACDPDLTDFDAITTFREVMFPKG 300
QY 301 RHLWRIYDITDVEFELIASFWPSLPADLQAAAYENPRDKILVFKDENFWMIRGYAVLPDY 360
Db 301 RHLWRIYDITDVEFELIASFWPSLPADLQAAAYENPRDKILVFKDENFWMIRGYAVLPDY 360
QY 361 PKSIIHTLGFPPGRVKKIDAAVCDKTRTKTYFFVGIWCMRDEMTQTMKGPPQVVKHFP 420
Db 361 PKSIIHTLGFPPGRVKKIDAAVCDKTRTKTYFFVGIWCMRDEMTQTMKGPPQVVKHFP 420
QY 421 ISIRVDAAFQYKGFPPFSRGSQKOFENIKTKNITRIMRTNTWFOCKEPKNSSGFDINKE 480
Db 421 ISIRVDAAFQYKGFPPFSRGSQKOFENIKTKNITRIMRTNTWFOCKEPKNSSGFDINKE 480
QY 481 KAHSGGKILYHKSLSLFIFGIVHLLKNTSIYQ 513
Db 481 KAHSGGKILYHKSLSLFIFGIVHLLKNTSIYQ 513

Search completed: November 15, 2004, 21:04:04
Job time : 95 secs